

OM of: TGFB3P to: EST:* out_format : pfs

Date: Oct 30, 2001 9:11 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/DUFFY097/runat_29102001_162247_25239/app_query.fasta_1.159
-DB=EST -Qfmt=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -FGAPOP=4.500
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DEPEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=100 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=DUFFY097 -CGCN1_1_3535 -NCPU=3
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT
-THREADS=1

Search information block:

Query: TGFB3P

Query length: 113

Database: EST:*

Database sequences: 10228115

Database length: 43145454

Search time (sec): 1008.120000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
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gb_est47:BG175423	+ 633.00	1270.49	1.2e-61	812	! BG175423 602337778F1 NCI_CGAP_M
gb_est29:AI432438	+ 633.00	1268.70	1.5e-61	964	! AI432438 AI532438 LVI_NFL001.NH
gb_est29:BF542567	+ 611.00	1230.72	2.0e-59	503	! BF542567 UI-R-C3-sm-a-12-0-UI.NH
gb_est83:BF101203	+ 605.00	1205.08	5.3e-58	1820	! BF101203 601754782F1 NCI_CGAP
gb_est50:BF670561	+ 535.00	1076.61	7.5e-51	477	! BF670561 114647 MARC LP1G Sus s
gb_est80:BF042894	+ 535.00	1075.81	8.4e-51	515	! BF042894 BP250019B10B3 Soares m
gb_est89:BF542438	+ 530.00	1066.57	2.7e-50	471	! BF542438 UI-R-AFI-aqf-f-07-0-UI
gb_est16:BF044612	+ 530.00	1065.66	3.1e-50	514	! BF044612 BP250020A20D5 Soares c
gb_est96:BG067564	+ 530.00	1063.90	3.8e-50	608	! BG067564 H3055G07-3 NIA Mouse
gb_est18:AI323791	+ 530.00	1062.72	4.5e-50	681	! AI323791 mm47e08.x1 Stratagene
gb_est76:BE575698	+ 522.00	1050.88	2.0e-49	445	! BE575698 dc62d10.x1 NICHD XGC H
gb_est49:AW600944	+ 519.00	1047.71	3.1e-49	336	! AW600944 RC1-BN0014-210100-012
gb_est13:AA915041	+ 510.00	1024.06	6.4e-48	560	! AA915041 AI15041 UI Soares_mamm
gb_est98:BG244370	+ 506.00	1010.23	3.8e-47	966	! BG244370 602356090F1 NCI_CGAP_M
gb_est53:AW919738	+ 503.00	1010.79	3.5e-47	510	! AW919738 EST351042 Rat gene ind
gb_est22:AI599959	+ 503.00	1010.41	3.7e-47	529	! AI599959 EST351662 Normalized r
gb_est18:AI323392	+ 503.00	1009.58	4.1e-47	573	! AI323392 mj33f01.x1 Soares mous
gb_est101:BG518882	+ 503.00	1007.18	5.6e-47	721	! BG518882 602578182F1 NCI_CGAP_M
gb_est53:AW580056	+ 500.00	1004.79	7.5e-47	505	! AW580056 EST370126 MAGE resequ
gb_est75:BE464068	+ 500.00	1003.56	8.8e-47	568	! BE464068 hx84h02.x1 NCI_CGAP_ki
gb_est27:AI951831	+ 500.00	1003.03	9.5e-47	598	! AI951831 wx38b08.x1 NCI_CGAP_P
gb_est91:BF126995	+ 500.00	1002.99	9.5e-47	600	! BF126995 yl1sc03.y1 Human Lens
gb_est14:AI323037	+ 498.00	1000.99	1.2e-46	727	! AI323037 qcl5c11.x1 Soares_feta
gb_est18:AI600952	+ 496.00	1001.32	1.2e-46	477	! AI600952 rc1-BN0014-210100-012
gb_est42:AW073988	+ 494.00	991.28	4.3e-46	572	! AW073988 xb06a06.x1 NCI_CGAP_G
gb_est16:AI089904	+ 492.00	989.04	5.7e-46	480	! AI089904 q418a08.x1 NCI_CGAP_B
gb_est46:AW512491	+ 492.00	985.94	8.5e-46	646	! AW512491 xx73d02.x1 NCI_CGAP_Ly
gb_est16:AI148173	+ 491.00	981.87	1.4e-45	785	! AI148173 q56d01.x1 NCI_CGAP_Br
gb_est85:BF287476	+ 490.00	983.96	1.1e-45	529	! BF287476 EST452067 Rat Gene Ind
gb_est1:AA000733	+ 488.00	982.03	1.4e-45	431	! AA000733 mg33b06.r1 Soares mous
gb_est24:AI743724	+ 487.00	973.83	4.0e-45	778	! AI743724 w574h04.x1 NCI_CGAP_P
gb_est77:BE645704	+ 486.00	976.96	2.7e-45	474	! BE645704 7e74h01.x1 NCI_CGAP_P
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gb_est52:AW823286	+ 481.00	966.04	1.1e-44	509	! AW823286 ur71c12.y1 NCI_CGAP_M
gb_est10:W160533	+ 481.00	965.31	1.2e-44	546	! W160533 wh88b09.x1 NCI_CGAP_C
gb_est10:W45844	+ 480.00	964.67	1.3e-44	478	! W45844 mc77e02.r1 Soares mouse
gb_est49:AW627667	+ 471.00	946.62	1.3e-43	466	! AW627667 hh89h10.x1 NCI_CGAP_G
gb_est97:BG180040	+ 468.00	941.33	2.6e-43	431	! BG180040 602329596F1 NIH_MGC_91

gb_est26:AI927187	- 463.00	928.09	1.4e-42	578	! AI927187 wo88c02.x1 NCI_CGAP
gb_est20:AI430179	+ 451.00	909.94	1.4e-41	317	! AI430179 me44c04.y1 Soares m
gb_est20:AI433146	- 448.00	898.97	5.9e-41	505	! AI433146 ti32a11.x1 NCI_CGAP
gb_est30:AU016729	- 447.00	895.56	9.2e-41	576	! AU016729 AU016729 Mouse two-
gb_est10:AA657145	- 438.00	878.12	8.6e-40	530	! AA657145 vr76d03.r1 Barstead
gb_est20:AI434956	- 438.00	877.41	9.4e-40	567	! AI434956 ti46f04.x1 NCI_CGAP
gb_est96:BG058804	- 437.50	876.54	1.0e-39	559	! BG058804 na1f0g09.x1 Soares
gb_est102:BG540633	- 437.00	870.68	2.2e-39	889	! BG540633 602570520F1 NIH_MGC
gb_est103:C86748	- 433.00	866.84	3.6e-39	599	! C86748 C86748 Mouse fertiliz
gb_99s4:CN803XHH	- 433.00	859.69	9.1e-39	1168	! AL265022 Tetraodon nigrovir
gb_est103:C86879	- 432.00	864.91	4.7e-39	583	! C86879 C86879 Mouse fertiliz
gb_est103:BF682484	- 428.50	852.20	2.4e-38	996	! BF682484 602117568F1 Soares
gb_est91:BF682484	- 426.00	855.62	1.5e-38	441	! BF682484 wb02f01.x1 NCI_CGAP
gb_est23:AI654506	- 426.00	855.18	1.6e-38	460	! AI654506 wb36d04.x1 NCI_CGAP
gb_est18:AA049522	- 426.00	854.80	1.7e-38	477	! AA049522 mj35f01.x1 Soares m
gb_est18:AI273619	- 422.00	846.19	5.2e-38	499	! AI273619 ql36c01.x1 Soares_N
gb_est18:AI272940	- 416.00	839.57	1.2e-37	292	! AI272940 ql36g01.x1 Soares_N
gb_est18:AI304490	- 416.00	835.08	2.1e-37	449	! AI304490 qo54e06.x1 NCI_CGAP
gb_est17:AI192407	- 414.00	833.67	2.6e-37	348	! AI192407 qc98c09.x1 Soares_P
gb_est20:AI421250	- 403.00	806.70	8.2e-36	540	! AI421250 tf14d02.x1 NCI_CGAP
gb_est49:AW600940	- 401.00	810.22	5.2e-36	261	! AW600940 RC1-BN0014-210100-0
gb_est29:AL530080	- 400.50	797.53	2.6e-35	798	! AL530080 RC1-BN0080 LTI_NFL001
gb_est49:AW600938	- 400.00	807.95	7.0e-35	267	! AW600938 RC1-BN0014-210100-0
gb_est11:AA021815	+ 399.50	799.23	2.1e-35	558	! AA021815 mh85d06.r1 Soares m
gb_est11:W98872	+ 395.00	792.77	4.9e-35	431	! W98872 mf89e01.r1 Soares mou
gb_est103:C87366	- 393.00	785.48	1.2e-34	587	! C87366 C87366 Mouse fertiliz
gb_est16:BG058796	- 388.00	779.23	2.8e-34	403	! BG058796 naf10f12.x1 Soares_N
gb_est16:AI157673	- 387.00	779.00	2.8e-34	339	! AI157673 ue48g10.r2 Soares_m
gb_est22:AI604914	- 387.00	777.19	3.2e-34	403	! AI604914 me44c04.x1 Soares m
gb_est19:AI360877	- 379.00	763.06	2.6e-33	328	! AI360877 qy01c06.x1 NCI_CGAP
gb_est22:AI634937	- 377.00	756.71	5.0e-33	408	! AI634937 tz74f09.x1 NCI_CGAP
gb_est1:AA016742	+ 375.00	749.47	1.3e-32	553	! AA016742 mh39e08.r1 Soares m
gb_est49:AW600947	- 374.00	755.93	5.5e-33	245	! AW600947 RC1-BN0014-210100-0
gb_est30:AW016439	- 364.50	729.91	1.5e-31	465	! AW016439 AU016439 Mouse two-
gb_est45:AW295761	- 351.00	703.78	4.4e-30	409	! AW295761 UI-H-B11-ath-a-02-0
gb_est110:W07801	+ 349.00	702.91	4.9e-30	301	! W07801 me44c04.r1 Soares mou
gb_est30:AU050770	+ 347.50	688.68	3.1e-29	878	! AU050770 AU050770 Paralichth
gb_est49:AW600942	- 343.50	693.29	1.7e-29	259	! AW600942 RC1-BN0014-210100-0
gb_est106:B36741	+ 341.00	680.15	9.1e-29	560	! B36741 yy90e06.r1 Soares mel
gb_est28:AI918883	- 337.00	668.99	3.8e-28	748	! BF682938 602117568F1 Soares
gb_est46:AW364559	- 333.50	668.28	4.2e-28	542	! AW364559 RC1-DT0028-131299-0
gb_est78:BF737006	+ 333.50	659.76	1.2e-27	915	! BF737006 601306767F1 NIH_MGC
gb_est17:AI179582	- 331.00	659.60	1.3e-27	571	! AI179582 EST2323304 Normalize
gb_est1:AA016946	- 321.50	640.98	1.4e-26	533	! AA016946 hx35a12.x1 Soares m
gb_est26:AI918883	- 321.00	643.17	1.0e-26	392	! AI918883 tu33b10.x1 NCI_CGAP
gb_est49:AW600960	- 317.50	640.10	1.6e-26	266	! AW600960 RC1-BN0014-210100-0
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gb_est20:AI414206	- 313.00	625.11	1.1e-25	465	! AI414206 md58e04.x1 Soares m
gb_est70:BF074350	- 305.00	607.72	9.9e-25	517	! BF074350 QV3-BT0571-030200-0
gb_est51:AW798167	- 304.00	608.93	8.5e-25	379	! AW798167 RC3-UM0046-290200-0
gb_est28:AL362754	+ 302.00	604.30	1.5e-24	400	! AL362754 AL362754 ICRFP 522
gb_est20:AI452742	- 301.00	602.37	2.0e-24	396	! AI452742 tj45a05.x1 Soares_N
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gb_est106:N55274	- 291.00	580.54	3.2e-23	456	! N55274 yv46g05.x1 Soares fet
gb_est22:AI610679	- 290.50	578.54	4.2e-23	639	! AI610679 tp71g12.x1 NCI_CGAP
gb_est91:BF723491	- 286.00	569.53	1.3e-22	494	! BF723491 ma33p126.y1 Soares_N
gb_est98:BG247154	- 284.00	567.72	1.7e-22	398	! BG247154 602361136F1 NCI_CGA
gb_est107:R36467	- 281.00	566.55	1.9e-22	248	! R36467 yh88d11.s1 Soares pla
gb_est49:AW591888	- 279.00	562.19	3.4e-22	255	! AW591888 RC1-DT0028-130100-0
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seq_name: gb_est46:AW412139

seq_documentation_block:

LOCUS AW412139 645 bp mRNA

DEFINITION uq46g03.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

ACCESSION AW412139

VERSION AW412139

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 645)
NCI-Cgap http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-Cgap clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

MGI:1045080
Seq primer: -40RP from Gibco
High quality sequence stop: 446.
Location/Qualifiers
1. 645
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/clone_lib="NCI-Cgap_Mam5"
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/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 159 a 196 c 175 g 115 t
ORIGIN
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Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
TGFB3P x AW412139 ..
Align seg 1/1 to: AW412139 from: 1 to: 645

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109 GCCCTGGACACCAATTACTGCTCCGCAACCTGGAGGAACTGCTGTGT 158
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
159 ACGCCCTTTATATTGACTTCGCGCAGGATCTAGGCTGGAATGGGTCC 208
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
209 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 258
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
259 CTCGCGCAGCAGACACACCATAGACGGTGTGGACTATACAAAC 308
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
309 CCTGAACCCAGAGCGCTGCTCGCCATGCTGCTCCCGCAGGACCTGG 358
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
359 AGCCCCGACCATCTTGTACTATGTGGGCAGAACCCCGCAGGTGGAGCAG 408

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
409 CTGTCCCAACATGGGTGAAGTCGTGTAAGTGACG 444
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seq_documentation_block:
LOCUS BG175423 812 bp mRNA EST 06-FEB-2001
DEFINITION 602337778F1 NCI-Cgap_Mam1 Mus musculus cDNA clone IMAGE:4460706 5', mRNA sequence.
ACCESSION BG175423 GI:12682126
VERSION BG175423
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 812)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10262 row: 1 column: 19
High quality sequence stop: 735.

FEATURES
source
1. 812
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/clone_lib="NCI-Cgap_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 197 a 210 c 245 g 160 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
TGFB3P x BG175423 ..
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
59 GCCCTGGACACCAATTACTGCTCCGCAACCTGGAGGAACTGCTGTGT 108
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
109 ACGCCCTTTATATTGACTTCGCGCAGGATCTAGGCTGGAATGGGTCC 158
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
159 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 208
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67


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209 CTCGCGAGCGACACAAACCCATAGACCGGTGCTGGACTATACACAC 258
67 rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
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259 CCTGAACCCAGAGCGCTCGCTCGCATCTGCTGGTCCCCAGGACCTGG 308
84 luProLeuThrIleLeuTyrTyValGlyArgThrProLysValGluGln 100
309 AGCCCTGACCATCTTGTACTATGTGGGCAGAACCCCAAGGTGGAGCAG 358
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seq_documentation_block:
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DEFINITION AL532438 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM014YD15 5
prime, mRNA sequence.
ACCESSION AL532438
VERSION AL532438.1 GI:12795931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 964)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..964
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue.type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : feng liang life
Technologies, a division of invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 245 a 248 c 269 g 200 t 2 others
ORIGIN
alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
TGFB3P x AL532438
Align seg 1/1 to: AL532438 from: 1 to: 964
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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311 GCCTTGACCACTTACTGCTTCCGCACTGGAGGAGACTGCTGT 360
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
361 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 410
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerClyProCysProTyr 50
|||||
411 ATGAACCTTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 450
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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461 CTCGCCAGTGCAGACACACACCCACAGCAGGCTGCTGGGACTGTACACAC 510
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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511 TCTGAACCCCTGAAGCATCTGCTCGCTTGTGCTGCTGCCAGGACCTGG 560
84 luProLeuThrIleLeuTyrTyValGlyArgThrProLysValGluGln 100
|||||
561 AGCCCTGACCATCTGCTACTATGTGGGAGGACCCCAAGTGGAGCAG 610
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
611 CTCCTCCAACTGGTGGTGAAGTCCTGTAATGTAGC 646
seq_name: gb_est89:BF542567
seq_documentation_block:
LOCUS BF542567 503 bp mRNA EST 11-DEC-2000
DEFINITION UI-R-C3-sm-a-12-0-UI.r1 UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-sm-a-12-0-UI 5', mRNA sequence.
ACCESSION BF542567
VERSION BF542567.1 GI:11633674
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 503)
Bonaldi,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1768868
Seq primer: M13 Forward.
Location/Qualifiers
1..503
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
```

generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within themixture. The subtracted library (UI-R-C3) was constructed as follows: PCR amplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldio, Lennon and Soares, Genome Research 6:791-806, 1996).

BASE COUNT 106 a 151 c 133 g 112 t 1 others
ORIGIN

alignment_scores:
Quality: 611.00 Length: 109
Ratio: 5.606 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.165

alignment_block:
TGFB3P x BF542567 ..

Align seg 1/1 to: BF542567 from: 1 to: 503

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4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
|||||
62 ACCGACTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCT 111
|||||
20 uTyrIleAspPheArgGlnAspLeuGlyTrpIlysrTrpValHisGluProL 37
|||||
112 CTACATTGACTTCGGCGAGGACTCTAGGTGGAAATGGGTCCACGAACTTA 161
|||||
37 ysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSer 53
|||||
162 AGGTTACTATGCGCAACTCTGCTCAGGCCCTTGCCCTTACCTCCGACG 211
|||||
54 AlaAspThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
|||||
212 TCAGACAAACCCACAGCAGCGTGTGGACTATACACACCTGAACCC 261
|||||
70 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
|||||
262 GGAGGCACTGGCTCGCCATGCTGTGTGCCCAAGACCTGGAGCCTCTGA 311
|||||
87 hrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
|||||
312 CCATCTTGACTATGTGGCAACCCCAAGGTGGAGCAGCTGTCCAC 361
|||||
104 MetValValLysSerCysLysCysSer 112
|||||
362 ATGGTGGTGAAGTCGTGTAAAGTGACG 388
|||||

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seq_name: gb_est83:BF101203

seq_documentation_block:
LOCUS BF101203 1820 bp mRNA EST 19-OCT-2000
DEFINITION 601754782F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3983588 5',
mRNA sequence.
ACCESSION BF101203
VERSION BF101203.1 GI:10883729
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1820)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLM9184 row: d column: 21
High quality sequence stop: 601.

FEATURES
Location/Qualifiers

1..1820
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3983588"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 513 a 533 c 590 g 184 t
ORIGIN

alignment_scores:
Quality: 605.00 Length: 112
Ratio: 5.402 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x BF101203 ..

Align seg 1/1 to: BF101203 from: 1 to: 1820

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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166 GCCTGGACACCAATTAATGCTTCCGCAACTGGAGGAGAACTGCTGTGT 215
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIlysrTrpValH 34
|||||
216 ACGCCCTCTTATATTGACTTCGGCAGGATCTAGGCTGGAAATGGGTCC 265
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
266 ACGAACCTAAGGTTACTATGCCAACTTCGTCAGGCCCTTGCCCATAC 315
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnThr 67
|||||
316 CTCGCGAGCGCAGACACACCACTAGCACGGTGTGGACTATATACAAC 365
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
366 CCTGAACCCAGAGCGCTCTGCCCTCGCATGCTGCCCGCCAGGACCTGG 415
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
416 AGCCCTTGACCACTCTGTACTATGTGGGAGAAC.CCCAAAGGTGGAGCAG 464
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
465 CTGTCCAACATGGTGGTGAAGTCGTGTAAAGTGACG 500
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seq_name: gb_est50:AW670561

seq_documentation_block:

LOCUS AW670561 477 bp mRNA EST 09-JUL-2000
DEFINITION 114647 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW670561
VERSION AW670561.1 GI:7527075
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithem@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 43 row: B column: 5
Seq primer: APTTAGGTGACACTATAG.
FEATURES
source
1. 477
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 114 a 138 c 135 g 90 t
ORIGIN
alignment_scores:
Quality: 535.00 Length: 94
Ratio: 5.691 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.936
alignment_block:
TGFB3P x AW670561 ..
Align seg 1/1 to: AW670561 from: 1 to: 477
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
195 GCCTGGACACCAACTACTCTCCGCAATTGGAGGAGAACTGCTGT 244
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValh 34
245 GCGCCCTCTCTACATTGACATTCGACAGGATCTGGGCTGGAAGTGGGTCC 294
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
295 ATGAACCTAAGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCGTAC 344
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
345 CTCGCGAGTCAGACACACACCCACAGCTCGTGGTGGTGTACAAAC 394
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
395 CCTGAACCCCAAGCCCTCGGCCCTCTCGTGTCTGGTGGCCCAACCTGG 444

84 luProLeuThrIleLeuTyrTyrValGlyArg 94
445 AGCCCTGACCATCTGTACTACGTGCGGAGG 476
seq_name: gb_est82:BF042894
seq_documentation_block:
LOCUS BF042894 515 bp mRNA EST 10-OCT-2000
DEFINITION BP250019B10B3 Soares normalized bovine placenta Bos taurus CDNA
clone BP250019B10B3 5', mRNA sequence.
ACCESSION BF042894
VERSION BF042894.1 GI:10759949
KEYWORDS EST.
SOURCE Cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 515)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimm g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCTCTCACTAAAG
Insert Length: 515 Std Error: 0.00
Plate: BP250019B10 row: B column: 3
Seq primer: AGCGGATACAAATTCACACAGGA
High quality sequence stop: 515.
FEATURES
Location/Qualifiers
1. .515
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BP250019B10B3"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7m3pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contibuted by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 126 a 113 c 111 g 165 t
ORIGIN
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x BF042894/rev ..
Align seg 1/1 to reverse of: BF042894 from: 1 to: 515
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17


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17  larqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
:|||||
402  TCGCCCTCTTACATGATTTTAAAGAGGATCTTGGATGGAAATGGATCC 353

34  isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
352  ATGAACCAAGGGTACAATGCTAACTTCTGTGTGGGGCATGCCATAT 303

51  LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
302  CTATGGAGTTCAGACACTCAACACACCAAGTCTCTCAGCCCTGTACAACAC 253

67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
252  CATAAATCCCGAAGCTTCCGGTCCCTTCCCTTGTGTGTCGCCAGGATCGG 203

84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
202  AACCACTGACCATCTCTATTACATTTGAATACGCCCAAGATCGAACAG 153

101  LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
152  CTTTCCAATATGATTGTCAAGTCTTGTAAATGCAGC 117
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seq_name: gb_est18:AI323791

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seq_documentation_block:
LOCUS      AI323791      681 bp      mRNA      EST      23-DEC-1998
DEFINITION mm47e08.x1 Stratagene mouse melanoma (#937312) Mus musculus cDNA
clone IMAGE:524678 3', similar to gb:X57413 Mouse mRNA for
transforming growth factor-beta2 (MOUSE);, mRNA sequence.
ACCESSION  AI323791
VERSION     AI323791.1  GI:4058220
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 681)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:318526
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 366.
Location/Qualifiers
1..681
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:524678"
/clone_lib="Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
/dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. From M2 cells, a highly metastatic derivative of the
K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACCAG
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FEATURES
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:524678"
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/tissue_type="melanoma"
/dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. From M2 cells, a highly metastatic derivative of the
K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACCAG
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3' -3' adaptor sequence: 5' CTCAGAGTTTTTTTTTTTTTTTTTTT 3'
BASE COUNT 164 a 151 c 163 g 200 t 3 others
ORIGIN

alignment_scores:
Quality: 530.00 Length: 112
Ratio: 5.048 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 78.571

alignment_block:
TGFB3P x AI323791/rev ..
Align seg 1/1 to reverse of: AI323791 from: 1 to: 681

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
461 GCTTTGGATGCTGCCTACTGCTTTAGAAATGTCAGGATAATTGCTGCCT 412

17 larqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
411 TCGCCCTCTTACATGATTTTAAAGAGGATCTTGGATGGAAATGGATCC 362

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
361 ATGAACCAAGGGTACAATGCTAACTTCTGTGTGGGCGATGCCCATAT 312

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
311 CTATGGAGTTCAGACACTCAACACACCAAGTCTCTCAGCCCTGTACAACAC 262

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|:::
261 CATAAATCCCGAAGCTTCGCTTCCCTTGTGTGTGTCCAGGATCTGG 212

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
211 AACCACTGACCATCTCTATTACATTTGAATACGCCCAAGATCGAACAG 162

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
161 CTTTCCAATATGATTGTCAAGTCTTGTAAATGCAGC 126

seq_name: gb_est76:BE575698

seq_documentation_block:
LOCUS      BE575698      445 bp      mRNA      EST      15-AUG-2000
DEFINITION dc62d10.x1 NICHD XGC Embi Xenopus laevis cDNA clone IMAGE:3401683
3', similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR
(HUMAN); gb:X57413 Mouse mRNA for transforming growth factor-beta2
(MOUSE);, mRNA sequence.
ACCESSION  BE575698
VERSION     BE575698.1  GI:9825497
KEYWORDS    EST.
SOURCE      African clawed frog.
ORGANISM    Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 445)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40up from Gibco
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34	isGluProLySGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyr	50
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51	LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh	67
411	CTCCGACGCGAGACACAAACCCATAGCAGGTGCTTGACATATACACAC	460
67	rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG	84
461	CCTGAACCCACAGGCGTCTGC.TGSCCATGTGCGT.CCCACGAGGACCTGG	508
84	luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln	100
509	AGCCCCCTGACCATCTTGTTACTATGTGGCAGAACCCCAAGGTGGAGCAG	558
seq_name: gb_est98:BG244370		
seq_documentation_block:		
LOCUS	BG244370	966 bp mRNA EST 13-FEB-2001
DEFINITION	602356090F01 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4484686 5',	
	mRNA sequence.	
ACCESSION	BG244370	
VERSION	GI:12754185	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-remail.nih.gov	
	Tissue procurement: Gilbert Smith, Ph.D.	
	CDNA Library Preparation: Life Technologies, Inc.	
	CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNL at:	
	http://image.llnl.gov	
	Plate: LLAM10325 row: c column: 23	
	High quality sequence stop: 656.	
FEATURES	Location/Qualifiers	
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	/clone_lib="NCI_CGAP_Mam1"	
	/tissue_type="tumor, biopsy sample"	
	/dev_stage="3 months, virgin"	
	/lab_host="DH10B"	
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;	
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.	
	Library constructed by Life Technologies. Investigator	
	providing samples: Gilbert Smith, NIH"	
BASE COUNT	228 a 273 c 251 g 214 t	
ORIGIN		
alignment_scores:		
Quality:	506.00	Length: 112
Ratio:	4.819	Gaps: 4
Percent Similarity:	93.750	Percent Identity: 91.964
alignment_block:		
TGFB3p x BG244370/rev	..	
Align seg 1/1 to reverse of: BG244370 from: 1 to: 966		

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681 CATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGTACGCCCCCTTGA 632
21 yrileAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProlys 37
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
631 TATGTGACTTCCGCGAGATCTAGC.TGGAAATGGGTCCAGCAACCTAAG 583
38 GlyTyr.TyAlaAsnPheCysSerGlyProCysProTyrLeuArgSerA 54
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
582 GGTACTAATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGG 533
54 laAspThr.ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
532 CAGACACAAACCCATAGACGGTCTTGGACTATACAAACACCCCTGAACCC 483
70 oGluAlaSerAlaSer.ProCysCysValProGlnAspLeuGluProLeu 86
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
482 AGAGCGCTCTGCTCTGCCATGTGCTGCCCTCCCGCAGGACCTGGAGCCCTG 433
87 ThrileLeuTyrTyValGlyArgThrProLysValGluGlnLeuSerAs 103
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
432 ACCATCTGTACTATGTGGCAGAACCCCAAGGTGGAGCAGCTGTCCAA 383
103 nMetValValLysSerCysLysCysSer 112
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 CATGGTGTGAAGTCGTGTAAGTGCAGC 355

```

seq_name: gb_est53:AW919738

```

seq_documentation_block:      510 bp      mRNA      25-MAY-2000
LOCUS      AW919738
DEFINITION      Rattus norvegicus cDNA clone RIGG52 5' end, mRNA sequence.
ACCESSION      AW919738
VERSION        AW919738.1 GI:8085539
KEYWORDS       EST.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.

```

```

REFERENCE      1 (bases 1 to 510)
AUTHORS        Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
                Kerlavage,A.R. and Adams,M.D.
TITLE          Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                Gene Index
JOURNAL        Unpublished (1998)
COMMENT        Contact: Lee, NH
                The Institute for Genomic Research
                9712, Medical Center Drive, Rockville, MD 20850, USA
                Tel: (301)-838-3529
                Fax: (301)-838-0208
                Email: nhlee@tigr.org
                This clone is available through the ATCC, contact the ATCC
                tel#703-365-2700 for further information
                Seq primer: M13 Reverse.

```

```

FEATURES             Location/Qualifiers
     source           1..510
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /clone="RIGG52"
     clone_lib="Rat gene index, normalized rat, norvegicus,
     Bento Soares"
     tissue_type="mix - brain, ovary, placenta, kidney, lung,
     liver, embryo, heart, muscle, spleen"
     lab_host="SOLR"
     note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
     XhoI; Estimated insert size approx.1 kb"
BASE COUNT      117 a. 165 c 131 g 96 t
ORIGIN

```

alignment_scores:

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Quality: 503.00      Length: 112
Ratio: 5.133      Gaps: 0
Percent Similarity: 87.500      Percent Identity: 77.679

alignment_block:
TGFB3P x AW919738
..
Align seg 1/1 to: AW919738 from: 1 to: 510

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||||||||||||||||||||||||||||||||||||||||||||||||||
157 GCCCTGGATACCAACTACTGCTTCAGCTCCACAGAGAACTGCTGTGT 206
17 largProLeuTyriIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||||||||||||||||||||||||||||||||||||||||||||||||||
207 ACGGACGCTGTACATGTGACCTTAGGAAGACCTGGTTGGAAGTGGATCC 256
34 isGluProLysGlyTyrTyAlaAsnPheCysSerGlyProCysProTyr 50
|||||||||||||||||||||||||||||||||||||||||||||||||||||
257 ACGAGCCCAAGGGCTACCATGCACACTTCTGTCTGGGGCCCTGCCCTAC 306
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| ::||| ::||| ::|||
307 ATTTGGAGCCTGGACACACAGTACACGAGGTCCTTGCCCTCTACAACCA 356
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
|||||||||||||||||||||||||||||||||||||||||||||||||||||
357 ACACAAACCCGGGTGCTCCGCATCACCGTCTGCGTGGCCGCGCTTTGG 406
84 luProLeuThrIleLeuTyrTyValGlyArgThrProLysValGluGln 100
|||||||||||||||||||||||||||||||||||||||||||||||||||||
407 AGCCACTGCCCATCGTCTACTAGTGGTGGTCCGAAGCCCAAGGTGGAGCAG 456
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||||||||||||||||||||||||||||||||||||||||||||||||||
457 TTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 492

```

seq_name: gb_est22:AI599959

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seq_documentation_block:      529 bp      mRNA      21-APR-1999
LOCUS      AI599959
DEFINITION      EST251662 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
                REMEX51 3' end, mRNA sequence.
ACCESSION      AI599959
VERSION        AI599959.1 GI:4609007
KEYWORDS       EST.
SOURCE         Rattus sp.
ORGANISM       Rattus sp.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1 (bases 1 to 529)
AUTHORS        Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
                Kerlavage,A.R. and Adams,M.D.
TITLE          Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                Gene Index
JOURNAL        Unpublished (1998)
COMMENT        Contact: Lee, NH
                The Institute for Genomic Research
                9712, Medical Center Drive, Rockville, MD 20850, USA
                Tel: (301)-838-3529
                Fax: (301)-838-0208
                Email: nhlee@tigr.org
                Seq primer: M13-21.

```

```

FEATURES             Location/Qualifiers
     source           1..529
                     /organism="Rattus sp."
                     /db_xref="taxon:10118"
                     /clone="REMEX51"
                     /dev_stage="embryo 8, 12, 18 dpc"
                     /note="Vector: p7T3Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT      88 a 142 c 194 g 105 t

```



```

DEFINITION 602578182F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3481700 5',
            mRNA sequence.
ACCESSION  BG518882
VERSION    BG518882.1 GI:13514180
KEYWORDS   EST,
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Cloning Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LIAW8510 row: d column: 21
            High quality sequence stop: 640.
FEATURES   Location/Qualifiers
            1..721
                /organism="Mus musculus"
                /strain="C57/B6"
                /db_xref="taxon:10090"
                /clone="IMAGE:3481700"
                /clone_lib="NCI_CGAP_Mam5"
                /tissue_type="tumor, gross tissue"
                /dev_stage="7 months"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
                Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Library constructed by Life Technologies. Investigators
                providing samples: Lothar Hennighausen/Robin Humphreys,
                NIH"
BASE COUNT 164 a 232 c 187 g 138 t
ORIGIN

alignment_scores:
    Quality: 503.00      Length: 112
    Ratio: 5.133        Gaps: 0
    Percent Similarity: 87.500 Percent Identity: 77.679

alignment_block:
TGFB3P x BG518882 ..
Align seg 1/1 to: BG518882 from: 1 to: 721
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
296 GCCTGGATACCAACTATTGCTTACGCTCCACAGAGAAGAACTGCTGTG 345
|||||
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
346 GCGGCAGCTGTACATTGACTTTAGGAGGACCTGGGTTGGAAGTGGATCC 395
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
396 ACGAGCCCAAGGGCTACCATGCTTGGGACCTTCTGTCTGGACCTTAT 445
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLysTrpAsnTh 67
::: ||| ||||| ::||| |||||
446 ATTTGGAGCTGGACACACAGTACAGCAAGGTCCTTGCCTCTACAACCA 495
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
496 ACACACCCGGCGCTTCGGCGCTACCGTCTCGCTGGCGCGAGGCTTTGG 545

```

```

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
546 AGCCACTGCCCATCGCTCTACTAGTGGTGCAGAGCCCAAGGTGGAGCAG 595
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
596 TTGTCCCAACATGATTGTGCGCTCTGCAAGTGCAGC 631
|||||
seq_name: gb_est53:AW958056

seq_documentation_block:
LOCUS      AW958056          505 bp      mRNA          EST          01-JUN-2000
DEFINITION EST370126 MAGE resequencs, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW958056
VERSION    AW958056.1 GI:8147739
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 505)
AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE      Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL    Unpublished (2000)
COMMENT    Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 115
FEATURES   Location/Qualifiers
            1..505
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequencs, MAGE"
                /note="Vector: pBluescriptSKm"
BASE COUNT 115 a 137 c 106 g 144 t 3 others
ORIGIN

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AW958056 ..
Align seg 1/1 to: AW958056 from: 1 to: 505
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
9 GCCTGGACACCAACTATTGCTTACGCTCCACGGAGAAGAACTGCTGCT 58
|||||
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
59 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 108
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
109 ACGAGCCCAAGGGCTACCATGCTCCAACTTCTGCTCGGCGCTTAC 158
::: ||| ||||| ::||| |||||
151 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||
159 ATTTGGAGCTGGACACAGTACAGCAAGTCTCTGCGCTGTACAACCA 208
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||

```

209 GCATAACCGGCGCTCGCGCGCGCGCTGCTGCTGCGCGCGAGGCGCTGG 258

84 luProLeuThrIleLeuTyrTyValglyArgThrProLysValGluGln 100

259 AGCCGCTGCCATCGTACTACGTGGCGCGCAAGCCCAAGCTGGAGCAG 308

101 LeuSerAsnMetValLysSerCysLysCysSer 112

309 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 344

seq_name: gb_est75:BE464068

seq_documentation_block:

LOCUS BE464068 568 bp mRNA EST 27-JUL-2000
DEFINITION hx84h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194547 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 TAR1 repetitive element ;
mRNA sequence.

ACCESSION BE464068

VERSION BE464068.1 GI:9509843

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 568)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -400P from Gibco

High quality sequence stop: 395.

FEATURES

source

1..568

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3194547"

/lab_host="NCI-CGAP_Kid11"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

prepared, and ss circles were made in vitro. Following RAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1322376-1323911, 1456007-1456775, and

1500552-1502855). Subtraction by Bento Soares and M.

Fatima Bonaldo.

96 a 159 c 203 g 110 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 500.00 Length: 112

Ratio: 5.102 Gaps: 0

Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x BE464068/rev ..

Align seg 1/1 to reverse of: BE464068 from: 1 to: 568

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

479 GCCTTGGACACCAACTATTCTCTTTCAGCTCCACGGAGAAGATTCTGCGT 430

17 laqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

429 GCGAAGCTGTACATTGACTTCGCAAGGACCTCGGTGGAAAGTGGATCC 380

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

379 ACGAGCCCAAGGCTACCATGCCAACTTTTTCCTCGGCGCTGCCCTAC 330

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

329 ATTTGGAGCGCTGGACACGACGATACGCAAGGTCCTGCGCTGTACAACCA 280

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

279 GCATAACCGGCGCTCGCGCGCGCTGCTGCTGCGCAGGCGCTGG 230

84 luProLeuThrIleLeuTyrTyrValglyArgThrProLysValGluGln 100

229 AGCCGCTGCCATCGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAG 180

101 LeuSerAsnMetValLysSerCysLysCysSer 112

179 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 144

seq_name: gb_est27:AI951831

seq_documentation_block:

LOCUS AI951831 598 bp mRNA EST 06-SEP-1999

DEFINITION wx38b08.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545911 3'

similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1

PRECURSOR (HUMAN); contains PTR7.t3 MER22 repetitive element ; mRNA

sequence.

ACCESSION AI951831

VERSION AI951831.1 GI:5744141

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 598)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies,

Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.

Consortium DNA Sequencing by: Washington University Genome

Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -400P from Gibco

High quality sequence stop: 425.

FEATURES

source

1..598

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2545911"

/clone_lib="NCI_CGAP_Pit1"

/tissue_type="four pooled pituitary adenomas"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies."

95 a 173 c 222 g 107 t

BASE COUNT

ORIGIN

```
/tissue_type="lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
from different adults (both approximately 40 years old)
together yielded 20ug of total RNA and 150ng mRNA for cDNA
library synthesis. A directionally cloned cDNA library in
the pCMVSPORT6 vector was constructed at Life Technologies
, essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pCAGTAGTTCTAGATCGGAGCGGCCG(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC). "
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BASE COUNT 91 a 170 c 216 g 122 t 1 others
ORIGIN

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x BF726995/rev ..

Align seg 1/1 to reverse of: BF726995 from: 1 to: 600

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
512 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTCGGT 463

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
462 GCGCAGCTGTACATGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 413

34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
412 ACGAGCCCAAGGGTACCATGCCAACTTCTGCTCGGGCCCTGCCCTTAC 363

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
362 ATTTGGAGCCTGGACGACGACGACGACGACGACGACGACGACGACGAC 313

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
312 GCATAACCCGGGCGCTCGGGCGGCGCTGCTGCTGCGCGAGCGCTGG 263

84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
262 AGCGCTGCCCATCGTGTACTACGTGGGCGCCCAAGCCCAAGGTGGAGCAG 213

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
212 CTGTCCCAACATGATCGTGCCTCTCTGCAAGTGACAGC 177

seq_name: gb_est16:A1131171

seq_documentation_block:
LOCUS A1131171 727 bp mRNA EST 27-OCT-1998
DEFINITION qcl5c11.1 xl Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone
IMAGE:1709684 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element TARI TARI
repetitive element ;, mRNA sequence.

ACCESSION A1131171
VERSION A1131171.1 GI:3601187
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

|||||:||||:||||:|||||
183 CTTGTCACATGATCGTGGCTCCTGCAAGTCAGC 148

seq_name: gb_est18:AI323037

seq_documentation_block:
LOCUS      AI323037       477 bp      mRNA      EST      23-DEC-1998
DEFINITION clone IMAGE:478105 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
            FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
            growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION  AI323037
VERSION    AI323037.1 GI:4057466
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 477)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:288849
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 415.
            Location/Qualifiers
1. .477
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:478105"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="vector: pT73D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
Skate Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      103 a      156 c      127 g      91 t
ORIGIN

alignment_scores:
Quality: 498.00      Length: 112
Ratio: 5.082      Gaps: 0
Percent Similarity: 87.500      Percent Identity: 76.786

```


alignment_block:

TGFB3P x AI323037 ..

Align seg 1/1 to: AI323037 from: 1 to: 477

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
141 GCCCTGGATACCAACTATTGCTTCCAGCTCCACAGAGAAGAACTGCTGTGT 190

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleAspValH 34
|||||
191 CGCGCAGCTGTACATTGACTTTAGAGAGGACCTGGGTTGGAAGTGGATCC 240

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
241 ACGAGCCCAAGGCTACCTCCCACTTCTGTCTGGGACCTGCCCTTAT 290

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||
291 ATTTGGAGCCCTGGACACACACATACAGCAAGTCTTGGCCCTCTACAACCA 340

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
341 ACACAACCCGGCGCTTGGCGCTCACCGTGTGGCTGGCGCAGGCTTTGG 390

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
391 AGCCACTCCCTCGTCTACGTACGTGGGTGCGCAAGCCCAATGTGGAGCAG 440

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
441 TTGTCCACATGATTTGGCGTCTCTGCAAGTGCAGC 476

seq_name: gb_est49:AW600952

seq_documentation_block: 325 bp mRNA EST 23-MAR-2000

LOCUS AW600952

DEFINITION RCL-BN0014-210100-012-f11 BN0014 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW600952

VERSION AW600952.1 GI:7305691

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.

AUTHORS The FAPESP/LICR Human Cancer Genome Project

TITLE Unpublished (1999)

JOURNAL Contact: Simpson A.J.G.

COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCL1&t2=RCL1&t3=2000-01-21&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 325.

FEATURES

source

1..325

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BN0014"

/dev_stage="Adult"

/note="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 98 a 76 c 63 g 88 t

ORIGIN

alignment_scores: Quality: 496.00 Length: 103
Ratio: 5.113 Gaps: 0
Percent Similarity: 94.175 Percent Identity: 79.612

alignment_block:
TGFB3P x AW600952 ..

Align seg 1/1 to: AW600952 from: 1 to: 325

10 AsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPheArgG1 26
|||||
10 AATGTGCAGGATAAATGTCGCTACGTCACATTACATTGATTCAAGAG 59

26 nAspLeuGlyTyrIleAspValHisGluProLysGlyTyrTyrAlaAsnP 43
:|||||
60 GGACCTAGGTGGAATGATACACAGAACCCAAAGGGTACAATGCCAACT 109

43 heCysSerGlyProCysProTyrLeuArgSerAlaAspThrHisSer 59
|||||
110 TCTGTGCTGGACATGCCCGTATTTATGGAGTTCAGACACTCAGCAGC 159

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||
160 AGGGTCTCGAGCTTATATATACATAAACCCAGAACATCTGCTCTCC 209

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||
210 TTGCTGCGTGTCCCAAGATTAGAACTCTAACCATTTCTACTACATTG 259

93 lyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCys 109
|||||
260 GCAAAACACCCCAAGATTGAACAGCTTCTTAATATGATTGTAAAGTCTTC 309

110 LysCysSer 112
|||||
310 AAATGCAGC 318

seq_name: gb_est42:AW073988

seq_documentation_block: 572 bp mRNA EST 13-OCT-1999

LOCUS AW073988

DEFINITION xb06a06.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575474 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA sequence.

ACCESSION AW073988

VERSION AW073988.1 GI:6028986

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 572)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.W.A.G.B. Consortium DNA Sequencing by: Washington University Genome Sequencing Center


```

86  eauthrleLeuTyrTyrValGlyArgThrProLysValGluInLeuSer 102
221  TGCCTCGGTGTTACTAGCTGGCGCAAGCCCAAGTGGAGCAGCTGTCC 172
103  AsnMetValLysSerCysLysCysSer 112
171  AACATGATCGTGGCTCCTCGCAAGTCGACG 142

seq_name: gb_est48:AW512491

seq_documentation_block:
LOCUS AW512491 646 bp mRNA EST 03-MAR-2000
DEFINITION xx75d02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2849475 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains element TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AW512491
VERSION AW512491.1 GI:7150569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 396.
FEATURES
Location/Qualifiers
source
1..646
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2849475"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Salt; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
BASE COUNT 115 a 178 c 208 g 144 t 1 others
ORIGIN

alignment_scores:
Quality: 492.00 Length: 110
Ratio: 5.125 Gaps: 0
Percent Similarity: 87.273 Percent Identity: 76.364

alignment_block:
TGFB3P x AW512491/rev ..

Align seg 1/1 to reverse of: AW512491 from: 1 to: 646

2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValAr 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 TTGCACACAAATATTGCTTCACCTCCAGGAGAACGACTGCTGCGTGC 444

18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
443 GCAGCTGTACATTGACTTCGCAAGGACCTCGCGTGGAGTGGATCCACG 394

35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
```

```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
393 AGCCCAAGGGCTACCATCCCAACTTTTGCCTCGGGCCCTGCACATT 344

52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
343 TGGAGCCTGGACACGACGACAGCAAGGTTCCTGGCCCTGTACACACGA 294

68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
293 TAACCCGGCGCCCTCGCGCGCGCGCTGTTCGCTGCCGCGGCGCTGGA 244

85 roLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeu 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
243 CGCTGCCCATGTGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAGCTG 194

102 SerAsnMetValValLysSerCysLysCys 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
193 TCCAACATGATTGTGCGCTCCTCGCAAGTGC 164

seq_name: gb_est16:AI148173

seq_documentation_block:
LOCUS AI148173 785 bp mRNA EST 26-OCT-1998
DEFINITION qb56d01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains PTR5.b3 TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AI148173
VERSION AI148173.1 GI:3675855
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 953 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 356.
FEATURES
Location/Qualifiers
1..785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1704097"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCACTCACTGGAGCGCGGCATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 137 a 217 c 267 g 164 t
ORIGIN
```

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alignment_scores:
  Quality: 491.00      Length: 112
  Ratio: 5.010        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 75.000

alignment_block:
  TGF3P x A1148173/rev ..

Align seg 1/1 to reverse of: A1148173 from: 1 to: 785

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||.....:|||||...: |||||.....
497 GCCCTGGACACCAATATGCTTCAGCTCCACGAGAAAGAACTGCTGGT 448

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||.....:|||||...: |||||.....
447 CGGCACGCTGTACATTGACTTCCCAAGGACCTCGGTGGAGGTGGATCC 398

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||...: |||||.....
397 ACGAGCCCAAGGGCTACCATGCTCCCAACTTTTGGCTCGGGCCCTGCCCTTAC 348

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
347 ATTTGGAGCTGGACACGCGAGTACAGCAAGTCTCGGCCCTGTACACCA 298

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||.....:|||||...: |||||.....
297 GCATACCCGGGCCCTCGGGCGCGCTGCTGCTCCGCGAGCGCTGG 248

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||.....:|||||...: |||||.....
247 AGCCACTGCCATCGTCTACTACGTGGCGCAAGCCCAAGGTGGAGCAG 198

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||.....:|||||...: |||||.....
197 CTGTCCCAACATGATCGTGGCGTCTCTGCAAGTGCAAC 162

seq_name: gb_est85:BF287476

seq_documentation_block:
  529 bp mRNA EST 28-NOV-2000
LOCUS BF287476
DEFINITION EST452067 Rat Gene Index, normalized rat, Rattus norvegicus cDNA
Rattus norvegicus cDNA clone RGIG52 3' sequence, mRNA sequence.
ACCESSION BF287476
VERSION BF287476.1 GI:11218546
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 529)
AUTHORS Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G.,
Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.
TITLE Generation of ESTs from Normalized Rat Embryo, Bonto Soares
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: EST351042
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
FEATURES
    Location/Qualifiers
        source
            1..529
                /organism="Rattus norvegicus"
                /db_xref="taxon:10116"
                /clone="RGIG52"
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/clone_lib="Rat Gene Index, normalized rat, Rattus
norvegicus cDNA"
/tissue_type="mixed tissue"
/lab_host="DH5-alpha"
/notes="Vector: p3T7Pac; Site_1: EcoRI; Site_2: NotI;
Combination of ROV, RBR, RKL, RPL, RLJ, REM, RNU, RSP
, RHE, RPC, RPN"
BASE COUNT 91 a 141 c 190 g 107 t
ORIGIN

alignment_scores:
  Quality: 490.00      Length: 112
  Ratio: 5.052        Gaps: 0
Percent Similarity: 86.607 Percent Identity: 76.786

alignment_block:
  TGF3P x BF287476/rev ..

Align seg 1/1 to reverse of: BF287476 from: 1 to: 529

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||.....:|||||...: |||||.....
477 GCCCTGGATACCAATATGCTTCAGCTCCACAGAAAGAACTGCTGTGT 428

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||.....:|||||...: |||||.....
427 ACGGCAGCTGTACATTGACTTAGGAAGGACCTGCTGGAGTGGATCC 378

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||...: |||||.....
377 ACGAGCCCAAGGGCTACCATGCTCCCAACTTCTGTGGGGCCCTGCCCTTAC 328

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
327 ATTTGGAGCTGGACACAGTACAGCAAGTCTTGCCTTTACACCA 278

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||.....:|||||...: |||||.....
277 ACACAAACCGGGTGTTCGCGATCACCGTGATCGTGGCGCAGGCTTGG 228

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||.....:|||||...: |||||.....
227 AGCCATCCCATCTCTTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 178

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||.....:|||||...: |||||.....
177 TGTCCCAACATGATCGTGGCGTCTCTGCAAGTGCAGC 142

seq_name: gb_est1:AA000733

seq_documentation_block:
  431 bp mRNA EST 18-JUL-1996
LOCUS AA000733
DEFINITION mg35006.r1 Soares mouse embryo NM013.5 14.5 Mus musculus cDNA
clone IMAGE:425747 5' similar to gb:X02812.cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION AA000733
VERSION AA000733.1 GI:1436599
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 431)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
```

WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:260299

Putative full length read

vector to vector length is 661

Seq primer: Etrprimer

High quality sequence stop: 321.

FEATURES

source

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1. .431
  /location/Qualifiers
  /organism="Mus musculus"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone_lib="Soares mouse embryo NbME13.5 14.5"
  /sex="unknown"
  /tissue_type="embryo"
  /dev_stage="13.5-14.5dpc total fetus"
  /lab_host="DH10B"
  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGACGCCGCGGAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru KO, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      94 a 140 c 113 g      84 t
ORIGIN

```

alignment_scores:

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Quality: 488.00      Length: 112
Ratio: 5.031         Gaps: 0
Percent Similarity: 86.607      Percent Identity: 75.000

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alignment_block:

TGFB3P x AA000733 ..

Align seg 1/1 to: AA000733 from: 1 to: 431

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1 AlaleuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
93 GCCCTGGATACCACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTG 142

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIysTrpValH 34
|||||
143 GCGCAGTGATACATTGACTTGTAGAGAGGACCTGGGTGGAGTGGATCC 192

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
193 ACGAGCCCAAGGCTACATGCCACACTTCGTCTGGGACCCCTGCCCTAT 242

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::: |||||
243 ATTTGGAGCTGGACACACAGTACAGCAAGTCTCTGCCCTCTACAACCA 292

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
293 ACACAACCCGGCGCTTCGGCGTCACCGTCTGCGTGGCGCGCTTATG 342

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
343 AGCCATGCCCCATCGTCTACTACTGCTGGGTGCGAAGCCCAAGGTGGAGCAG 392

```

```

101 LeuSerAsnMetValVallysSerCysLysCysSer 112
|||||
393 TTGTCCACATGATGTGGCTCCTGCAAGTGCAGC 428

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seq_name: gb_est24:AI743724

seq_documentation_block:

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LOCUS      AI743724          778 bp      mRNA          EST          19-DEC-1999
DEFINITION      wq53b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2368787 3' similar to gb:X02812.cdsl TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN);contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION      AI743724
VERSION        AI743724.1      GI:5112012
KEYWORDS       EST.
SOURCE        human.
ORGANISM      Homo sapiens

```

```

REFERENCE      1 (bases 1 to 778)
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT        Tumor Gene Index
                Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaps-r@mail.nih.gov
                This clone is available royalty-free through LLNL ; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Insert Length: 863 Std Error: 0.00
                Seq primer: -40Up from Gibco
                High quality sequence stop: 449.

```

FEATURES

source

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1. .778
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:2368787"
  /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
  /lab_host="DH10B"
  /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      131 a 223 c 269 g 151 t      4 others
ORIGIN

```

alignment_scores:

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Quality: 487.00      Length: 113
Ratio: 4.969         Gaps: 1
Percent Similarity: 86.726      Percent Identity: 76.106

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alignment_block:

TGFB3P x AI743724/rev ..

Align seg 1/1 to reverse of: AI743724 from: 1 to: 778

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1 AlaleuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
484 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGT 435

```

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 434 GCGGAGCTGTACATTTGCTCCGAAAGGACCTCGCTGGAAGTGGATCC 385
 34 isGlupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 384 ACGAGCCCAAGGGCTACCATGCTGCTGGGCGCCCTGCCCTAC 335
 51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 334 ATTGTGAGCGCTGGACACGACGATACAGCAAGGTCTTGGCCCTGTACAACCA 285
 67 rleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 284 GCATAACCGGCGCGCTCGGCGGCCCTGCTGCGTGGCGAGCGCTGG 235
 84 lu.ProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
 234 AACCCCTGCGCATCGTGTACTACGTGGGCGCCCAAGCCCAAGTGGAGCA 185
 100 nLeuSerAsnMetValLysSerCysLysCysSer 112
 184 GCTGTCCACATGATCGTGGCGCTCTCGCAAGTGCAGC 148

seq_name: gb_est77:BE645704

seq_documentation_block:
 LOCUS BE645704 474 bp mRNA EST 05-SEP-2000
 DEFINITION 7e74h10.x1 NCI-CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288259 3'
 similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN);contains element TAR1 repetitive element ;, mRNA
 sequence.

ACCESSION BE645704
 VERSION BE645704.1 GI:9970015
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 474)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov

Seq primer: -400P from Gibco.
 Location/Qualifiers
 1. .474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3288259"
 /clone_lib="NCI-CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; plasmid DNA from the
 normalized library NCI-CGAP_Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 1101192-1101959, and 1217928-1220615).
 * Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 75 a 138 c 176 g 85 t
 ORIGIN
 alignment_scores:
 Quality: 486.00 Length: 109
 Ratio: 5.116 Gaps: 0
 Percent Similarity: 87.156 Percent Identity: 76.147
 alignment_block:
 TGF3P x BE645704/rev ..

Align seg 1/1 to reverse of: BE645704 from: 1 to: 474
 4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
 473 ACCAACATTTGCTTACGCTCCACGGAGAAGAACTGCTGCGTGGCGAGCT 424
 20 uTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProL 37
 423 GTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGGCCA 374
 37 ySGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSer 53
 373 AGGGCTACCATGCCAACTTTTGCCTCGGGCCCTGCCCTACATTGGAGC 324
 54 AlaAspThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
 323 CTGACACGACGATACAGCAAGTCTTGGCCCTGTACACCAACGACATACCC 274
 70 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
 273 GGGCGCTCGGCGCGCTGCTGCGTGGCGAGCGCTGGAGCGCGCTGC 224
 87 hrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
 223 CCATGTGTACTACGTGGGCCCAAGCCCAAGTGGAGCGAGCTGTCCAAC 174
 104 MetValLysSerCysLysCysSer 112
 173 ATGATCGTGGCTCTCTGCAAGTGCAGC 147

seq_name: gb_est27:AI991139

seq_documentation_block:
 LOCUS AI991139 589 bp mRNA EST 27-OCT-1999
 DEFINITION wu38g03.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone
 IMAGE:2522356 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 TAR1
 repetitive element ;, mRNA sequence.

ACCESSION AI991139
 VERSION AI991139.1 GI:5838043
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400P from Gibco
 High quality sequence stop: 459.
 Location/Qualifiers
 1. .589
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2522356"

FEATURES
 source

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 509)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Other_ESTs: ur7lc12.x1 Contact: Robert Strausberg, Ph.D. Email: cgapb-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov/image/html/iresources.shtml MGI:1058490 Seq primer: -40RP from Gibco High quality sequence stop: 418.

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i: 302
/organism="Mus musculus"
/strain="129 - C57/B6 - FVB"
/db_xref="taxon:10090"
/clone_image="3155734"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"

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/lab_host= D10B
/note="Organ: mammary: Vector: pCMV-SPORT6; Site 1: SalI;
```

```

site_2: NOD1; Cloned unidirectionally: Primer: Vargo et al.,
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999).
BASE COUNT      134 a    156 c    123 g    94 t     2 others
ORIGIN

alignment_scores:
Quality:      481.00          Length:      94
Ratio:        5.228           Gaps:       0
Percent Similarity: 97.872   Percent Identity: 94.681

alignment_block:
TGFB3P x AW823286      ..

Align seg 1/1 to: AW823286 from: 1 to: 509

1 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
228 GCCCTGGACACAATTAAGTCCTCCGCCAACCTGGAGGAGAAGTGTGTGT 277
|||||

17 largProLeuTyrIleAspPheArgGlnAspleuGlyTrpLysTrpValH 34
|||||
278 ACGCCCCCTTTATATTGACTTCCGCACAGATCTAGCTGGAAATGGTCC 327
|||||

34 lsGluProLvsGLYTVrTvAlaAsnPheCysSerGlyProCvsProtvIr 50
|||||
```

328 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 377

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
378 CTC CGCAGCGCAGACACAAACCCATAGCAGGGGCTTGGACTATACAACAC 427
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
428 CCTGAACCCAGAGCGTCTGCCTGCC.TGCTGCGCCGCCNANGACCTGG 476
84 luProLeuThrIleLeuTyrTyrValGlyArg 94
477 AGCCCCCTGACCATCTGTACTATGTGGCAGA 508


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seq_name: gb_est24:AI760533

seq_documentation_block:
LOCUS      AI760533          546 bp      mRNA      EST      20-DEC-1999
DEFINITION wh8b09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2387801 3'
            similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION  AI760533
VERSION    AI760533.1 GI:5176200
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 546)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/hrp/image/image.html
            Insert length: 714 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 465.

FEATURES             Location/Qualifiers
     source           1..546
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2387801"
                     /clone_lib="NCI_CGAP_CLL1"
                     /tissue_type="B-cell, chronic lymphocytic leukemia"
                     /lab_host="DH10B"
     note="vector: pT7T3D-Pac (Pharmacia) with a modified
     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
     was primed with a Not I - oligo(dT) primer [5',
     TGTACCAATCTCAAGTGGGAGCGCGCATCTTTTTTTTTTTTTTTTTTT
     T 3']; double-stranded cDNA was ligated to Eco RI
     adaptors (Pharmacia), digested with Not I and cloned into
     the Not I and Eco RI sites of the modified pT7T3 vector.
     Library is normalized, and was constructed by Bento
     Soares and M.Fatima Bonaldo."
BASE COUNT      86 a 157 c 204 g 98 t 1 others
ORIGIN

alignment_scores:
Quality: 481.00      Length: 108
Ratio: 5.117        Gaps: 0
Percent Similarity: 87.037 Percent Identity: 75.926

alignment_block:
TGFB3P x AI760533/rev ..

Align seg 1/1 to reverse of: AI760533 from: 1 to: 546

5 AsnTyrCysPheArgAsnLeuGluAsnCysCysValArgProLeuTy 21
|||||
464 AACTATTGCTTCAGCTCCACGAGAGAACTGCTCGTGGCGACGCTGA 415
|||||

21 rIleAspPheArgGlnAsnLeuGlyTrpLysTrpValHisGluProLysG 38
|||||
414 CATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAG 365
|||||

```

```

38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
|||||
364 GTTACCATGCGCAACTTCTGCTGGGCGCTGCCCCCTACATTTGGAGCGCTG 315
|||||

55 AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProG1 71
|||||
314 GACACGACGTACAGCAGGCTCTGGCCCTGTACACACGACGATACCCGGG 265
|||||

71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
|||||
264 CGCCTCGGCGCGCGCTGCTGCGTGGCGAGGCGCTGGAGCGCTGCCCA 215
|||||

88 leuLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
|||||
214 TCGTGTACTACGTGGCGCGAAGCCCAAGGTGGAGCAGCTGTCCAACATG 165
|||||

105 ValValLysSerCysLysCysSer 112
|||||
164 ATCGTGGCTCTCGCAAGTCGAGC 141
|||||

seq_name: gb_est110:W45844

seq_documentation_block:
LOCUS      W45844          478 bp      mRNA      EST      23-MAY-1996
DEFINITION mc77e02.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
            clone IMAGE:354554 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
            FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
            growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION  W45844
VERSION    W45844.1 GI:1330578
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 478)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE     The WashU-HHMI Mouse EST Project
JOURNAL   Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:226354
Seq primer: ETPrimer
High quality sequence stop: 466.

FEATURES             Location/Qualifiers
     source           1..478
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:354554"
                     /clone_lib="Soares mouse embryo NBME13.5 14.5"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
     note="vector: pT7T3D-Pac (Pharmacia) with a modified
     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
     was primed with a Not I - oligo(dT) primer [5',
     TGTTACCAATCTGAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT
     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
     14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
     State Univ., from 2 ]; double-stranded cDNA was ligated to

```

Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 106 a 155 c 126 g 90 t 1 others
ORIGIN

alignment_scores:
Quality: 480.00 Length: 112
Ratio: 4.898 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x W45844 ..

Align seg 1/1 to: W45844 from: 1 to: 478

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
141 GCCTGGATACCACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTG 190

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
191 GCGGCA.CTGTACATTGACTTTAGGAAGACCTGGCTTGAAGTGCATCC 239

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
240 ACGAGCCCAAGGCTACCACTTGTCTGGGACCCCTGCCCTAT 289

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67
:::
290 ATTGGAGCTGGACACAGTACACAGAGTCTTGCCTCTACAAACA 339

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
340 ACACAAACCGGGCGCTTCGCGTCCACCGTCTCGCGCCGAGTATATGG 389

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
390 AGCCACTGCCCATCGCTCTACTAGTGGTGGCAAGCCCAAGGTGGAGCAG 439

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
440 TTGTCCAACATGATTGCGCTCGCTCGCAAGTGCAGC 475

seq_name: gb_est49:AW627667

seq_documentation_block: 466 bp mRNA EST 31-MAR-2000
LOCUS h989h10.x1 NCI_CGAP_GUL Homo sapiens cDNA clone IMAGE:2970019 3'
DEFINITION similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
sequence.

ACCESSION AW627667
VERSION AW627667.1 GI:7374457
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 466)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 378.

FEATURES
Location/Qualifiers
1..466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2970019"
/clone_lib="NCI_CGAP_GUL"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."

BASE COUNT 77 a 136 c 167 g 86 t
ORIGIN

alignment_scores:
Quality: 471.00 Length: 107
Ratio: 5.065 Gaps: 0
Percent Similarity: 86.916 Percent Identity: 74.766

alignment_block:
TGFB3P x AW627667/rev ..

Align seg 1/1 to reverse of: AW627667 from: 1 to: 466

6 TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl 22
|||||
466 TATTGCTTCAGCTCCACGGAGAAGAACTGTTGCGTGGCGAGCTGTACAT 417

22 eAspPheArgGlnAspLeuGlyTyrLysTyrValHisGluProLysGlyT 39
|||||
416 TGACTCCGCAAGGACTTCGGTTGGAGTGGATCCACGAGGCCAAGGGCT 367

39 yrTyAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp 55
|||||
366 ACCATGCCAACTTTGCTCGGGCCCTGCCCTACATTTGGAGCCTGGAC 317

56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl 72
|||||
316 ACGCAGTACAGCAAGGTCTTGGCCCTGTACAACACGACATAACCCGGCGC 267

72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL 89
|||||
266 CTCGGCGCGCGCTGCTCGCGTGGCGAGCGCTGGAGCGCTGCCCATCG 217

89 euTyTyTyValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
:::|||||
216 TGTACTACGTGGCGCCCAAGCCCAAGGTGGAGTGGACGCTGTCCAATGATC 167

106 ValLysSerCysLysCysSer 112
|||||
166 GTGGCTCTCTGCAAGTGCAGC 146

seq_name: gb_est97:BG180040
seq_documentation_block:
LOCUS BG180040 431 bp mRNA EST 06-FEB-2001
DEFINITION 602329596F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431214 5',
mRNA sequence.

ACCESSION BG180040
VERSION BG180040.1 GI:12686743
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 431)
NTH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: o column: 23
High quality sequence stop: 338.
Location/Qualifiers
1. 431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431214"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 95 a 126 c 148 g 62 t
ORIGIN

alignment_scores:
Quality: 468.00 Length: 106
Ratio: 5.087 Gaps: 0
Percent Similarity: 86.792 Percent Identity: 75.472

alignment_block:
TGFB3P x BG180040 ..
Align seg 1/1 to: BG180040 from: 1 to: 431

7 CysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAs 23
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
17 TGCTTACGCTCCAGGAGAGAACTGCTGCGGAGCTGTATATGA 66
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
23 pPheArgGluAspLeuGlyTrpLysTrpValHisGluProLysGlyTyr 40
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
67 CTTCCGCAAGGACCTCGCTGGAAGTGGATCCAGCCGAGGCTACC 116
40 YrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThr 56
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
117 ATGCCAACTTCTGCTCGGCCCTGCCCTACATTTGGAGCTGGACAG 166
57 ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSe 73
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
167 CAGTACAGCAAGGCTCTGGCCCTGTACAAACCAGCATAAACCGGCGCTC 216
73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
217 GGGCGCGCGCTGCTGCGCGCGAGCGCTGGAGCGCTGCCCATCGTGT 266
90 YrTrpValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
267 ACTACGTGGGCGGCAAGCCCAAGGTGGAGGAGCGCTGTCCACATGATCGT 316
107 LysSerCysLysCysSer 112
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
317 CGCTCCTGCAAGTGCAGC 334

seq_name: gb_est26-AI927187
```

```

seq_documentation_block:
LOCUS AI927187 578 bp mRNA EST 08-MAR-2000
DEFINITION wo86c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462402 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
sequence.
ACCESSION AI927187
VERSION AI927187.1 GI:5663151
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1358 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.
Location/Qualifiers
1. 578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2462402"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT 127 a 166 c 175 g 105 t 5 others
ORIGIN

alignment_scores:
Quality: 463.00 Length: 112
Ratio: 4.874 Gaps: 0
Percent Similarity: 84.821 Percent Identity: 72.321

alignment_block:
TGFB3P x AI927187/rev ..
Align seg 1/1 to reverse of: AI927187 from: 1 to: 578

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
475 GCTTTGGATACATACTATTGNTTACCTCTATGGAGAGAANAATGCTGT 426
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
425 GTGGCAGCTGTACATTGACTTCGCAAGGACTTTGGTGAAGTGGATCC 376
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
375 ACGAGCCCAAGGGCTACCATGCCAACTTTTGGCTGGGCGCTGCCCTAC 326
```

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyraSnTh 67
 :: ||| ||||| ::||| |||||::||| |||||
 325 ATTGGAGCGCTGACGACGACGAGTACAGCAAGGTCTGGCCCTGTACAAACCA 276
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGluAspLeuG 84
 ||||| |||||::|||::||| ||||| ||||| |||||
 275 GCATAACCCGGCGCGCTGGCGCGCGGTGNTGCGTCCGACAGGGGCTGG 226
 84 luProLeuThrIleLeuTyTyTyValGlyArgThrProLysValGluGln 100
 ||||| |||||::|||::||| ||||| ||||| ||||| |||||
 225 AGCGCTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 176
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 ||||| |||||::|||::||| ||||| ||||| ||||| |||||
 175 CTGTCCAACATGATGTCGGCTCTCTGCAAGTGCAGC 140

seq_name: gb_est20:AI430179

seq_documentation_block:
 LOCUS AI430179 317 bp mRNA EST 15-MAR-2000
 DEFINITION me44c04.y1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
 clone IMAGE:390342.5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); gb:N32745 mouse transforming
 growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
 ACCESSION AI430179
 VERSION AI430179.1 GI:4276015
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 317)
 REFERENCE Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Willson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 CONTACT Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 MGI:242174
 Seq primer: -40RP from Gibco
 High quality sequence stop: 306
 POLYA=No.

FEATURES

source
 1..317
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:390342"
 /clone_lib="Soares mouse embryo NBME13.5 14.5"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer 15'
 TGTTCACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M.Patima Bonaldo.

BASE COUNT 65 a 98 c 89 g 65 t
 ORIGIN

alignment_scores:
 Quality: 451.00 Length: 99
 Ratio: 5.184 Gaps: 0
 Percent Similarity: 87.879 Percent Identity: 78.788

alignment_block:
 TGFB3P x AI430179 ..

Align seg 1/1 to: AI430179 from: 1 to: 317

14 AsnCysCysValAlaTgProLeuTyTyTyIleAspPheArgGlnAspLeuGlyTr 30
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 6 AACGTCTGTGTGGCGGACCTGTACATTGACTTTAGGAGGACCTGGGTG 55
 30 pLysTrpValHisGluProLysGlyTyTyTyAlaAsnPheCysSerGlyp 47
 |||||::|||::||| ||||| ||||| ||||| ||||| ||||| |||||
 56 GAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGAC 105
 47 roCysProTyTyLeuArgSerAlaAspThrHisSerThrValLeuGly 63
 ||||| |||||::||| ||||| ||||| ||||| ||||| ||||| |||||
 106 CTGCCCCCTATATTGGAGCCTGGACACACAGTACAGCAAGGTCTCTGCC 155
 64 LeuTyraSnThrLeuAsnProGluAlaSerAlaSerProCysCysValPr 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 156 CTCACAAACCAACCAACCCGGCGCTTCGGCGTCCCGTCTCGGTGCC 205
 80 oGlnAspLeuGluProLeuThrIleLeuTyTyTyValGlyArgThrProL 97
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 206 GCAGGCTTTGGAGGCACATGCCCATGCTCTACTACGTGGTGCACAGCCCA 255
 97 ysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 256 AGGTGGAGCAGTTGTCCAAACATGATTGTGGCTCTCTGCAAGTGCAGC 302

seq_name: gb_est20:AI433146

seq_documentation_block:

LOCUS AI433146 505 bp mRNA EST 30-MAR-1999
 DEFINITION ti32a11.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132156 3'
 similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
 sequence.
 ACCESSION AI433146
 VERSION AI433146.1 GI:4287132
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 505)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 2004 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 376.

FEATURES

Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2132156"
 /clone_lib="NCI_CGAP_Gas4"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_host="DH10B"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.69 kb. Life Technologies catalog #:
 11549-011"

BASE COUNT 76 a 147 c 187 g 95 t
 ORIGIN

alignment_scores:

Quality: 448.00 Length: 101
 Ratio: 5.091 Gaps: 0
 Percent Similarity: 87.129 Percent Identity: 76.238

alignment_block:

TGFB3P x A1433146/rev ..

Align seg 1/1 to reverse of: A1433146 from: 1 to: 505

```

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
447 GAGAGAACTGCTGCGCGCAGCTGTACATTGACTTCGCGAAGACCT 398
|||||
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||
397 CGCTGGAGTGGATGACAGCCAGCCAGGCTACCATGCCAATCTCTGCC 348
|||||
45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||
347 TCGGGCCCTGCCCTTACATTTGGAGCCTGGACACGCAGTACAGCAAGTC 298
|||||
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||
297 CTGGCCCTGTACAACACGACATAACCGCGCGCTCGCGGCGCGCTGCTG 248
|||||
78 sValProGlnAspLeuGluProLeuThrIleLeuTyrValGlyArgT 95
|||||
247 CGTGGCGGCGCGCTGGAGCGCGCTGCCCTCGTGTACTGCGGCGCGCA 198
|||||
95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
|||||
197 AGCCCAAGTGGAGCAGCTGTCCACATGATGTCGTCGCTCTGCAAGTGC 148
|||||
112 Ser 112
|||
147 AGC 145

```

seq_name: gb_est30:AU016729

seq_documentation_block:

LOCUS AU016729 576 bp mRNA EST 15-OCT-1998
 DEFINITION AU016729 Mouse two-cell stage embryo cDNA Mus musculus CDNA clone
 J0728H08 3', mRNA sequence.
 ACCESSION AU016729
 VERSION AU016729.1 GI:3371733
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 576)
 AUTHORS Ko,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E.,

TITLE Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
 Systematic analyses of genes expressed in 2-cell stage mouse
 embryos (The ERATO/Doi Project at Wayne State University) (Ko
 ,M.S.H. et al.)
 JOURNAL Unpublished (1998)
 COMMENT Contact: Hirofumi Doi
 Doi Bioasymmetry Project, ERATO
 Japan Science and Technology Corporation (JST)
 WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
 Email: hdbioa.jst.go.jp.

FEATURES

Location/Qualifiers
 1..576
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="J0728H08"
 /clone_lib="Mouse two-cell stage embryo cDNA"
 /dev_stage="two-cell stage embryo"
 BASE COUNT 144 a 123 c 134 g 164 t 11 others
 ORIGIN

alignment_scores:

Quality: 447.00 Length: 114
 Ratio: 4.298 Gaps: 2
 Percent Similarity: 91.228 Percent Identity: 76.316

alignment_block:

TGFB3P x AU016729/rev ..

Align seg 1/1 to reverse of: AU016729 from: 1 to: 576

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlu.AspCysCysV 17
|||||
452 GCTTGGATGCTGCCTACTGCTTTAGAAATGTCAGGAATAATGCTGCC 403
|||||
17 alArgProLeuTyrIleAsp.PheArgGlnAspLeuGlyTrpLysTrpVa 33
|||||
402 TTTCGCCCTTTTACATTGAATTTTAAAGAGGATCTTGGATGGAATGAT 353
|||||
33 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProt 50
|||||
352 CCATGAACCCAA.GGGTACATGCTTAACCTTCTGTGCTGGGNGATGCCAT 304
|||||
50 YrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsn 66
|||||
303 ATCTATGGAGTTCAGACACTCAACACACCAAGCTCTCAGCCTGTACAAC 254
|||||
67 ThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLe 83
|||||
253 ACCATAAATCCGGAAT.TCCGCTTCCCTTGTGCTGTGTGCCAGGATCT 205
|||||
83 uGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG 100
|||||
204 GGAACTGCTGACCATCTCTATTACATTGGAATAGCCCAAGATCGAAC 155
|||||
100 InLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
154 ACCTTTCCTCAATATGATGTCAAGTCTTGTAAATGCAGC 117

```

seq_name: gb_est10:AA657145

seq_documentation_block:

LOCUS AA657145 530 bp mRNA EST 04-NOV-1997
 DEFINITION vr26d03.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
 IMAGE:1121765 5', similar to gb:J03241 TRANSFORMING GROWTH FACTOR
 BETA 3 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth
 factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
 ACCESSION AA657145
 VERSION AA657145.1 GI:2593299
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1168)

AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saunin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1168)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source Location/Qualifiers

1. 1168

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="066G06"

/clone.lib="c"

/note="Genoscope sequence ID : COBG066BD03LP1-end : T7"

BASE COUNT 308 a 300 c 299 g 258 t 3 others

ORIGIN

alignment_scores:

Quality: 433.00 Length: 135

Ratio: 4.656 Gaps: 3

Percent Similarity: 68.889 Percent Identity: 60.741

alignment_block:

TGFB3P x CNS03XHH/rev ..

Align seg 1/1 to reverse of: CNS03XHH from: 1 to: 1168

12 GluGluAsnCysValArgProLeuTyrIleAspPheArgGlnAspLe 28

1100 CAGGACAACTGCTGCTGGGTGCTCATACATCGACTTCAGGAGGACCT 1051

28 uGlyTrpLysTrpVal.HisGluProLysGlyTyrTyrAla.AsnPheCy 44

1050 GGGCTGGAGGTGGATCCCATGAGCCGAGGCTACGAGGCCCACTCTG 1001

44 sSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisSer.... 59

1000 CGCTGGGGCTGTCCGTACCTGTGTGAGCGCGACACCCAGCATTCCAAGG 951

59

950 TACCGATGAAGGCTGGGACCCAGCGGTTGGCTCGAGTCTCTGTGGGC 901

60

900 TTCTGGGCTTTCTGGACTCTGTCTGCTGACCGTTCTCATCTTCAGGTGT 851

62 uGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysV 79

850 GGGTTTGTACAAACACATCAACCCGGAAGCTGACGCTCGCTTCTGTG 801

79 alProGluAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThr 95

800 TCTCCAGGACCTGGAGCGCTCTCACATCCCTCTACTATACGCGCAAGACG 751

96 ProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSe 112

750 CCCAAATTGACAGCTTTCACACATGAAGGTCAAGTCTCTGCAAGTGCAG 701

112 r 112

700 c 700

seq_name: gb_est103:C86879

seq_documentation_block:

LOCUS C86879 583 bp mRNA EST 11-MAR-1998

DEFINITION C86879 Mouse fertilized one-cell-embryo CDNA Mus musculus CDNA clone J0235C05 3', mRNA sequence.

ACCESSION C86879

VERSION C86879.1 GI:2918836

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 583)

AUTHORS Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., Delalma,G.E., Liang,Y., Kaigul,G.J., Sharara,R., Paonessa,P.D. and Doi,H.

TITLE Systematic analyses of genes expressed in fertilized mouse eggs(The ERATO/Doi Project at Wayne State University)

JOURNAL Unpublished (1998)

COMMENT Contact: Hirofumi Doi

Doi Bioasymmetry Project, ERATO

Japan Science and Technology Corporation (JST)

WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan

Email: hd@bioa.jst.go.jp.

FEATURES

Location/Qualifiers

1. 583

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="J0235C05"

/clone.lib="Mouse fertilized one-cell-embryo cdna"

/dev_stage="fertilized one-cell-embryo"

BASE COUNT 142 a 124 c 134 g 166 t 17 others

ORIGIN

alignment_scores:

Quality: 432.00 Length: 113

Ratio: 4.454 Gaps: 2

Percent Similarity: 85.841 Percent Identity: 74.336

alignment_block:

TGFB3P x C86879/rev ..

Align seg 1/1 to reverse of: C86879 from: 1 to: 583

2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCys.Vala 18

450 TTGGATGCTGCCTACTGCTTTAGAAAGTNCAGGTATATGTCGCCCTTC 401

18 rgProLeuTyrIleAspPhe.ArgGlnAspLeuGlyTrpLysTrpValHI 34

400 GCNCTCTTTACATTGATTTTAAAGAGGANTCTTGGATGGAAATGGATCCA 351

34 sGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrL 51

350 TGAACCCCAA.GGGTACAATGCTNACTTCTGTCTGGGGCATGCCCATATC 302

51 euArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThr 67

301 TTGGAGTTTCAGACACTCAACACNAAAGTCTCAGCTGTACAAACACN 252

68 LeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

251 NTNAATCCGAAGCTTCGCTTCCCTTGTGTGTGTGTGTGTGTGTGTGTGA 202

84 uProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnL 101

201 ACCACTGACCATCTNTATTACATTGGAATACGCCCAAGATCGAAGACG 152

```

101 euSerAsnMetValLysSerCysLysCysSer 112
|||||
151 TTTCCAATATGATTCGAAGTCTGTGTAATGCAGC 117

seq_name: gb_est91-BF682484

seq_documentation_block:
LOCUS BF682484 996 bp mRNA EST 21-DEC-2000
DEFINITION 602117568r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 3', mRNA sequence.
ACCESSION BF682484
VERSION BF682484.1 GI:11956379
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nlm.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8476 row: h column: 18
High quality sequence start: 37
High quality sequence stop: 636.
High quality sequence stop: 636.
Location/Qualifiers
1..996
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3468737"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT7T3Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 239 a 243 c 317 g 197 t
ORIGIN

alignment_scores:
Quality: 428.50 Length: 114
Ratio: 4.559 Gaps: 4
Percent Similarity: 82.456 Percent Identity: 72.807

alignment_block:
TGFB3P x BF682484/rev ..

Align seg 1/1 to reverse of: BF682484 from: 1 to: 996

2 LeuAspThrAsnTrpCysPheArgAsnLeuGluGluAsnCys.CysVala 18
|||||
434 CTGATACCTACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTC 385
|||||

18 rgProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValHis 34
||
384 GGCAGCTGTACATTGACTTTAGGAAGACCTGGGTTGGAAGTGGATCCAC 335
|||||

35 GluProLysGlyTyTrpTyrlleAlaAsnPheCysSerGly.ProCysProTyrl 51

```

```

|||||
334 GAGCCCAAGGGCTACCATGCCAACTTCTGCTGGACCCCTGCCCTATA 285
|||||
51 euArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrlleAsnThr 67
:: ||| ||||| ::||| |||||::|||
284 TTTGGAGCCTGGACACACAGTACAGCAAGGCTCTTGGCCCTT...CCCCCA 238
|||||
68 Leu.AspProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
237 ACACAACCCGGCGCTTCGGCGTCAACCGTGTGCGTGGCGGAGGCTTGG 188
|||||
84 luProLeuThrIleLeuTyrlleValGlyArgThrProLysValGluGln 100
|||||
187 AGCCACTGCCCATCGCTACTACGTGGGTGCGCAAGCCCAAGGTGGAGCAG 138
|||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
137 TTGTCCAACATGATGTGCGCTCCTGCAAGTGCAGC 102

seq_name: gb_est25:AI824845

seq_documentation_block:
LOCUS AI824845 441 bp mRNA EST 16-DEC-1999
DEFINITION wb02f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304505 3'
similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element TAR1 MER22 repetitive element ;,
mRNA sequence.
ACCESSION AI824845
VERSION AI824845.1 GI:5445516
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 441)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nlm.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 347.
Location/Qualifiers
1..441
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2304505"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3Pac (Pharmacia) with a modified
polylinker; plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 66 a 129 c 165 g 81 t
ORIGIN

```

```

alignment_scores:
  Quality: 426.00      Length: 97
  Ratio: 5.071         Gaps: 0
  Percent Similarity: 86.598  Percent Identity: 76.289

alignment_block:
  TGF3P x AI824845/rev ..

Align seg 1/1 to reverse of: AI824845 from: 1 to: 441

16 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleAsp 32
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
439 TCGTGGCGGACGCTGATGACCTCCGGAAGGACCTCGGCTGGAAGTG 390
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

32 pValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysP 49
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
389 GATCCACGAGCCCAAGGCTACCACTGCACTCTGCTCGGGCCCTGCC 340
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

49 roTyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyr 65
|||||  |||  |||||  |||||  |||||  |||||  |||||  |||||
339 CCTACATTTGGAGCTGGACAGCGCAGTACAGCAAGGCTCTGGCCCTGTAC 290
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

66 AsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAs 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
289 AACCAAGATACCCGGCGCTCGCGCGCGCTGCTGCTGCCGACAGGC 240
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

82 pLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValG 99
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
239 GCTGAGCGGCTGCCATCGTGCTACTAGTGGCGCGCAAGCCAGGTGG 190
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

99 LuGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
189 AGCAGCTGTCAACATGATCGTGGCTCTCTGCAAGTGCAGC 149
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

```

```
seq_name: gb_est23:AI654506
```

```

seq_documentation_block:
LOCUS   AI654506      460 bp      mRNA      EST      17-DEC-1999
DEFINITION   wb63404.x1 NCI-CGAP_G66 Homo sapiens cDNA clone IMAGE:2310343 3'
              similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
              PRECURSOR (HUMAN); contains PTRS.t3 PTR5 MSRI repetitive element ;
              mRNA sequence.
ACCESSION   AI654506
VERSION     AI654506.1  GI:4738485
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
             Email: cgaps@mail.nih.gov
             Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
             R. Emmert-Buck, M.D., Ph.D.
             CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
             CDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Insert Length: 519 Std Error: 0.00
             Seq primer: -400P from Gibco
             High quality sequence stop: 206.
FEATURES
             Location/Qualifiers
             1..460
                /organism="Homo sapiens"
                /db_xref="taxon:9606"

```

```

/clone="IMAGE:2310343"
/clone_lib="NCI-CGAP_G66"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI-CGAP_G64 was prepared, and ss circles were made in
vitro. Following RAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      68 a 131 c 166 g 93 t 2 others
ORIGIN

```

```

alignment_scores:
  Quality: 426.00      Length: 101
  Ratio: 4.953         Gaps: 0
  Percent Similarity: 85.149  Percent Identity: 74.257

alignment_block:
  TGF3P x AI654506/rev ..

Align seg 1/1 to reverse of: AI654506 from: 1 to: 460

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
458 GAAAGAAGTGTGCTGGTGGCGGAGCTGTACATGCTCCGCAAGGACCT 409
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

28 uGlyTyrLysTyrValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
408 CGGCTGGAAGTGGATCCCGGAGCCCAAGGCTACCATGCCAATTNTGCC 359
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
358 TCGGGCCCTGCCCTACATTTGGAGCCTGGCAGCAGCTACAGCAAGGTC 309
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
308 CTGGCCCTGTACACAGCATACCCGGCGCCTCGGCGCGCGGTGNTG 259
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArg 95
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
258 CGTGGCGGAGGCGCTGGAACCGCTGCCCATTTGTACTAGTGGCGCGCA 209
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
208 AGCCCAAGTGGAGCAGCTGTCCAACATGATCGTGGCTCTCTGCAAGTGC 159
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
112 Ser 112
158 AGC 156

```

```
seq_name: gb_est1:AA049522
```

```

seq_documentation_block:
LOCUS   AA049522      477 bp      mRNA      EST      09-SEP-1996
DEFINITION   mj35f01.r1 Soares mouse embryo NM013.5 14.5 Mus musculus CDNA
              clone IMAGE:478105 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
              FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
              growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION   AA049522
VERSION     AA049522.1  GI:1529194
KEYWORDS    EST.
SOURCE      house musculus
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 477)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

```



```

/db_xref="taxon:9606"
/clone="IMAGE:1912354"
/clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      66 a 128 c 163 g      92 t
ORIGIN

```

```

alignment_scores:
  Quality: 416.00      Length: 93
  Ratio: 5.073        Gaps: 0
  Percent Similarity: 88.172  Percent Identity: 77.419

alignment_block:
TGFB3P x AI304490/rev ..

```

Align seg 1/1 to reverse of: AI304490 from: 1 to: 449

```

20 LeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluPr 36
|||||
444 CTGTACATTGACTCGCAAGACCTCGGCTGGAAAGTGGATCCACGAGCC 395
|||||
36 oLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyrLeuArgS 53
|||||
394 CAAGGGCTACCATGCGCAACTTTTGCTCGGGCCCTGCCCTACATTGGA 345
|||||
53 erAlaAspThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsn 69
|||||
344 GCCTGGACACGCGAGTACAGCAAGTCTGGCCCTGTACACACGACATAC 295
|||||
70 ProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLe 86
|||||
294 CCGGGCGCTCGGCGCGCGTCTGCTGCGCGCGCGCGTGGAGCGGCT 245
|||||
86 uThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSera 103
|||||
244 GCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGTGGAGCGAGCTGTCCA 195
|||||
103 snMetValValLysSerCysLysCysSer 112
|||||
194 ACATGATCGTGGCTCTCTGCAAGTGCAGC 166
|||||

```

seq_name: gb_est17:AI192407

```

seq_documentation_block: 348 bp mRNA EST 28-OCT-1998
LOCUS AI192407
DEFINITION qc98c09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:1722256 3', similar to gb:Y00083 TRANSFORMING GROWTH FACTOR
BETA 2 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI192407
VERSION AI192407.1 GI:3743616
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the

```

```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 157.
FEATURES
  source
    1..348
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:1722256"
    /clone_lib="Soares_pregnant_uterus_NbHPU"
    /sex="female"
    /dev_stage="adult"
    /lab_host="DH10B"
    /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
    Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
    oligo(dT) primer [5',
    AACTGGAAGAAATTCGGCGCCCTTTTTTTTTTTTTTTTTTTT 3'],
    double-stranded cDNA was ligated to Eco RI adaptors
    (Pharmacia), digested with Not I and cloned into the Not I
    and Eco RI sites of the modified pT7T3 vector. Library
    went through one round of normalization. Library
    constructed by M. Fatima Bonaldo."
BASE COUNT      91 a 78 c 85 g      93 t      1 others
ORIGIN

```

```

alignment_scores:
  Quality: 414.00      Length: 88
  Ratio: 5.111        Gaps: 0
  Percent Similarity: 92.045  Percent Identity: 78.409

```

alignment_block:
TGFB3P x AI192407/rev ..

Align seg 1/1 to reverse of: AI192407 from: 1 to: 348

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
265 GCTTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTCGTGCTT 216
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
215 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGTGGAAATGGATAC 166
|||||
34 isGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyr 50
|||||
165 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCGTAT 116
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
115 TTATGGAGTTTCAGACACTCAGCACAGAGGGTCTCGAGCTTATATAATAC 66
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
65 CATAAATCCAGAGCATCTGCTTCTCCTTCGTGCGTCCCAAGATTAG 16
|||||
84 luProLeuThrIle 88
|||||
15 AACCTCTAACCAT 2

```

seq_name: gb_est20:AI421250

```

seq_documentation_block:
LOCUS AI421250 540 bp mRNA EST 28-MAR-1999
DEFINITION tf1402.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2096163 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AI421250
VERSION AI421250.1 GI:4267181
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```



```

41 laasnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThr 57
|||||
159 CCAACTTCTGTGAGCATGCCGCTATTATGAGTTCCAGACACTCAG 110
|||||
58 HisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAl 74
|||||
109 CACAGCAGGCTCTGAGCTTATATATACATAAATCCAGAAGCATCTGC 60
|||||
74 aSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr 91
|||||
59 TTTCTCTGCTGCTGCTCCAGATTAGAACCTCTAACCAATCTCTATT 10
|||||
91 yrVal 92
|||||
9 ACATC 5

seq_name: gb_est29:AL530080

seq_documentation_block:
LOCUS AL530080 798 bp mRNA EST 13-FEB-2001
DEFINITION AL530080 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YM06 3
prime, mRNA sequence.
ACCESSION AL530080
VERSION AL530080.1 GI:12793573
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 142 a 228 c 274 g 145 t 9 others
ORIGIN

alignment_scores:
Quality: 400.50 Length: 110
Ratio: 4.500 Gaps: 1
Percent Similarity: 80.909 Percent Identity: 66.364

alignment_block:
TGPB3P x AL530080/rev ..

Align seg 1/1 to reverse of: AL530080 from: 1 to: 798

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

```

```

402 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCT 353
17 larProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIysTrpValH 34
|||||
352 GCGCAGCTGTACATTAACCTCCGCAAGACCTCGCTGGGAGTGGATCC 303
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
302 ACAGAGCCCAAGGGCTWCCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 253
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ||| |||||::: |||||
252 ATTTGGAGCCTGGACACAGGACAGCAAGGTCTCGCCCTGTACAACA 203
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
202 GCATAACCCGGGCTCGCGGGGCC...GTGCGCGTGGCGAGCGCTGG 156
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
155 AGCGCTGCCCTTCGTGTACTACGTGGCGCCGCAAGCCCAAGGTGGGCG 106
|||||
101 LeuSerAsnMetValValLysSerCysLys 110
|||||
105 CTGTCCAAACATGGTGTGCTCTCTGCAAG 76

seq_name: gb_est49:AW600938

seq_documentation_block:
LOCUS AW600938 267 bp mRNA EST 23-MAR-2000
DEFINITION RC1-BN0014-210100-012-c03_1 BN0014 Homo sapiens cDNA, mRNA
sequence.
ACCESSION AW600938
VERSION AW600938.1 GI:7305677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
210100-012-c03_1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 257.
Location/Qualifiers
1..267
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/notes="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 69 a 52 c 62 g 84 t
ORIGIN

```

```

alignment_scores:
  Quality: 400.00      Length: 86
  Ratio: 5.063         Gaps: 0
  Percent Similarity: 91.860  Percent Identity: 80.233

alignment_block:
  TGF3P x AW600938/rev ..

Align seg 1/1 to reverse of: AW600938 from: 1 to: 267

27 AspLeuGlyTyrLysTrpValHisGluProLysGlyTyrTyrAlaAsnPh 43
265 GATCTAGGTTGAAATGATACCAACCAAGGTTACATGCCAATTT 216
43 ecysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisserT 60
215 CTGTCTGGAGCATGCCGCTATTTATGAGTTCACACACTCAGCACAGCA 166
60 hrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPro 76
165 GGGTCTGAGCTTATATATACCAATAATCCAGAAATCCAGAGCATCTGCTACTCT 116
77 CysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValCl 93
115 TGCTCGGTGCCAGATTAGAACTTAAACCTTAAACCTTCTACTATGG 66
93 YargThrProLysGluValGluGlnLeuSerAsnMetValValLysSerCysL 110
65 CAACACACCAAGATTGACACGCTTCTAATATGATTGTAAGTCTTGCA 16

110 yscysSer 112
115 AATGAGCAGC 8

seq_name: gb_est1:AA021815

seq_documentation_block:
LOCUS      AA021815      558 bp      mRNA      21-JAN-1997
DEFINITION  mh85d06.r1 Soares mouse placenta 4NbMpl3.5 14.5 Mus musculus CDNA
            clone IMAGE:457739 5', similar to gb:X02812.cdsl TRANSFORMING GROWTH
            FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
            growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION  AA021815
VERSION    AA021815.1 GI:1485570
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 558)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:274627
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 454.
Location/Qualifiers
1..558
            /organism="Mus musculus"

FEATURES
source

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457739"
/clone_lib="Soares mouse placenta 4NbMpl3.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      130 a      172 c      150 g      105 t      1 others
ORIGIN

alignment_scores:
  Quality: 399.50      Length: 103
  Ratio: 4.540         Gaps: 2
  Percent Similarity: 85.437  Percent Identity: 74.757

alignment_block:
  TGF3P x AA021815 ..

Align seg 1/1 to: AA021815 from: 1 to: 558

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
222 GCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGT 271
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
272 GCGGCAGTNGTACATTGACTTTAGGAAGGACCTGGGTGGAGTGGATCC 321
34 isGluProLysGlyTyrTyrAlaAsnPhCysSerGlyProCysProTyr 50
322 ACGAGCCCAAGGCTACCATGCCAATCTCTGTGGGACCCCTGCCCTAT 371
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
372 ATTTGGAGCTGGACACACAGTACAGCAAGGCTCTTCCCTCTACACCA 421
67 rLeuAsnProGluAlaSerAlaSerProCysCysValPro.GlnAspLeu 83
422 ACACAAACCCGGCGCTTCGGCGTCCACCGTGGTGGCGGACGT...TTG 468
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
469 GAGCCACTGCCCATCTCTACTACTGCTGGTGGTGGTGGTGGTGGTGG 517
100 nLeuSer 102
518 GTTGTC 524

seq_name: gb_est111:W98872

seq_documentation_block:
LOCUS      W98872      431 bp      mRNA      16-JUL-1996
DEFINITION  mf89e01.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA
            clone IMAGE:421464 5', similar to gb:X02812.cdsl TRANSFORMING GROWTH
            FACTOR BETA 1 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  W98872
VERSION    W98872.1 GI:1428996
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:256016
Seq primer: ETPprimer
High quality sequence stop: 1.
Location/Qualifiers
1..431
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:421464"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: pPT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      91 a 138 c 117 g 85 t
ORIGIN

alignment_scores
Quality: 395.00 Length: 107
Ratio: 4.438 Gaps: 0
Percent Smilarity: 83.178 Percent Identity: 71.028

alignment_block:
TGFB3P x W98872
..
Align seg 1/1 to: W98872 from: 1 to: 431
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
98 GCCTGGATACCAACATATGCTTCACCTCCACAGAGAAGACTGCTGTG 147
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
148 GCGGCAGTGCTACATTGACTTTAGGAAGGACCTGGCTTGAAGTGGATCC 197
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
198 ACAGGCCCAAGGCTACCATGCCAACTTCTGTCTGGGACCCCTCCCTAT 247
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::| |||||:|||||

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```

248 ATTGTGGAGCCCTGGACACACAGTACAGCAAGGTCTTGGCCCTCTACAACA 297
67 rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||||| ||||||| ||||||| ||||||| |||||||
298 ACACAACCCGGCGCTTCGGGTCTACCGTGTGCTGCGCGCAGTT.TGGG 346
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:
347 AGCCACTGGTCTATGCTACTACGTGGGAGCAAGCCCGAGTTGTG.CAG 395
101 LeuSerAsnMetValValLys 107
||||| ||||||| |||:::
396 TTGTCCACATGATGTCGC 416
seq_name: gb_est103:C87366

seq_documentation_block:
LOCUS      C87366      587 bp      mRNA      EST      11-MAR-1998
DEFINITION C87366 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA
clone J0244G10 3', mRNA sequence.
ACCESSION C87366
VERSION   C87366.1 GI:2919323
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 587)
AUTHORS   Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
Doi,H.
TITLE      Systematic analyses of genes expressed in fertilized mouse eggs(The
ERATO/Doi Project at Wayne State University)
JOURNAL    Unpublished (1998)
COMMENT    Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WEG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bio.jst.go.jp.
FEATURES
source
1..587
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0244G10"
/clone_lib="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
BASE COUNT      147 a 128 c 140 g 166 t 6 others
ORIGIN

alignment_scores
Quality: 393.00 Length: 110
Ratio: 4.052 Gaps: 3
Percent Smilarity: 88.182 Percent Identity: 71.818

alignment_block:
TGFB3P x C87366/rev ..
Align seg 1/1 to reverse of: C87366 from: 1 to: 587
6 TyrCysPheArgAsnLeuGlu.GluAsnCysCysVal.ArgProLeuTyr 21
438 TACTCGCTTTAGAAATGTGAGGATAATGCTGCTTNGCCCTCTTAC 389
22 IleAsp.PheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG 38
388 ATGGAATTTTAAGAGGNATCTGGATGGATGGATCATCAACCCAA.G 340
38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
||||| ||||||| |||:|||||
339 GGTACAATGCTAACTTCGTCTGCTGGGGCATGCCCATATCTATGGAGTTCA 290
::: ||| ||||| ::::| |||||:|||||

```

55 AspThrThrHisSerThrValLeuGlyLeuTyrrAsnThrLeuAsnProGln 71
||||| ||||| :|||:|||||:::|||||
289 GACATCAACACACAAAGTCCTCAGCGCTGTACAACACCATAAATCCGA 240
71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
_|||||:|||||:|||||:|||||:|||||:|||||:
239 ACT_TCCGGTTCCTTGCTGTGTGCCAGGATCTGGAACCACTGACCA 191
88 lLeuTyrrTyrrValglyArgThrProLysValGlnLeuSerAsnMet 104
:|||||:|||||:|||||:|||||:|||||:|||||:
190 TTTCTATTACATTGGAAATAGCCCAAGATCGAACAGCTTCCAATATG 141

105 ValValLysSerCysLysCysSer 112
:|||||:|||||:|||||:|||||:|||||:
140 ATTGTCAAAGTCTTTGAATGCAGC 117

BASE COUNT	80 a	105 c	131 g	87 t
ORIGIN	scores (university of iowa).			
alignment_scores:				
Quality:	388.00			Length: 111
Ratio:	4.409			Gaps: 0

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Percent Similarity: 79.279 Percent Identity: 64.865

alignment_block:
TFGB3P x BG058796/rev ..

Align seg 1/1 to reverse of: BG058796 from: 1 to: 403

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysva 17
334 GGCCTGGACACCAACTAGTCTTCAGCTGCAGTAGAGAAATGATGAGT 285
17 largProLeuTyrIleaspPheArgGlnAspLeuGlyTrpLysTrpValH 34
284 TCGACAGCTGTACATTGACTTCGCAAGGACATAGTCTGGAAGTGAGATCC 235
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
234 ACGAGCCCAAGGGCTACCATGCCCAACTCTGCATCGGGCCCTGCCCTAC 185
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
184 ATTTGGAGCTGGACGCGAGTACAGCAAGGTCTGTGCCCTGATCAAGCA 135
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnaspLeuG 84
134 GCATAACCCGGGGCGCTTGGCGGCGCGTGGTGGCTTCTTCAGGTGCTGG 85
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
84 ACCCGTGGCCATGTGTACTACGTGGCCCGCAAGCCCAAGGTGGAGCAG 35
101 LeuSerAsnMetValValLysSerCysLysCys 111
34 CTGTCCAACATGATCGTGCCTCTCTGCAAGTGC 2

```

```
source
1. .339
/organism="Mus musculus"
/db_xref="taxon:10090"
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```

|||||
407 CTCGGCTGGAGTGGATCCAGAGCCCAAGGGCTACCATGCCACTCTGT 358
|||||
44 sSerGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrV 61
|||||
357 CTCGGGCCCTGCCCTTACATTTGGAGCTGGACACGAGTACAGCAAG 308
|||||
61 allLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCys 77
|||||
307 TCCTGGCCCTGTACACACAGCATAAACCGGGCGCTCGCGCGCGCTGC 258
|||||
78 CysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyAr 94
|||||
257 TGCCTGCCGACGAGCGCTGGAGCGCTGCCATCGTACTACGTGGGCG 208
|||||
94 gThrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysC 111
|||||
207 CAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGGCTCTCTGCAAGT 158
|||||
111 ysSer 112
|||||
157 GCAGC 153

```

seq_name: gb_est1:AA016742

seq_documentation_block: 553 bp mRNA EST 21-JAN-1997
 LOCUS AA016742 mh39e08.r1 Soares mouse placenta 4NbMPL3.5 14.5 Mus musculus cDNA
 DEFINITION clone IMAGE:444902 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
 growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

ACCESSION AA016742

VERSION AA016742.1 GI:1479043

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:270238

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 432.

Location/Qualifiers

1..553

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:444902"

/clone_lib="Soares mouse placenta 4NbMPL3.5 14.5"

/sex="unknown"

/tissue_type="placenta"

/dev_stage="adult"

/lab_host="DH108"

/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)

1st strand cDNA was primed with a Not I - oligo(gt) primer

15'

TGTTACCAATCTGAAGTGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT
 T 3'); double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 129 a 168 c 150 g 106 t
 ORIGIN

alignment_scores:

Quality: 375.00 Length: 113

Ratio: 4.213 Gaps: 2

Percent Similarity: 78.761 Percent Identity: 65.487

alignment_block:

TGFB3P x AA016742 ..

Align seg 1/1 to: AA016742 from: 1 to: 553

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

|||||

222 GCCCTGGATACCACTATTGCTTTCAGCTCCACAGAGAACTGCTGTGT 271

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34

|||||

272 CGCGCAGCTGTACATTGACTTTAGGAAGACCTGGGTTGGAAGTGGATCC 321

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

|||||

322 ACGAGCCCAAGGGCTACCATGCACTTCTCTGGGACCTTGCCTAT 371

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67

|||||

372 ATTTGGAGCTGGACACACAGTACACAAAGTCTTGCCTCTACAACCA 421

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

|||||

422 ACACAACCGGGCGCTTGGCGCTCACCGTCTGCTGCGTGGCGG.....ACGT 455

84 luProLeuThrIleLeuTyrTyr.ValGlyArgThrProLysValGluG 100

|||||

466 TTGGAGCCACTGCCATCGTCTACTAGTGGTCCCAAGCCAGGTTCAGCA 515

100 nLeuSerAsnMetValValLysSerCysLysCysSer 112

|||||

516 GTTGTGTC.AACATGATTGTGCGCTGCTGTCAGTGCAGCT 551

seq_name: gb_est49:AW600947

seq_documentation_block: 245 bp mRNA EST 23-MAR-2000

LOCUS AW600947

DEFINITION RC1-BN0014-210100-012-e04_1 BN0014 Homo sapiens cDNA, mRNA

sequence.

ACCESSION AW600947

VERSION AW600947.1 GI:7305686

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 245)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE THE FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1st2-RC1-BN0014-210100-012-e04_1st3-2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 233.
Location/Qualifiers

FEATURES
source
1..245
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/notes="Organ: breast normal; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 67 a 43 c 62 g 73 t
ORIGIN

alignment_scores:
Quality: 374.00 Length: 79
Ratio: 5.123 Gaps: 0
Percent Similarity: 92.405 Percent Identity: 83.544
alignment_block:
TGFB3P x AW600947/rev ..

Align seg 1/1 to reverse of: AW600947 from: 1 to: 245
34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProty 50
|||||
244 CAGCAACCCAGAGGTACAAATGCCAACTTCGTGCTGGAGCATGCCGTA 195
|||||
50 rleuargSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnT 67
|||||
194 TTTATGGAGTTTCAGACACTCAGCACAGCAGGCTCTGAGCTTATATA 145
|||||
67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
|||||
144 CCTTAATCCAGAACATCTGCTCTCTCTGCTGGTGTCCCAAGATTGA 95
|||||
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG 100
|||||
94 GAACCTCTAACCATTCCTACTACATTGGCAAAACACCCAGATTGAACA 45
|||||
100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
44 GCTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 8

seq_name: gb_est30:AU016439
seq_documentation_block:
LOCUS AU016439 465 bp mRNA EST 15-OCT-1998
DEFINITION AU016439 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0725B08 3', mRNA sequence.
ACCESSION AU016439
VERSION AU016439.1 GI:3371443
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 465)
AUTHORS Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Karqul, G.J., Sharara, R. and Doi, H.
TITLE Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko, M.S.H. et al.)
JOURNAL Unpublished (1998)

COMMENT Contact: Hirofumi Doi
Doi Biosymetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bioa.jst.go.jp.

FEATURES
Location/Qualifiers
source
1..465
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="J0725B08"
/clone_lib="Mouse two-cell stage embryo cDNA"
/dev_stage="two-cell stage embryo"
BASE COUNT 123 a 97 c 112 g 127 t 6 others
ORIGIN

alignment_scores:
Quality: 364.50 Length: 104
Ratio: 4.238 Gaps: 3
Percent Similarity: 82.692 Percent Identity: 70.192

alignment_block:
TGFB3P x AU016439/rev ..
Align seg 1/1 to reverse of: AU016439 from: 1 to: 465
12 GluGluAsnCysCysValArgPro...LeuTyrIleAspPheArgGlnAs 27
::: ||||| ||| :::||||| |||||
423 CAGNATAATGTCTGNCCTTCGCCCTCTCTTTTACATTGATTTTANGGGA 374
|||||
27 pLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsn.Phe 43
|||||
373 TGTGGNATGAAATGGATCCCATGACCAAGGTCACCAATGCACTTTC 324
|||||
44 CysSerGlyProCysProTyrLeuArgSerAlaAspThrThr.HisSerT 60
::: ||||| ||||| |||||
323 TGTGCTGGGGCATGCCCATATCTATGAGGTTCAGACACTTCAACACACCA 274
|||||
60 hrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPro 76
|||||
273 AGTCTCTACGCTGTACACACCACTAATCCGNACT.TCCGCTTCCCT 225
|||||
77 CysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||
224 TGTGTGTGTCTCCAGGATCTGGAACCACTGACCATCTCTATTACATTGG 175
|||||
93 yargThrProLysValGluGlnLeuSerAsnMetValValLysSerCysL 110
::: ||||| ||||| |||||
174 AAATAGCCCAAGATCGAAGAGCTTCCAATATGATTGTCAAGTCTTGTA 125
|||||
110 yScysSer 112
|||||
124 AATGCAGC 117

seq_name: gb_est45:AW295761
seq_documentation_block:
LOCUS AW295761 409 bp mRNA EST 16-JAN-2000
DEFINITION UI-H-B11-afh-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721675 3', mRNA sequence.
ACCESSION AW295761
VERSION AW295761.1 GI:6702397
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nhl.nih.gov
The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA sequence: 102-157,
>GC-rich#Low.complexity
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers

```

1. 409
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2721675"
/lab_host="NCI_CGAP_Sub3"
/note="vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLI1, NCI_CGAP_Le12,
NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
985608-986759, 1101192-1101959, 1217928-1220615);
NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
was performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG_LIB=NCI_CGAP_Pr22
TAG_TISSUE=prostate
TAG_SEQ=AACTG"

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BASE COUNT 57 a 115 c 153 g 84 t

ORIGIN

alignment_scores:

Quality: 351.00 Length: 82
Ratio: 5.014 Gaps: 0
Percent Similarity: 85.366 Percent Identity: 74.390

alignment_block:

TGFB3P x AW295761/rev ..

Align seg 1/1 to reverse of: AW295761 from: 1 to: 409

31 LysTrpValHisGluProLysGlyTyrTyraAlaAsnPhcCysSerGlyPr 47

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

409 AAGTGGATCCAGCGCCGAAGGGCTACCATCCCAACTTCTGCTCGGGCC 360

```

47 oCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyL 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
359 CTGCCCTTACATTTGGAGCGCTGGACACGACGAGTACAGCAAGGTCTGGCCC 310
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
64 eutyAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
309 TGTAAACACGACATAAACCGCGCTCGCGCGCGCGCTGCTGCGTGGCG 260
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 GlnAspLeuGluProLeuThrThrLeuTyrTyraValGlyArgThrProly 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
259 CAGGCGCTGGAGCGCTGCCCATCGTGTACTGCTGGCGCGCGCAAGCCAA 210
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
97 sValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
209 GGTGAGCAGCGTGTCCACATGATGCTGCGCTCTGCAAGTGCAGC 164
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
seq_name: gb_est110.W70801

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seq_documentation_block:

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LOCUS W70801 301 bp mRNA EST 17-JUN-1996
DEFINITION me44c04.r1 Soares mouse embryo NbMEI3.5 14.5 Mus musculus cDNA
clone IMAGE:390342 5' similar to gb:X02812.cdsl TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION W70801
VERSION W70801.1 GI:1380934
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:242174
Seq primer: mob.REGA+ET
High quality sequence stop: 289.

```

FEATURES

source

Location/Qualifiers

```

1. 301
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:390342"
/clone_lib="Soares mouse embryo NbMEI3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCGCGAGATTTTCTTTTCTTTTCTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of

```


FEATURES
source
Location/Qualifiers
1. .259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESPEX PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 69 a 48 c 62 g 80 t
ORIGIN
alignment_scores:
Quality: 343.50 Length: 79
Ratio: 4.838 Gaps: 1
Percent Similarity: 89.873 Percent Identity: 78.481
alignment_block:
TGFB3P x AW600942/rev ..
Align seg 1/1 to reverse of: AW600942 from: 1 to: 259
34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy 50
|||||:||||| :|||||:|||||:|||||
241 CACGACCCAAAG...GTACATCCCACTCTGTGCGAGCATGCCGTA 195
50 rLeuArgSerAlaAspThrHrHisSerThrValLeuGlyLeuTyrAsnT 67
|||||:|||||:|||||:|||||:|||||:|||||
194 TTTATGAGTTCAGACACTCAGCACACGAGTCTGTGAGCTTATATA 145
67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
|||||:|||||:|||||:|||||:|||||:|||||
144 CCATAATCCAGAGCATCTGCTCTCTGCTGCGTGTCCAGATTA 95
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG1 100
|||||:|||||:|||||:|||||:|||||:|||||
94 GAACCTCTAACCATCTCTACTACATTTGGCAAAACACCAAGATTGA 45
100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||
44 GCTTCTAATATGGTTGTAAGTCTTGCAATGCAGC 8
seq_name: gb_est106:N36741
seq_documentation_block:
LOCUS N36741 560 bp mRNA EST 16-JAN-1996
DEFINITION yx90e06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone
IMAGE:269026 5' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR
BETA 2 PRECURSOR (HUMAN);contains element OPR repetitive element ;,
mRNA sequence.
ACCESSION N36741
VERSION N36741.1 GI:1157883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
1 (bases 1 to 560)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tap,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 470
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 470.
FEATURES
source
Location/Qualifiers
1. .560
/organism="Homo sapiens"
/db_xref="GDB:3878668"
/db_xref="taxon:9606"
/clone_lib="IMAGE:269026"
/clone_lib="Soares melanocyte 2NBHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: p7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGAGTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT 195 a 102 c 107 g 154 t
ORIGIN
alignment_scores:
Quality: 341.00 Length: 74
Ratio: 5.015 Gaps: 0
Percent Similarity: 91.892 Percent Identity: 81.081
alignment_block:
TGFB3P x N36741 ..
Align seg 1/1 to: N36741 from: 1 to: 560
39 TyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAs 55
|||||:|||||:|||||:|||||:|||||:|||||
8 TACAATGCCAACTCTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGA 57
55 pThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluA 72
|||||:|||||:|||||:|||||:|||||:|||||
58 CACTCAGCACACGAGGTCCTGAGCTTATATATACCATTAATCCAGAAG 107
72 laSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIle 88
|||||:|||||:|||||:|||||:|||||:|||||
108 CATCTGCTCTCCNTGCTCGTGTGCCAAGATTAGAACCTCTTAACCAT 157
89 LeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVa 105
|||||:|||||:|||||:|||||:|||||:|||||
158 CTCTACTACATTGGCAAAACACCAAGATTGAACAGCTTTCTAATATGAT 207
105 lVallysSerCysLysCysSer 112
:|||||:|||||:|||||:|||||:|||||:|||||
208 TGTAAGTCTTGCAAAATGCAGC 229
seq_name: gb_est91:BF682938
seq_documentation_block:
LOCUS BF682938 748 bp mRNA EST 21-DEC-2000
DEFINITION 602117568F1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 5', mRNA sequence.
ACCESSION BF682938
VERSION BF682938.1 GI:11956937
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 748) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: M. Bento Soares, Ph.D. cDNA Library Preparation: Bento Soares and M. Fatima Bonaldo cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8476 row: h column: 18 High quality sequence start: 26 High quality sequence stop: 746. Location/Qualifiers 1..748 /organism="Mus musculus" /db_xref="taxon:10090" /clone_lib="IMAGE:3468737" /clone_lib="Soares_mammary_gland_NMLMG" /sex="female (lactating)" /tissue_type="mammary gland" /lab_host="DH10B" /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." BASE COUNT 189 a 220 c 189 g 150 t ORIGIN alignment_scores: Quality: 337.00 Length: 79 Ratio: 4.884 Gaps: 0 Percent Similarity: 87.342 Percent Identity: 75.949 alignment_block: TGFB3P x BF682938 .. Align seg 1/1 to: BF682938 from: 1 to: 748 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 512 GCCCTGGATACCACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGT 561 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 562 CGCGCAGCTGTACATTGACTTAGGAGACCTGGTTGGAAGTGATCC 611 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 612 ACAGACCCAGAGGGTACCATGCCAACTTCTGCTGGGACCCCTGCCCTAT 661 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 662 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCTTGCCCTCTCAACAA 711 67 rLeuAsnProGluAlaSerAlaSerProCysCysVal 79 712 CACAAACCGGGCGCTTCGGGTCACCGTGTGGGTG 747 seq_name: gb_est8:AA533093 seq_documentation_block: 542 bp mRNA EST 21-AUG-1997 LOCUS AA533093

DEFINITION nj19q04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:992982 3' similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ; mRNA sequence. ACCESSION AA533093 VERSION AA533093.1 GI:2277189 EST. KEYWORDS SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 542) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1687 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 142. Location/Qualifiers 1..542 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:992982" /clone_lib="NCI_CGAP_AA1" /tissue_type="adrenal adenoma" /lab_host="SOLR (kanamycin resistant)" /note="Organ: adrenal gland; Vector: Bluescript SK-; Site.1: EcoRI; Site.2: XhoI; Cloned unidirectionally, Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.6 kb." BASE COUNT 92 a 152 c 196 g 102 t ORIGIN alignment_scores: Quality: 395.00 Length: 115 Ratio: 3.564 Gaps: 5 Percent Similarity: 81.739 Percent Identity: 66.957 alignment_block: TGFB3P x AA533093/rev .. Align seg 1/1 to reverse of: AA533093 from: 1 to: 542 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeu.GluGluAsnCysCysV 17 473 AGCCTTGACACCACTATTGCTTCAGCTCCGCGAGAAGAA...CTGCTGG 427 17 aLArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpVal 33 426 TCGGCAGCTGTACATTGA.TTCCCGCAAGACCTCGCTGGAATTTGGATC 378 34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy 50 377 CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCCTCGGGCCTGCCCTA 328 50 rLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn. 66 327 CATTTGGAGCCTGGACACGACGTACAGCAAGGTCTCTGGCCTGTACAACC 278

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189 GCCCTGGACCAACTATTGCTTACGCTCCACGGAGAAAGAACTGCTGCGT 238

17 largProLeuTyrrilleAspPheArgGlnAspLeuGlyTrpLysnrvpValH 34
||||| ||||||| ||||||| :||| ||||||| ||||||| |||:|
239 GGGCAGCTGTACATTGACTTCCGCAAGGACCTCGCTGGAAGTGATCC 288

34 isGluProLysGlyTyrrTyrrAlaAsnPheCysSerGlyProCysProTyrr 50
||||| ||||||| ||||||| :||| ||||||| ||||||| |||:|
289 ACGAGCCCAAGGGCTACCATGTCACAACTTCTGCTCGGGCCCTGCCCTAC 338

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrrAsnTh 67
::: ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| |||
339 ATTGGAGCTGGACGACGACGATGACAGGTCCTGGCCCTGACACCA 388

67 rLeuAsnProGluAla.SerAlaSerProCysCysValProGln 81
||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| :|
389 GCATAACCCGGCGCTCGGGGG...CCGTGCTGCTGCCGAA 429

seq_name: gb_est17:A1179582

seq_documentation_block:
LOCUS A1179582 571 bp mRNA EST 20-JAN-1999
DEFINITION EST223304 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
RSPCJ23 3' end, mRNA sequence.
ACCESSION A1179582
VERSION A1179582.1 GI:3730220
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 571)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES
source
1..571
/organism="Rattus sp."
/db_xref="ATCC (inhost):2033997"
/db_xref="taxon:10118"
/clone="RSPCJ23"
/clone_lib="Normalized rat spleen, Bento Soares"
/notes="Organ: spleen; Vector: pTYT3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 144 a 111 c 121 g 195 t
ORIGIN

alignment_scores:
Quality: 331.00 Length: 72
Ratio: 4.940 Gaps: 0
Percent Similarity: 93.056 Percent Identity: 80.556

alignment_block:
TGF3P x A1179582/rev ..

Align seg 1/1 to reverse of: A1179582 from: 1 to: 571

41 AlaAsnPheCysSerGlyProCysProTyrrLeuArgSerAlaAspThrTh 57
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
569 GCTAACTCTGTGCGGCATCGCCCTATCTGTGGAGTTCAGACACACA 520

57 rHisSerThrValLeuGlyLeuTyrrAsnThrLeuAsnProGluAlaSerA 74

```



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/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      57 a 117 c 150 g 67 t 1 others
ORIGIN

```

```

alignment_scores:
  Quality: 321.00      Length: 82
  Ratio: 4.586        Gaps: 0
  Percent Similarity: 85.366      Percent Identity: 73.171

```

```
alignment_block:
```

```
TGFB3P x A1918883/rev ..
```

```
Align seg 1/1 to reverse of: A1918883 from: 1 to: 392
```

```

31  LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPr 47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
387 AAGTGGATCCACGAGCCAAAG.GGCTACCATGCCNACTTCTGCCTCGGGCC 339

47  oCysProTyrLeuArgSerAlaAspThrHisSerThrValLeuGlyL 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
338 CTGCCCCATATTGGAGCCTGGACCGCAGTACAGCAAGTCTCGGCC 289

64  eutyAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
288 TGTACACACGACATAACCGCGCGCTCGCGCGCGTCTCGGTGCGG 239

81  GlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLy 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
238 CAGCGCGTGGAGCGCTGCGCCTACTAGTCTAGTGGCGCGCAAGCCAA 189

97  svalGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 GGTGGACAGCTGTCCAACATGATGCGTGGCGCTCTCGAAGTGCAGC 143

```

```
seq_name: gb_est49:AW600960
```

```

seq_documentation_block:
LOCUS      AW600960      266 bp      mRNA      23-MAR-2000
DEFINITION RCI-BN0014-210100-012-h01_1 BN0014 Homo sapiens cDNA, mRNA
sequence.
ACCESSION  AW600960
VERSION    AW600960
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 266)
            HCGP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome

```

```

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
210100-012-h01_1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 218.

```

FEATURES

```

source
  1..286
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="BN0014"
    /dev_stage="Adult"
    /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
    Site_2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the pUC 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."
BASE COUNT      72 a 51 c 59 g 84 t
ORIGIN

```

```

alignment_scores:
  Quality: 317.50      Length: 88
  Ratio: 4.178        Gaps: 4
  Percent Similarity: 86.364      Percent Identity: 71.591

```

```
alignment_block:
```

```
TGFB3P x AW600960/rev ..
```

```
Align seg 1/1 to reverse of: AW600960 from: 1 to: 266
```

```

26  GlnAspLeuGlyTyrLysTrpValHisGluPro.LysGlyTyrTyrAlaA 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
260 GAGGATTTAGT...GAAATGATACACGAGCCAAAG...TACAATGCCAA 217

42  snPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHis 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
216 CTCGTGTC...TGGAGATGCCGCTATTATTGGAGTTCAGACACTCAGCAC 170

59  SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 AGCAGGGTCTGAGCTTATATAATACCAATAATCCAGAGCATCTGCTTC 120

75  rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrv 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 TCCTTGCTGCGTGTCCCAAGATTTAGAACCTCTAACCATTTCTTACTACA 70

92  alGlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 TTGCCAAACACCCCAAGATTGAACAGCTTCTTAATGATTGTTAAAGTCT 20

```

```
seq_name: gb_est46:AW364559
```

```

seq_documentation_block:
LOCUS      AW364559      391 bp      mRNA      04-FEB-2000
DEFINITION RCI-DT0028-131299-011-a06 DT0028 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW364559
VERSION    AW364559
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 391)
            HCGP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
            Contact: Simpson A.J.G.

```



```
391 TGATTTAAGAGGATCTGTGGAGGAATGATCCCAATAACCCAAAG...G 345
39 yrYrAlaAsnPhcCysSerGlyProCysProTyrLeuArgSerAlaAsp 55
   ::::::::::::::::::::|
344 TACAATGCTAATCTGTGTGGGCATGCCATATCTATGAGTTTCAGAC 295
   ::::::::::::::::::::|
56 ThrThr.HisSer..ThrValLeuGlyLeuTyrAsnThr.LeuAsnProGl 71
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
294 ACTCTAACACACAAAAGTCTCGCTGAGCTGTACACACCCATAAATCCGA 245
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
244 AGCTTCGCTCCCTTCGCTGTGTGTCGCCAGGATCTGGAACCACTGACCA 195
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
194 TTCTCTATTACATTGGAATACGCCCAAGATCGAACAGCTTCCAATATG 145
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
105 ValValLysSerCysLysCysSer 112
   ::::::::::::::::::::|
144 ATTGTCAAGTCTGTGTAATGCAGC 121
```

seq_name: gb_est70:BE074350

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seq_documentation_block:
LOCUS BE074350 517 bp mRNA EST 09-JUN-2000
DEFINITION QV3-BT0571-030200-078-d08 BT0571 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE074350
VERSION BE074350.1 GI:8422187
KEYWORDS EST.
SOURCE human.
```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 517)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV3-BT0571-030200-078-d08&t3=2000-02-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 516.
Location/Qualifiers

FEATURES
source 1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0571"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```
BASE COUNT 130 a 131 c 150 g 106 t
ORIGIN
alignment_scores:
Quality: 305.00 Length: 58
Ratio: 5.259 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.276
alignment_block:
TGFB3p x BE074350 ..
Align seg 1/1 to: BE074350 from: 1 to: 517
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```
55 AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl 71
   ::::::::::::::::::::|
8 AACACACCCACAGCAGCGTCTGGGACTGTACAACACTCTGAACCCGGA 57
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58 AGCATCTGCCTCGCTTCTGGTGGTCCCGAGGACCTGGAGCCCTGACCA 107
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
108 TCCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAGCTCTCCAACATG 157
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
105 ValValLysSerCysLysCysSer 112
   ::::::::::::::::::::|
158 GTGGTGAAGTCTGTGTAATGTAGC 181
```

seq_name: gb_est51:AW798167

```
seq_documentation_block:
LOCUS AW798167 379 bp mRNA EST 16-MAY-2000
DEFINITION RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW798167
VERSION AW798167.1 GI:7850141
KEYWORDS EST.
SOURCE human.
```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 379)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC3-UM0046-290200-011-a06&t3=2000-02-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 379.
Location/Qualifiers
source 1..379
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0046"

```

/dev_stage="Adult"
/notes="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      84 a 128 c 98 g 69 t
ORIGIN

alignment_scores:
  Quality: 304.00      Length: 66
  Ratio: 5.241         Gaps: 0
  Percent Similarity: 87.879 Percent Identity: 75.758

alignment_block:
  TGF3P x AW798167 ..

Align seg 1/1 to: AW798167 from: 1 to: 379

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||.....:|||||.....:|||||.....:|||||.....:
163 GCCCTGGACRCCCACTATGCTTCAGCTCCACGGAGAACTGCTGCGT 212

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||.....:|||||.....:|||||.....:|||||.....:
213 GCGGAGCTGTACATTGACTTCGCAAGGACCTCGCTGGAAGTGGATCC 262

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||.....:|||||.....:|||||.....:
263 ACGAGCCCAAGGCTACCATGCAACTTCTGCTCGGCGCTGCGCCCTAC 312

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
::: ||| ||||| :||| :||| :||| :||| :||| :||| :|||
313 AFTTGGAGCTGGACCGACGATACAGCAAGGTCTCGGCGCTGTACAAC 360

seq_name: gb_est28:AL362754

seq_documentation_block:
LOCUS      AL362754      400 bp      mRNA      EST      04-AUG-2000
DEFINITION AL362754 ICRFP 522 and 523 Mus musculus cDNA clone K9222B41 5',
mRNA sequence.
ACCESSION  AL362754
VERSION     AL362754.1 GI:9692237
KEYWORDS   EST.
SOURCE      house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 400)
AUTHORS    Eickhoff,H., Schuchardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J.,
            Malik,A., Tandon,N., Wolski,E., Rohlf,E., Nyarsik,L., Reinhardt,R.,
            Nietfeld,W. and Lehrach,H.
TITLE      Tissue gene expression analysis using arrayed normalized cDNA
            libraries
JOURNAL    Genome Res. (2000) In press
COMMENT    Contact: MPIWG
            Abt.Lehrach
            Max Planck Institut Fuer Molekulare Genetik
            Innessstrasse 73, Berlin, 14195 Germany
            The cDNA libraries ICRFP 522 and 523 were normalized with
            oligonucleotide fingerprinting, resulting in a unique subset of
            5376 cDNA clones.
            Location/Qualifiers
            source
              1..400
              /organism="Mus musculus"
              /strain="Black 6"
              /db_xref="taxon:10090"
              /clone="K9222B41"
              /clone_lib="ICRFP 522 and 523"
              /tissue_type="embryo"

/dev_stage="9 and 12 pc embryo"
BASE COUNT      108 a 105 c 91 g 96 t
ORIGIN

alignment_scores:
  Quality: 302.00      Length: 66
  Ratio: 5.033         Gaps: 0
  Percent Similarity: 90.909 Percent Identity: 72.727

alignment_block:
  TGF3P x AL362754 ..

Align seg 1/1 to: AL362754 from: 1 to: 400

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||.....:|||||.....:|||||.....:|||||.....:
202 GCTTGGATGCTGCTACTACTGCTTTAGAAATGTCAGGATAATTGCTGCCT 251

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||.....:|||||.....:|||||.....:|||||.....:
252 TCGCCCTCTTTACATTGATTTTAAGAGGGATCTTGGATGGAATGGATCC 301

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||.....:|||||.....:|||||.....:
302 ATGAACCCAAAGGTCACATGCTAACTTCTGCTGGGGCATGCCCATAT 351

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
352 CTTAGGAGTTCAGACACTCAACACACAAAGTCTCAGCCTGTACAAC 399

seq_name: gb_est20:AI452742

seq_documentation_block:
LOCUS      AI452742      396 bp      mRNA      EST      13-APR-1999
DEFINITION tJ45a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2144432 3' similar to gb:X02812 cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.t3 MSRI repetitive
element ;, mRNA sequence.
ACCESSION  AI452742
VERSION     AI452742.1 GI:4287481
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 396)
AUTHORS    NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: ccgaps-r@mail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Insert Length: 529 Std Error: 0.00
            Seq primer: -40UP from Gibco.
            Location/Qualifiers
            source
              1..396
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:2144432"
              /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
              /lab_host="DH10B"
              /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
              a modified polylinker; Site_1: Not I; Site_2: Eco RI;
              Equal amounts of plasmid DNA from five normalized
              libraries were mixed, and ss circles were made in vitro. In
              Following HAP purification, this DNA was used as tracer in
              a subtractive hybridization reaction. The driver was
              PCR-amplified cDNAs from pools of 5,000 clones made from
              the same 5 libraries. The pools consisted of the following
              libraries and cloneIDs: Soares NbHSF pool 1;

```



```
seq_name: gb_est22:AI610679
seq_documentation_block:
LOCUS      AI610679      501 bp      mRNA      EST      13-MAY-1999
DEFINITION tpf7g12 x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188102 3',
            similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN);contains PTRS.t3 PTR5 repetitive element ;, mRNA
            sequence.

```

```

60 .....Thr.ValLeuGlyLeuTyrAsnThrL 68
      |||||:::|||||||
325 AGAGAAAAGAGAGATrAArGCAGAGGTCCTGGCCCTGTACAArCAGC 276

68 euAsnProGluAlaSerAlaSerProCysValProGlnAspLeuGlu 84
      |||||
275 ATAACCGGGCGCCTCGCGCGCGCGTCTCGTGGCGCAGCGGCTGAA 226

```

Query Match 99.8%; Score 633; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 1 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 112
|||||
Db 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 112

RESULT 6

US-08-481-377-25
; Sequence 25, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:

; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA

; COUNTRY: US
; ZIP: 90067

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.377
; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/00666
; FILING DATE: 12-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WETHERELL, JR. Ph.D., JOHN R.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: FD2279 PCT

; TELEPHONE: (619) 455-5100

; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: TGF-beta 3

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..114

US-08-481-377-25

Query Match 99.8%; Score 633; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||

Db 3 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62
|||||

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 112
|||||

Db 63 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 114

RESULT 7

US-08-491-835-23

; Sequence 23, Application US/08491835
; Patent No. 5821056

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Jubas & Lubitz

; STREET: 1880 Century Park East, Suite 500

; CITY: Los Angeles

; STATE: California

; COUNTRY: US

; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/491,835

; FILING DATE: 23-OCT-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/00685

; FILING DATE: 12-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Wetherell, Jr. Ph.D., John R.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: FD3288

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 455-5100

; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: TGF-beta3

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..114

Query Match 99.8%; Score 633; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||

Db 3 ALDNTYCFRNLENCVRLYIDFRODLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62
|||||

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 112
|||||

Db 63 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVVKCKCS 114
|||||

RESULT 8

US-09-153-733A-25

; Sequence 25, Application US/09153733A
; Patent No. 6025475

; GENERAL INFORMATION:

; APPLICANT: JOHNS HOPKINS UNIVERSITY

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3

; NUMBER OF SEQUENCES: 29

NAME: Wetherell, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-09-172-062-23

Query Match 99.8%; Score 633; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 63 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 11
PCT-US94-00624-635-24
Sequence 24, Application US/08624635
Patent No. 6204047
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Cunningham No. 6204047een
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-08-624-635-24

Query Match 99.8%; Score 633; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 63 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 12
PCT-US94-00666-25
Sequence 25, Application PC/TUS9400666
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
PCT-US94-00666-25

Query Match 99.8%; Score 633; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 62
QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 13

PCT-US94-00685-23
; Sequence 23, Application PC/TUS9400685
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
PCT-US94-00685-23

Query Match 99.8%; Score 633; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 62
QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 14

US-08-581-529B-21
; Sequence 21, Application US/08581529B
; Patent No. 5770444
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin

; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,529B
; FILING DATE: 15-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
US-08-581-529B-21

Query Match 99.8%; Score 633; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
Db 4 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 63
QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 64 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 115

RESULT 15

US-08-455-559-27
; Sequence 27, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN

; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-455-559-27

Query Match 99.8%; Score 633; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHTST 60
Db 4 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHTST 63
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 64 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 115

RESULT 16
US-08-581-528A-21
Sequence 21, Application US/08581528A
Patent No. 5986058
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-JUL-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/081001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-528A-21

Query Match 99.8%; Score 633; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHTST 60
Db 4 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHTST 63
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 64 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 115

RESULT 17
US-09-097-616-21
Sequence 21, Application US/09097616
Patent No. 6090563
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-097-616-21

Query Match 99.8%; Score 633; DB 3; Length 115;

Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 4 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 63
|||||
Qy 61 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 112
|||||
Db 64 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 115
|||||

RESULT 18

US-09-145-060-27
Sequence 27, Application US/09145060
Patent No. 6245896

GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
US-09-145-060-27

Query Match

99.8%; Score 633; DB 4; Length 115;

Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 4 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 63
|||||
Qy 61 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 112
|||||
Db 64 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 115
|||||

RESULT 19

PCT-US94-00657-27

Sequence 27, Application PC/TUS9400657

GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 115 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: TGF-beta-3

FEATURE:

NAME/KEY: Protein

LOCATION: 1..115

PCT-US94-00657-27

Query Match

99.8%; Score 633; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 4 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 63
|||||

Qy 61 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 112
|||||

Db 64 VLGLYNTLNPEASASPCCVPODLEPLTILYYVGRTPKVEQLSNMVYKSKCS 115
|||||

RESULT 20

PCT-US94-07762-21

```

; Sequence 21, Application PC/TUS9407762
;
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A., PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD2349
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
;
PCT-US94-07762-21

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Query Match          99.8%; Score 633; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. NO. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLNCCVRPIYIDFRQDLGNKWKWVHEPKGYANFCGSGPCPYLRSADTTTST 60
    |||||
Db 4 ALDNTYCFRNLNCCVRPIYIDFRQDLGNKWKWVHEPKGYANFCGSGPCPYLRSADTTTST 63
    |||||
QY 61 VLGLYNTLNPEASASPCCVQDPLEPLTILTYVVGRTPKVEQLSNMVKSKCKS 112
    |||||
Db 64 VLGLYNTLNPEASASPCCVQDPLEPLTILTYVVGRTPKVEQLSNMVKSKCKS 115
    |||||

RESULT 21
PCT-US94-07799-21
; Sequence 21, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07799
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A., PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD-2348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; PCT-US94-07799-21

Query Match          99.8%   Score 633; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPGPYILRSADTTHTST 60
        |||||||
Db       4 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPGPYILRSADTTHTST 63

Qy      61 VLGLYNTLNPRASAPCCVPQDLEPLTLTYVGRTPKVEQLSNMVVKCKGS 112
        |||||||
Db       64 VLGLYNTLNPRASAPCCVPQDLEPLTLTYVGRTPKVEQLSNMVVKCKGS 115

RESULT 22
PCT-US91-01861-3
; Sequence 3, Application PC/TUS9101861
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Method of Predisposing Mammals to
; TITLE OF INVENTION: Accelerated Tissue Repair
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01861
; FILING DATE: 19910320
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Ser. No. 07/504,495
; FILING DATE: 4 April 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 637
; TELECOMMUNICATION INFORMATION:

```


QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 412

RESULT 25
PCT-US91-04541-2
; Sequence 2, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-04541-2

Query Match 99.8%; Score 633; DB 5; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.le-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 412

RESULT 26
5262319-2
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO: 2:
; LENGTH: 412
5262319-2

Query Match 99.8%; Score 633; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.le-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTTST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKCS 412

RESULT 27
US-08-927-433-4
; Sequence 4, Application US/08927433
; Patent No. 6107476
; GENERAL INFORMATION:
; APPLICANT: Erlander, Mark G.
; APPLICANT: Huang, Shaoming
; APPLICANT: Jackson, Michael A.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-927-433-4


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; CLONE: TGF-beta-3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
US-09-177-860A-31

Query Match      98.7%; Score 626; DB 3; Length 115;
Best Local Similarity 99.1%; Pred. No. 1.3e-60;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60
Db 4 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 63

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112
Db 64 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 115

RESULT 31
US-09-123-233-8
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:11:
; LENGTH: 455
5168051-11

Query Match      96.5%; Score 612; DB 6; Length 455;
Best Local Similarity 97.3%; Pred. No. 2.2e-58;
Matches 109; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60
Db 344 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHSS 403

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112
Db 404 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTAKVEQLSNMNVKSKCS 455

RESULT 32
US-09-123-233-8
; Sequence 8, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biological active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-123-233-8
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Query Match      93.8%; Score 595; DB 3; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.9e-57;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60
Db 1 ALDNYCFRSSTKCCVRLYIDFRKDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112
Db 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112

RESULT 33
US-09-123-233-10
; Sequence 10, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biological active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-123-233-10

Query Match      93.2%; Score 591; DB 3; Length 112;
Best Local Similarity 91.1%; Pred. No. 7.8e-57;
Matches 102; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60
Db 1 ALDNYCFRNVDNCCLRLYIDFRKDLGKWKVHEPKGYANFCGPGCPYLRSDTTHST 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112
Db 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMNVKSKCS 112

RESULT 34
US-09-123-233-12
; Sequence 12, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biological active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 12:
```


APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..98
OTHER INFORMATION: /note= "TGF-B3 SEQUENCE"
US-08-478-097A-3

Query Match 85.38; Score 541; DB 3; Length 98;
Best Local Similarity 99.08; Pred. No. 1.7e-51;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 15 CCVRPLYIDFQDLGKWKVHPEKGYANFCGPGPYLRSADTTHSTVLGLYNTLNPEASA 74
Db 1 CCVRPLYIDFQDLGKWKVHPEKGYANFCGPGPYLRSADTTHSTVLGLYNTLNPEASA 60
Qy 75 SPCCVPQDPLETLITYYVGRTPKVEQLSNMVKSKCS 112
Db 61 SPCCVPQDPLETLITYYVGRTPKVEQLSNMVKSKCS 98
RESULT 38
US-07-979-441-2
Sequence 2, Application US/07979441
Patent No. 5462925
GENERAL INFORMATION:
APPLICANT: OGAWA, YASUSHI
APPLICANT: SCHMIDT, DAVID
APPLICANT: DASCH, JAMES
TITLE OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,441
FILING DATE: 19921120
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/614,306
FILING DATE: 16-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CIOTLI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 220952024800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-979-441-2
Query Match 84.48; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDTNYCFRNLENCVRLPYIDFQDLGKWKVHPEKGYANFCGPGPYLRSADTTHST 60
Db 1 ALDAAVCFRNVDNCCRLPYIDFKRDGLGKWKVHPEKGYANFCGPGPYLRSADTTHST 60
Qy 61 VLGLYNTLNPEASAPCCVPQDPLETLITYYVGRTPKVEQLSNMVKSKCS 112
Db 61 VLGLYNTLNPEASAPCCVPQDPLETLITYYVGRTPKVEQLSNMVKSKCS 112
RESULT 39
US-08-486-057B-42
Sequence 42, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-057B-42

Query Match 84.4%; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
||| |||||:~:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTHSR 60
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
||| |||||:~:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASASPCVQDLEPLTILYYIGKTPKIEQLSNMIVKSKCS 112

RESULT 40
US-08-470-837-32
Sequence 32, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimmi, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051

REFERENCE/DOCKET NUMBER: 30630-IUS01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-837-32

Query Match 84.4%; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
||| |||||:~:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAVCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTHSR 60
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
||| |||||:~:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASASPCVQDLEPLTILYYIGKTPKIEQLSNMIVKSKCS 112

RESULT 41
US-08-789-588-42
Sequence 42, Application US/08789588
Patent No. 5922846
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-789-588-42

Query Match 84.4%; Score 535; DB 2; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHT 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 42
US-08-691-794-5
Sequence 5, Application US/08691794
Patent No. 6057428
GENERAL INFORMATION:

APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.
APPLICANT: Li, Bing
TITLE OF INVENTION: Variants of Vascular Endothelial Cell
TITLE OF INVENTION: Growth factor, Their Uses, and Processes for their
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,794
FILING DATE: 02-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,827
FILING DATE: 25-AUG-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/567,200
FILING DATE: 05-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63758/WHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids

TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-691-794-5

Query Match 84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHT 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 43
US-09-123-233-4
Sequence 4, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:

CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-233-4

Query Match 84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHT 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 ALDAAFCFRNVQDNCCLRLPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 44
US-08-927-433-3
Sequence 3, Application US/08927433
Patent No. 6107476
GENERAL INFORMATION:

APPLICANT: Erlanger, Mark G.
APPLICANT: Huang, Shaoming
APPLICANT: Jackson, Michael A.
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson

```
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-927-433-3

Query Match      84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLEENCVRPLYIDFRDLGKWKVHPEKGYANFCGPGPYLRSADTTHST 60
   ||| |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAAYCFRNVDNCCRLPLRIDFKRDLGKWKVHPEKGYANFCAGACPYLWSSDTQHSR 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASAPCCVSDLEPLTILYVIGKTPKIEQLSNMIVKSKCS 112

RESULT 45
US-08-481-377-24
; Sequence 24, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,377
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00666
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
```

```
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; US-08-481-377-24

Query Match      84.4%; Score 535; DB 1; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLEENCVRPLYIDFRDLGKWKVHPEKGYANFCGPGPYLRSADTTHST 60
   ||| |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAAYCFRNVDNCCRLPLRIDFKRDLGKWKVHPEKGYANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSDLEPLTILYVIGKTPKIEQLSNMIVKSKCS 114

RESULT 46
US-08-491-835-22
; Sequence 22, Application US/08491835
; Patent No. 5821056
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-08-491-835-22

Query Match 84.4%; Score 535; DB 2; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVDNCCRLPLYIDFKRDLGKWKIHEPKGYNANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSKCS 114

RESULT 47
US-09-153-733A-24
; Sequence 24, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/153.733A

ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 2
NAME/KEY: Protein
LOCATION: 1..114
US-09-153-733A-24

Query Match 84.4%; Score 535; DB 3; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;

Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVDNCCRLPLYIDFKRDLGKWKIHEPKGYNANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSKCS 114

RESULT 48
US-08-946-092A-22
; Sequence 22, Application US/08946092A
; Patent No. 6030617
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,092A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta2
NAME/KEY: Protein
LOCATION: 1..114
US-08-946-092A-22

Query Match 84.4%; Score 535; DB 3; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVDNCCRLPLYIDFKRDLGKWKIHEPKGYNANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSKCS 114

```
RESULT 49
US-09-172-062-22
; Sequence 22, Application US/09172062
; Patent No. 6191261
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,062
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-09-172-062-22

Query Match 84.4%; Score 535; DB 4; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
Db 3 ALDAAYCFRNVQDNCCURPLYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 114

RESULT 50
US-08-624-635-23
; Sequence 23, Application US/08624635
; Patent No. 6204047
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Cunningham, No. 6204047een
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
; NUMBER OF SEQUENCES: 26
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,635
; FILING DATE: 16-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,078
; FILING DATE: 08-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-08-624-635-23

Query Match 84.4%; Score 535; DB 4; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
Db 3 ALDAAYCFRNVQDNCCURPLYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 114

RESULT 51
PCT-US94-00666-24
; Sequence 24, Application PC/TUS9400666
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/006666
;; FILING DATE: 12-JAN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WETHERELL, JR. Ph.D., JOHN R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: FD2279 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta 2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..114
PCT-US94-00666-24

Query Match 84.4%; Score 535; DB 5; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDNYCFRNLENCVRPLYIDFRQDLGWKWHPEKGYANFCGPGPYLRSADTTHT 60
Db 3 ALDAAFCFRNVQNCCLRPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 62
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYYIGTKPKIEQLSNMIVKSKCS 114

RESULT 52
PCT-US94-00685-22
;; Sequence 22, Application PC/TUS9400685
;; GENERAL INFORMATION:
;; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Spensley Horn Jubas & Lubitz
;; STREET: 1880 Century Park East, Suite 500
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: US
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/00685
;; FILING DATE: 12-JAN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wetherell, Jr. Ph.D., John R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: FD3288
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..114
PCT-US94-00685-22

Query Match 84.4%; Score 535; DB 5; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDNYCFRNLENCVRPLYIDFRQDLGWKWHPEKGYANFCGPGPYLRSADTTHT 60
Db 3 ALDAAFCFRNVQNCCLRPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 62
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYYIGTKPKIEQLSNMIVKSKCS 114

RESULT 53
US-08-581-529B-20
;; Sequence 20, Application US/08581529B
;; Patent No. 5770444
;; GENERAL INFORMATION:
;; APPLICANT: Lee, Se-Jin
;; APPLICANT: Huynh, Thanh
;; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/581,529B
;; FILING DATE: 15-APR-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lisa A. Haile, Ph.D.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/082001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 678-5070
;; TELEFAX: (619) 678-5099
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 115 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta-2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..115
US-08-581-529B-20

Query Match 84.4%; Score 535; DB 1; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;

QY	1	ALDNTCFRNLBENCVCVRPLYIDFRQDLGHWKWHPEKGYANFCSGPCPYLRSDTTHST	60
DB	4	ALDAAFCFRNVQNCCLURPLYIDFKRDLGHWKWHPEKGYANFCAGACPKYLRWSDTOHSR	63
QY	61	VLGLYNTLNPEASASPCCVQDLEPTILYIVYGTRPVEQLSNMVKSCRS	112
DB	64	VLSYNTINPEASASPCCVSQDLEPTILYIVGTRPKIEQLSNMVKSCRS	115

```

US-08-581-528A-20
:
: Sequence No. 20, Application US/08581528A
:
: Patent No. 5986058
:
: GENERAL INFORMATION:
:
: APPLICANT: Lee, Se-Jin
:
: APPLICANT: Hyunh, Thanh
:
: TITLE OF INVENTION: GROWTH DIFFERENTIAL
:
: NUMBER OF SEQUENCES: 21
:
: CORRESPONDENCE ADDRESS:
:
:

```

ADDRESS: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581.528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/081001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-528A-20
Query Match 84.4%; Score 535; DB 2; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGPPYLRSDTTHST 60
Db 4 ALDAAFCFRNVQDNCCLRLPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASPCCVPDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 64 VLSLYNTINPEASPCCVSODLEPLTILYVIGTKPKIEQLSNMIVKSKCS 115
RESULT 57
US-09-097-616-20
Sequence 20, Application US/09097616
Patent No. 6090563
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-097-616-20
Query Match 84.4%; Score 535; DB 3; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGPPYLRSDTTHST 60
Db 4 ALDAAFCFRNVQDNCCLRLPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASPCCVPDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 64 VLSLYNTINPEASPCCVSODLEPLTILYVIGTKPKIEQLSNMIVKSKCS 115
RESULT 58
US-09-177-860A-30
Sequence 30, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-177-860A-30

Query Match 84.4%; Score 535; DB 3; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHPEKGYANFCGPGCPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 ALDAAVCFRNVDNCLRLPYIDFKRDLGKWKVHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 VLSLYNTINPEASASPCCVSQDLEPLTILYVYIGTKPKIEQLSNMIVKSKCS 115

RESULT 59
US-09-145-060-26
Sequence 26, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
US-09-145-060-26

Query Match 84.4%; Score 535; DB 4; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHPEKGYANFCGPGCPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 ALDAAVCFRNVDNCLRLPYIDFKRDLGKWKVHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 VLSLYNTINPEASASPCCVSQDLEPLTILYVYIGTKPKIEQLSNMIVKSKCS 115

RESULT 60
PCI-US94-00657-26
Sequence 26, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
PCI-US94-00657-26

Query Match 84.4%; Score 535; DB 5; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHPEKGYANFCGPGCPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 ALDAAVCFRNVDNCLRLPYIDFKRDLGKWKVHPEKGYANFCAGACPYLWSSDTQHSR 63


```
; FILING DATE: 06-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 01-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 597D1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-132-405-2

Query Match      84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.5%; Pred. No. 4.le-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGWKWHPEKGYVYANFCGCPYLRSDTTHST 60
    ||| |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 ALDAAVCFRNVQDNCCLRPYIDFKDLGWKWHPEKGYNANFCAGACPYLWSSDTQHSR 362

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
    || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VLSLYNTINPEASASPCCVSQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 414

RESULT 64
US-08-395-939A-2
; Sequence 2, Application US/08395939A
; Patent No. 5604204
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudman, Christopher G.
; TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
; TITLE OF INVENTION: GROWTH
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,939A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/132405
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 1-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P0597D1C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-395-939A-2

Query Match      84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.5%; Pred. No. 4.le-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGWKWHPEKGYVYANFCGCPYLRSDTTHST 60
    ||| |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 ALDAAVCFRNVQDNCCLRPYIDFKDLGWKWHPEKGYNANFCAGACPYLWSSDTQHSR 362

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
    || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VLSLYNTINPEASASPCCVSQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 414

RESULT 65
PCT-US91-01861-2
; Sequence 2, Application PC/TUS9101861
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Method of Predisposing Mammals to
; TITLE OF INVENTION: Accelerated Tissue Repair
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01861
; FILING DATE: 19910320
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Ser. No. 07/504,495
; FILING DATE: 4 April 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: AMINO ACID
```



```

; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-057B-41

Query Match 78.9%; Score 500; DB 1; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 AIDTNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCPYLRSDTTHST 60
DB 1 AIDTNYCFSTENKCCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCPYLRSDTTHST 60
QY 61 VLGLYNTLNPEASASPCVCPQDLEPLTILYYGRTPKVEQLSNMIVVSKCS 112
DB 61 VLALYLNQHNPGASAPCCVQALEPLPIYVYVGRKPKVEQLSNMIVVSKCS 112

RESULT 72
US-08-459-850-36
; Sequence 36, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; NUMBER OF SEQUENCES: 44
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-459-850-36

Query Match 78.9%; Score 500; DB 1; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 AIDTNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCPYLRSDTTHST 60
DB 1 AIDTNYCFSTENKCCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCPYLRSDTTHST 60
QY 61 VLGLYNTLNPEASASPCVCPQDLEPLTILYYGRTPKVEQLSNMIVVSKCS 112
DB 61 VLALYLNQHNPGASAPCCVQALEPLPIYVYVGRKPKVEQLSNMIVVSKCS 112

RESULT 73
US-08-459-214-36
; Sequence 36, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
```

```

; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-837-30

Query Match          78.9%; Score 500; DB 1; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0

Qy   1  ALDNYCFRNLEENCVRPLYIDFRDLGKWKVWHEPKGYVANFCSGPCPYLRSDTDT
      ||||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db   1  ALDNYCFSSTKEKNCCVRQLYIDFRDLGKWKVWHEPKGYHANFCGLGPCPYIWSLDT
      ||||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Qy   61 VLGLYNTLNPNASAPCCVPQDEPLTILYYVGRTPKVEQLSNMVKSCKS 112
      || || | || || | || || || || || || || || || || || || || || || ||
Db   61 VLALYNQHPGASAAPCCVPQAELPLPIVVYGKKPKVEQLSNMIVRSCKS 112
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RESULT    75
US-08-789-588-41
; Sequence 41, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown

```



```

; ; REFERENCE/DOCKET NUMBER: FD2279 PCT
; ;
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: (619) 455-5100
; ; TELEFAX: (619) 455-5110
; ; INFORMATION FOR SEQ ID NO: 23:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 114 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; IMMEDIATE SOURCE:
; ; CLONE: TGF-beta 1
; ; FEATURE:
; ; NAME/KEY: Protein
; ; LOCATION: 1..114
; ;
; ; US-08-481-377-23

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Query Match          78.98; Score 500; DB 1; Length 114;
Best Local Similarity 76.88; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
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[illegible]

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; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-08-491-835-21

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Query Match 78.9%; Score 500; DB 2; Length 114;
Best Local Similarity 76.8%; Pred..No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps

[illegible]

RESULT 82
 US-09-153-733A-23
 Sequence 23, Application US/09153733A
 Patent No. 6025475
 GENERAL INFORMATION:
 APPLICANT: JOHNS HOPKINS UNIVERSITY
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
 STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CITY: LOS ANGELES
 STATE: CALIFORNIA
 COUNTRY: US
 ZIP: 90067
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/153,733A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/481,377
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: WETHERELL, JR. Ph.D., JOHN R.
 REGISTRATION NUMBER: 31,678
 REFERENCE/DOCKET NUMBER: FD2279 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 TELEFAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 114 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: TGF-beta 1
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..114
 US-09-153-733A-23

Query Match	78.9%	Score 500;	DB 3;	Length 114;
Best Local Similarity	76.8%	Pred. No. 5.3e-47;		
Matches 86; Conservative	11;	Mismatches 15;	Indels 0;	Gaps 0;

QY 1 ALDNTNCFRNLENCVRLYIDFRDLGWKWHHPKGYANFCSGPCPYLRSADTTHST 60
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 3 ALDNTNCFSTKNCVRLYIDFRDLGWKWHHPKGYHANFCLGCPYIWSLDTQYSK 62
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMIVSKCS 112
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 63 VLALYNQHPGASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVSKCS 114
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |

RESULT 83

US-08-946-092A-21
; Sequence 21, Application US/08946092A
; Patent No. 6030617
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,092A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/491,835
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114

US-08-946-092A-21

Query Match 78.9%; Score 500; DB 3; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLYIDFRDLGWKWHHPKGYANFCSGPCPYLRSADTTHST 60
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 3 ALDNTNCFSTKNCVRLYIDFRDLGWKWHHPKGYHANFCLGCPYIWSLDTQYSK 62
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMIVSKCS 112
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 63 VLALYNQHPGASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVSKCS 114
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |

RESULT 84

US-09-172-062-21
; Sequence 21, Application US/09172062
; Patent No. 6191261
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,062
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114

US-09-172-062-21

Query Match 78.9%; Score 500; DB 4; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLYIDFRDLGWKWHHPKGYANFCSGPCPYLRSADTTHST 60
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 3 ALDNTNCFSTKNCVRLYIDFRDLGWKWHHPKGYHANFCLGCPYIWSLDTQYSK 62
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMIVSKCS 112
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |
Db 63 VLALYNQHPGASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVSKCS 114
| | | | | : | : | | | | | | | | | | | | | | | | | | | : | : | |

RESULT 85

US-08-624-635-22
; Sequence 22, Application US/08624635
; Patent No. 6204047
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Cunningham, No. 6204047een
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:


```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
PCT-US94-00685-21

```

Query Match 78.9%; Score 500; DB 5; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ALDNTNYCFRNL	EE	NCCV	RP	LYID	PRO	D	L	G	K	W	K	H	E	P	K	G	Y	A	N	F	C	S	G	P	C	P	I	R	S	A	D	T	T	H	S	T	60											
Db	3	ALDNTNYCF	SE	TE	K	N	C	C	V	R	Q	Y	I	D	R	K	D	L	G	K	W	K	H	E	P	K	G	Y	A	N	F	C	S	G	P	C	P	I	R	S	A	D	T	T	H	S	T	62		
Qy	61	V	L	G	I	N	T	L	N	P	E	A	S	A	S	P	C	C	V	P	Q	D	L	E	P	L	T	I	L	Y	V	G	R	T	P	K	V	E	Q	L	S	N	M	V	K	S	C	K	S	112
Db	63	V	I	A	L	N	O	H	N	F	G	A	S	A	A	P	C	C	V	P	Q	A	L	E	P	L	T	I	V	Y	V	G	R	K	P	R	V	E	Q	L	S	N	I	V	R	S	C	K	S	114

RESULT 86
US-08-581-529B-19
; Sequence 19, Application US/08581529B
; Patent No. 5770444
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581.529B
; FILING DATE: 15-APR-1996
; CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-529B-19

Query Match 78.9%; Score 500; DB 1; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels

Qy	1	ALD	NY	CERN	LENN	CCRV	PL	YID	RQ	DL	GW	KW	HE	PK	GY	AN	FC	SG	CP	YLR	AS	DT	TH	ST	60		
Db	4	ALD	NY	CF	SST	EK	CC	RQ	LY	ID	RQ	DL	GW	KW	HE	PK	GY	AN	FC	SG	CP	YLR	AS	DT	TH	ST	63
Qy	61	VL	GL	NT	LN	PS	AS	PC	CP	OD	LE	PL	TY	LV	GR	TP	KV	EQ	LN	SV	CK	GS	112				
Db	64	VL	AL	NO	HP	CA	SA	PC	CP	OD	LE	PL	TY	LV	GR	TP	KV	EQ	LN	SV	CK	GS	115				

RESULT 89
 US-08-455-559-25
 ; Sequence 25, Application US/08455559
 ; Patent No. 5801014
 ; GENERAL INFORMATION:
 ; APPLICANT: LEE, SE-JIN
 ; APPLICANT: HUYNH, THANH
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SPENSLEY HORN JUBAS & LOBITZ
 ; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 ; CITY: LOS ANGELES
 ; STATE: CALIFORNIA
 ; COUNTRY: US
 ; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,559
 ; FILING DATE: 31-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/003,144
 ; FILING DATE: 12-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WETHERELL, JR. PH.D., JOHN R.
 ; REGISTRATION NUMBER: 31,678
 ; REFERENCE/DOCKET NUMBER: PD2280
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/455-5100
 ; TELEFAX: 619-455-5110
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 115 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; IMMEDIATE SOURCE:
 ; CLONE: TGF-beta-1
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..115
 ; US-08-455-559-25

Query Match	78.9%	Score 500;	DB 1;	Length 115;
Best Local Similarity	76.8%;	Pred. No. 5.3e-47;		
Matches 86;	Conservative 11;	Mismatches 15;	Indels 0;	Gaps 0;

[illegible]

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
NAME/KEY: Protein
LOCATION: 1..115
US-09-097-616-19

Query Match 78.9%; Score 500; DB 3; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPCYLRSADTTHST 60
Db 4 ALDTNYCFSTSKNCCVRQLYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYYVGRTPKVEQLSNMIVRSCKCS 112
Db 64 VLALYNQHNPGASAPCCVQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 115

RESULT 93
US-09-177-860A-29
Sequence 29, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-177-860A-29
Query Match 78.9%; Score 500; DB 3; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPCYLRSADTTHST 60
Db 4 ALDTNYCFSTSKNCCVRQLYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYYVGRTPKVEQLSNMIVRSCKCS 112
Db 64 VLALYNQHNPGASAPCCVQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 115
RESULT 94
US-09-145-060-25
Sequence 25, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear

```

; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
US-09-145-060-25

Query Match      78.9%; Score 500; DB 4; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSPGCPYLRSADTTHT 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| :|
Db 4 ALDNTYCFSSTEKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 95
PCT-US94-00657-25
; Sequence 25, Application PC/TUS9400657
; GENERAL INFORMATION:
; APPLICANT: SE-JIN LEE
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00657
; FILING DATE: 1/12/94
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. P.H.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-00657-25

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSPGCPYLRSADTTHT 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| :|
Db 4 ALDNTYCFSSTEKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 96
PCT-US94-07762-19
; Sequence 19, Application PC/TUS9407762
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A. PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-07762-19

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSPGCPYLRSADTTHT 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| :|
Db 4 ALDNTYCFSSTEKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 97
PCT-US94-07799-19
; Sequence 19, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
```

```

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 96
PCT-US94-07762-19
; Sequence 19, Application PC/TUS9407762
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A. PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-07762-19

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCSPGCPYLRSADTTHT 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| :|
Db 4 ALDNTYCFSSTEKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 97
PCT-US94-07799-19
; Sequence 19, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
```

CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07799
FILING DATE: 08-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: FD-2348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tgf-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
PCT-US94-07799-19

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-132-405-1

Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-46;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
Db 279 ALDTNYCFSSSTEKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGPGPYIWSLDTQYSK 338
QY 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVVGRTPKVQEQLSNMIVRSCKCS 112
Db 339 VLALYNQHNPGASAPCCVPQALEPLPIVYVVGKPKVQEQLSNMIVRSCKCS 390

RESULT 100
US-08-395-939A-1
Sequence 1, Application US/08395939A
Patent No. 5604204
GENERAL INFORMATION:
APPLICANT: Ammann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
TITLE OF INVENTION: GROWTH
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P0597D1C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid

TOPOLOGY: linear
US-08-395-939A-1

Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-46;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
Db 279 ALDTNYCFSSSTEKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGPGPYIWSLDTQYSK 338
QY 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVVGRTPKVQEQLSNMIVRSCKCS 112
Db 339 VLALYNQHNPGASAPCCVPQALEPLPIVYVVGKPKVQEQLSNMIVRSCKCS 390

Search completed: October 30, 2001, 08:53:20
Job time: 139 sec

Db	121	GCCAACTCTGCTAGGCCCTTGCCCATACCTCCGAGTGCAGACACAAACCCACAGCAG	180
QY	181	gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctcgtctgtcgtgcgc	240
Db	181	GTCTGGGACTGTACAACTCTGAACCTTGACATCTGCCTCGCTTGTCTGCTGCCCC	240
QY	241	caggacctggagccctgacctctctgtactatgttggaggagcccccaaaagtggagcag	300
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QY	301	ctctcaacatggtggtgaagctcttgtaaatgtagtga	339
Db	301	CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGTGA	339
RESULT	2		
LOCUS	A23753	339 bp mRNA	PAT 25-JAN-1995
DEFINITION	TGF-beta3 coding region.		
ACCESSION	A23753		
VERSION	A23753.1	GI:825587	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 339)		
AUTHORS	McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.		
TITLE	Novel hybrid transforming growth factors		
JOURNAL	Patent: EP 0542679-A 3 19-MAY-1993;		
FEATURES	CIBA-GEIGY AG		
Source	1..339		
BASE COUNT	74 a 104 c 86 g 75 t		
ORIGIN	/organism="Homo sapiens"		
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Best Local Similarity	100.0%; Pred. No. 2.7e-83;		
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Db	1	GCTTGGACACCAATTACTCTCCGAACCTGGAGGAACTGCTGTGCGCCCCCTC	60
QY	61	tacattgacttccgacaggatctgggtggaagtgggtccatgaacctaaaggtctactat	120
Db	61	TACATTGACTTCGCAGAGATCTGGCTGGAAGTGGTCCATGAACCTAAGGGCTACTAT	120
QY	121	gcaacttctgtcagcccttgcccatacctccgcagtcagtcagacacacccccacagcag	180
Db	121	GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACAAACCCACAGCAG	180
QY	181	gtctgggactgtacaacactctgaacctgaagcatctgcctcgtcgtgcgc	240
Db	181	GTCTGGGACTGTACAACTCTGAACCTGAAGCATCTGCCCTGCTGCTGCGTGC	240
QY	241	caggacctggagccctgacctctgtactatgttggaggagcccccaaaagtggagcag	300
Db	241	CAGGACTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG	300
QY	301	ctctcaacatggtggtgaagctcttgtaaatgtagtga	339
Db	301	CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGTGA	339
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LOCUS	A48553	339 bp DNA	PAT 07-MAR-1997
DEFINITION	Sequence 5 from Patent WO9603432.		
ACCESSION	A48553		

VERSION	A48553.1	GI:2302323	
KEYWORDS	unidentified.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 339)		
AUTHORS	Cerletti,N.		
TITLE	NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEI		
JOURNAL	Patent: WO 9603432-A 5 08-FEB-1996;		
COMMENT	CIBA GEIGY AG (CH)		
FEATURES	Other publication AU 3109595 960222.		
source	Location/Qualifiers		
	1..339		
	/organism="unidentified"		
	/db_xref="taxon:32644"		
CDS	1..336		
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	/protein_id="CAA03115.1"		
	/db_xref="GI:2302324"		
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BASE COUNT	74 a 104 c 86 g 75 t		
ORIGIN			
Query Match	100.0%; Score 339; DB 9; Length 339;		
Best Local Similarity	100.0%; Pred. No. 2.7e-83;		
Matches 339; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	gcttggacacaattactctccgaacttggagagaactgctgtgcgcgccttc	60
Db	1	GCTTGGACACCAATTACTCTCCGAACCTGGAGGAACTGCTGTGCGCCCCCTC	60
QY	61	tacattgacttccgacaggatctgggtggaagtgggtccatgaacctaaaggtctactat	120
Db	61	TACATTGACTTCGCAGAGATCTGGCTGGAAGTGGTCCATGAACCTAAGGGCTACTAT	120
QY	121	gcaacttctgtcagcccttgcccatacctccgcagtcagtcagacacacccccacagcag	180
Db	121	GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACAAACCCACAGCAG	180
QY	181	gtctgggactgtacaacactctgaacctgaagcatctgcctcgtcgtgcgc	240
Db	181	GTGCTGGGACTGTACAACTCTGAACCTGAAGCATCTGCCCTGCTGCTGCGTGC	240
QY	241	caggacctggagccctgacctctgtactatgttggaggagcccccaaaagtggagcag	300
Db	241	CAGGACTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG	300
QY	301	ctctcaacatggtggtgaagctcttgtaaatgtagtga	339
Db	301	CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGTGA	339
RESULT	4		
LOCUS	A48567	339 bp DNA	PAT 07-MAR-1997
DEFINITION	Sequence 5 from Patent WO9603433.		
ACCESSION	A48567		
VERSION	A48567.1	GI:2302337	
KEYWORDS	unidentified.		
SOURCE	unclassified.		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 339)		
AUTHORS	Cerletti,N.		
TITLE	NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN		
JOURNAL	Patent: WO 9603433-A 5 08-FEB-1996;		

QY 181 gtctgggactgtacaacactctgaaccctgaagcatctgcctcgcttgcctgctgccc 240
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Db 181 GTCTGGGACTGTACAACTCTGAACCTCTGAAGCATCTGCCTCGCTTGCCTGCGTCCC 240
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Db 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
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Db 301 CTCTCCAACATGTTGTGAAGTCTTGTAAATGTAGTGA 339
RESULT 7
I56856 I56856 339 bp DNA PAT 07-OCT-1997
LOCUS Sequence 3 from patent US 5650494.
ACCESSION I56856
VERSION I56856.1 GI:2477269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for recombining recombinantly produced TGF-beta-like
proteins
JOURNAL Patent: US 5650494-A 3 22-JUL-1997;
FEATURES Location/Qualifiers
source 1..339
/organism="unknown"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN
Query Match 100.0%; Score 339; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 ctctccaaactgtgtgaagcttctaataatagctga 339
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Db 301 CTCTCCAACATGTTGTGAAGTCTTGTAAATGTAGTGA 339
RESULT 8
HUMTGF3A HUMTGF3A 2529 bp mRNA PRI 14-JAN-1995
LOCUS Human transforming growth factor-beta 3 (TGF-beta3) mRNA, complete
DEFINITION cds.
ACCESSION J03241
VERSION J03241.1 GI:339551
KEYWORDS transforming growth factor.

SOURCE Human placental and umbilical cord (cell line A673), cDNA to mRNA,
from library lambda-gt10.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Homnidae; Homo.
1 (bases 1 to 2529)
AUTHORS ten Dijke,P., Hansen,P., Iwata,K.K., Pieler,C. and Foulkes,J.G.
TITLE Identification of another member of the transforming growth factor
type beta gene family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988)
MEDLINE 88263019
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
C.Pieler 12-SEPT-1988 The authors have found that this transforming
growth factor contains multiple growth inhibitory elements.
FEATURES Location/Qualifiers
source 1..2529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14Q24"
gene 263..1501
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CDS 263..1501
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/note="transforming growth factor-beta3"
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LGLEISHCPCHTFQPNGDILENIHEVMELKFKGVNEDDGHGDLGLKQKDDHNP
HLILMIPPHRLDNPQGGOKKARALDNTFCRNLENCVRRPLYIDFRDGLGKWKVH
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BASE COUNT 617 a 671 c 660 g 581 t
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Query Match 100.0%; Score 339; DB 97; Length 2529;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcttggacaccaattactgcttcgcgaacttggagagaactgctgtgccccctc 60
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Db 1163 GCTTTGGACACCAATTAAGTCTGCCAATCTGGAGGAGAACTGCTGTGCGCCCCCTC 1222
QY 61 tacattgaacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
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Db 1223 TACATTGACTTCGCAGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 1282
QY 121 gccaaacttctgcagcccttgcctaccctcccgagtcagacacacacacacagcag 180
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Db 1283 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGAGTGCAGACACACACCCACAGCAG 1342
QY 181 gtctgggactgtacaacactctgaaccctgaagcatctgctcgcttgcctgctgctgccc 240
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Db 1343 GTGCTGGGACTGTACAACTCTGAACCTCTGAAGCATCTGCCTCGCTTGCCTGCGTCCC 1402
QY 241 caggacctggagccctgaccactctgtactatgttggagagaccctcccaagtggagcag 300
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Db 1403 CAGGACCTGGAGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1462
QY 301 ctctccaaactgtgtgaagcttctaataatagctga 339
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Db 1463 CTCTCCAACATGTTGTGAAGTCTTGTAAATGTAGTGA 1501
RESULT 9
HSTGFB3M HSTGFB3M 2574 bp mRNA PRI 12-SEP-1993
LOCUS Human mRNA for transforming growth factor-beta 3 (TGF-beta 3).
DEFINITION

ACCESSION X14149
VERSION X14149.1 GI:37095
KEYWORDS growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 2574)
JOURNAL Direct Submission
REFERENCE Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
AUTHORS 2 (bases 1 to 2574)
JOURNAL Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L., Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and Chen, E.Y.
TITLE A new type of transforming growth factor-beta, TGF-beta 3
JOURNAL EMBO J. 7 (12), 3737-3743 (1988)
MEDLINE 89091120
COMMENT See <J03241> for alternative sequence of TGF-beta 3.
FEATURES
source Location/Qualifiers
1..2574
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/db_xref="taxon:9606"
/chromosome="14q24"
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/cell_line="A172 glioblastoma"
254..1492
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SKRNEIRQLPQILRDEHIAKQYIGKNLPTRGTAEMLSFDVDTVREMLLRRES
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ORIGIN
Query Match 100.0%; Score 339; DB 93; Length 2574;
Best Local Similarity 100.0%; Pred. No. 2.le-83;
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Db 1454 CTCTCCAAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 1492

RESULT 10

LOCUS I03320
DEFINITION Sequence 11 from Patent US 4886747.
ACCESSION I03320
VERSION I03320.1 GI:270714
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1899)
AUTHORS Derynck, R.M.A. and Goeddel, D.V.
TITLE Nucleic acid encoding TGF-beta, and its uses
JOURNAL Patent: US 4886747-A 11 12-DEC-1989; Genentech, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
1..1899
/organism="unknown"
BASE COUNT 515 a 425 c 452 g 507 t
ORIGIN
Query Match 99.5%; Score 337.4; DB 10; Length 1899;
Best Local Similarity 99.7%; Pred. No. 6e-83;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 578 CTCTCCAAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 616

RESULT 11

LOCUS I05432
DEFINITION Sequence 2 from Patent EP 0267463.
ACCESSION I05432
VERSION I05432.1 GI:590974
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 498)
AUTHORS Iwata, K.K., Gold, L.I. and Stephenson, J.R.
TITLE Tissue-derived tumor growth inhibitors, methods of preparation and uses thereof
JOURNAL Patent: EP 0267463-A2 2 18-MAY-1988;
FEATURES
source Location/Qualifiers
1..498
/organism="unknown"
BASE COUNT 122 a 137 c 129 g 110 t

QY 121 gcaaatcttgctcagcccttgccatacctccgagtcagtcagagacacacacacacagcagc 180
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Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCCCAAAAGTGAGCAG 300
QY 301 ctctccaaacatggtggtgaagctctgtaaatgtagc 336
Db 301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
RESULT 14
A48555
LOCUS A48555 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 7 from Patent WO9603432.
ACCESSION A48555
VERSION A48555.1 GI:2302325
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Carletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL PROTEIN
PATENT: WO 9603432-A 7 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES
source 1..336
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CDS 1..336
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NMVVKSCKCS"
mat_peptide 133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 75 a 109 c 86 g 66 t
ORIGIN
Query Match 87.8%; Score 297.6; DB 9; Length 336;
Best Local Similarity 92.9%; Pred. No. 7.7e-72;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 gctttggacacacaaattactgtcttcgcaacttgagagagaactgtgtgccccctc 60
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Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCCCAAAAGTGAGCAG 300
QY 301 ctctccaaacatggtggtgaagctctgtaaatgtagc 336
Db 301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
RESULT 15
A48569
LOCUS A48569 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 7 from Patent WO9603433.
ACCESSION A48569
VERSION A48569.1 GI:2302339
KEYWORDS .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Carletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 7 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
FEATURES
source 1..336
/organism="unidentified"
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mat_peptide 1..132
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CDS 1..336
/note="Protein sequence is in conflict with the conceptual translation"
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NMVVKSCKCS"
mat_peptide 133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 75 a 109 c 86 g 66 t
ORIGIN
Query Match 87.8%; Score 297.6; DB 9; Length 336;
Best Local Similarity 92.9%; Pred. No. 7.7e-72;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 gctttggacacacaaattactgtcttcgcaacttgagagagaactgtgtgccccctc 60
Db 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCTGGCGCAGCTG 60
QY 61 tacattgacttcgacaggaatctgggctggaagtgggtccatgaacctaaagggtactact 120
Db 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
QY 121 gcaaatcttgctcagcccttgccatacctccgagtcagtcagagacacacacacacagcag 180
Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCACTGAGTGCAGACACAACCCACAGCAG 180
QY 181 gtgctggagctgtacaacactctgaacccctgaagcatctgctcgcttctgctgctgccc 240
Db 181 GTGCTGGGACTGTACACACTCTGAACCCCTGAACCATCTGCCTCGCTTGTGCTGCGTGC 240
QY 241 caggacctggagcccttgaccatctgtactatgttgggagagaccccccacaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCCCAAAAGTGAGCAG 300


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ACCESSION      BC005513
VERSION        BC005513.1  GI:13529607
KEYWORDS
SOURCE        house mouse.
ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        1 (bases 1 to 2164)
JOURNAL      Strausberg, R.
              Direct Submission
              Submitted (27-MAR-2001) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK       NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert.Strausberg@nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              Center, Stanford University School of Medicine, Stanford, CA 94305
              Web site: http://www-shgc.stanford.edu
              Contact: (Dickson, Mark) mcd@paxil.stanford.edu
              Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
              R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 8 Row: f Column: 13.
Location/Qualifiers
FEATURES      1. .2164
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              /clone="IMAGE:3492763"
              /tissue_type="Mammary tumor metastatized to lung. Tumor
              arose spontaneously from a senescent normal mammary
              (clonal) outgrowth infected with the virus MMTV."
              /clone_lib="NCI CGAP_Lu29"
              /lab_host="DH10B"
              /note="Vector: pCMV-SPORT6"
              <1. .1090
              /codon_start=2
              /product="Similar to transforming growth factor, beta 3"
              /protein_id="AAH05513.1"
              /db_xref="GI:13529608"
              /translation="GRVSPPEPVMTHPYQVLALYNSTRELLEEMHGEREGCTOE
              TSEYAKIEIHKFDIQLGAEHNEALAVCPKITSKVFNFVSVKNGTNLFAEPR
              VLRVPNPSKRTQRIELFQILRPDEHIAKORYIGGNLPTRTGAEWLSFDVDTVRE
              WLLRRSNLGLSIIHCPTFPQNGDILENVHEVMEIKFGVDNEDDHGRGLGRK
              KODHNPHLILAMIPPHRLDSPGQSORKRALDNTNCFNLENCVVRPLYIDFRQ
              DLGKWHPEKGYANFPCSPCPLRSADTHTSVILGLYNTLNPASASPCCPVDLE
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BASE COUNT   634 a 541 c 550 g 439 t
ORIGIN
Query Match 85.8%; Score 291; DB 94; Length 2164;
Best Local Similarity 91.2%; Pred. No. 4e-70;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 1 gctttgacacaaattactgtccgcaacttgagagaaactgtgtgctgcgccccctc 60
Db 752 GCCCTGGACACCAATTAAGTCTCCGCAACCTGGAGAGAACTGCTGTGACGCCCTT 811
Qy 61 tacattgactccgacagagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 812 TATATTGACTTCGGCAGGACTAGGCTGGAATAAGGGTCCACGAACCTAAGGGTTACTAT 871
Qy 121 gccaaactctgctcaggcccttgcccatacctccgagtgagagacacacacagcagc 180
Db 872 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCGCAGACACAAACCCATAGCAGC 931

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Qy 181 gtgctgggactgtacaaacactgtgaacccctgaagcatctgtcctcgcttgcgtgccc 240
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Qy 241 caggacctggagccctcaccatcctgtactactgttgaggagaccccccaagtgagcag 300
Db 992 CAGGACCTGGAGCCCTGACCATCTTGTACTATGTGGGAGAACCCCAAGGTGGAGCAG 1051
Qy 301 ctctccaaactgtgtgaagtcttgaatgtagctga 339
Db 1052 CTGTCAACATGTTGTTGAAGTCGTGTGAAGTCAGCTGA 1090
RESULT 19
LOCUS      MUSTGFB3 2879 bp mRNA ROD 27-APR-1993
DEFINITION mouse transforming growth factor beta-3 mRNA, complete cds.
ACCESSION M32745
VERSION M32745.1 GI:201949
KEYWORDS transforming growth factor.
SOURCE Mouse cell line AKR-2B, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2879)
AUTHORS Miller, D.A., Lee, A., Matsui, Y., Chen, E.Y., Moses, H.L. and
Derynck, R.
TITLE Complementary DNA cloning of the murine transforming growth factor-
beta-3 (TGF-beta-3) precursor and the comparative expression of
TGF-beta-3 and TGF-beta-1 messenger RNA in murine embryos and adult
tissues
JOURNAL Mol. Endocrinol. 3, 1926-1934 (1989)
MEDLINE 90190650
FEATURES Location/Qualifiers
source 1. .2879
/organism="Mus musculus"
/db_xref="taxon:10090"
<1. .2879
/note="TGF beta-3 mRNA"
611. .1843
/note="transforming growth factor beta-3 (TGF beta-3)
precursor (start site 611 could be 368 or 477)."
/codon_start=1
/db_xref="GI:201950"
/translation="MHQLRALVLLALNLATISLSLSTCTTILDFGHIKKRVAEIRGO
ILSKRLTSPPEPVMTHPYQVLALYNSTRELLEEMHGEREGCTQETSESEYAKG
IHKFDIQLGAEHNEALAVCPKITSKVFNFVSVKNGTNLFAEPRVLRVPNPSK
RTEIRIELFQILRPDEHIAKORYIGGNLPTRTGAEWLSFDVDTVREWLLRRSNL
LEIHSICPCHTFQNGDILENVHEVMEIKFGVDNEDDHGRGLGRKOKDHHNPHL
ILAMIPPHRLDSPGQSORKRALDNTNCFNLENCVVRPLYIDFRQDLGKWHPEP
KGYANFPCSPCPLRSADTHTSVILGLYNTLNPASASPCCPVDLEPLTILYVGR
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mat_peptide 1505. .1840
BASE COUNT 673 a 811 c 724 g 671 t
ORIGIN
Query Match 85.8%; Score 291; DB 94; Length 2879;
Best Local Similarity 91.2%; Pred. No. 3.8e-70;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 1 gctttgacacaaattactgtccgcaacttgaggagaaactgtgtgctgcgccccctc 60
Db 1505 GCCCTGGACACCAATTAAGTCTCCGCAACCTGGAGAGAACTGCTGTGACGCCCTT 1564
Qy 61 tacattgactccgacagagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 1565 TATATTGACTTCGGCAGGACTAGGCTGGAATAAGGGTCCACGAACCTAAGGGTTACTAT 1624
Qy 121 gccaaactctgctcaggcccttgcccatacctccgagtgagagacacacacagcagcag 180

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unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Carletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 9 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
FEATURES
source Location/Qualifiers
1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide 1..132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"
CDS 1..336
/note="protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HYBRID TGF-BETA2-3"
/protein_id="CAA03124.1"
/db_xref="GI:2302342"
/translation="ALDAAYCFRNVQDNCLRLPLYIDFKRDLGKWKWIHEPRKYNANFC SGPCPYLRSDATTHSTVLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLS NMVVKCKCS"
mat_peptide 133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 81 a 94 c 84 g 77 t
ORIGIN
Query Match 81.78; Score 276.8; DB 9; Length 336;
Best Local Similarity 89.08; Pred. No. 4.3e-66;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 1 gcttggacacaaattactgctcgcgaacttgaggagaaactgctgtgccccctc 60
Dy 1 GCTTGGATGGCGCTATTGCTTTAGAAATGTGCGGATATTTGCTGCTACGTCACATT 60
Qy 61 tacattgactccgacagagatgggtggaagtgggtccatgaacctaaagggtactat 120
Dy 61 TACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATACAGAACCCCAAGGGTACAA 120
Qy 121 gcaactctgctcagggccctggccatacctcgcagtcagtcagacacacacagcag 180
Dy 121 GCCAACTTCCTGCTCAGGCGCTGGCCATPACCTCCGACGTGAGACACACACAGCAG 180
Qy 181 gtgctggagactgtacaacactgaacctgaagcatctgctgccttgcgtgccc 240
Dy 181 GTGCTGGGACTGTACACACTCTGAACCTTGAGCATCTGCTGCTTGTGCTGCTGCC 240
Qy 241 caggacctggagccctgaccatcctgtactatgttggaggagaccccccaaaagtggagcag 300
Dy 241 CAGGACCTGGAGCCCTGACCATCCTGTACTATGTGGAGGAGACCCCAAGTGGAGCAG 300
Qy 301 ctctccaaactggtggtagaagcttctgtaaatgtagc 336
Dy 301 CTCCTCAACATGGTGGTGAAGTCTGTGTAATGTAGC 336
RESULT 23
CHKGFB 2187 bp mRNA VRT 28-APR-1993
LOCUS Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete cds.
DEFINITION M31154
VERSION M31154.1 GI:212758
KEYWORDS transforming growth factor-beta.
SOURCE Chicken embryo chondrocyte, cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2187)
AUTHORS Jakowlew,S.B., Dillard,P.J., Kondalish,P., Sporn,M.B. and

Roberts,A.B.
TITLE Complementary deoxyribonucleic acid cloning of a novel transforming growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes
JOURNAL Mol. Endocrinol. 2, 747-755 (1988)
MEDLINE 89096966
FEATURES
source Location/Qualifiers
1..2187
/organism="Gallus gallus"
/db_xref="taxon:9031"
40..1278
/note="transforming growth factor beta precursor"
/codon_start=1
/protein_id="AAA49089.1"
/db_xref="GI:212759"
/translation="NMVYQRAIVLVLSSLFATVSLASCTTLDLEHIKKKVEAIR GOILSKRLTSPSPESVGAHPVQIILALYNSTRELLEEMEERKEESCQNTSESYVA KEIHKFDMIOGIPHEHNLGICPKGVTSNVFRNVSAEKNSTNLFAEFRLVLPNPS SKRSEQRLEFQILRPDDEHIAKQYLSGRNVQTRGSPWLSFDVDTVRWLLHRESN LGLEISIHCPCHTFQPNQDLEHLEHLEIKFKGIDSEDDYRGDLGRLLKQDLHNP HLILMLPPHRLSEPTLGQRKKRALDITNYCFRNLNENCCVRPLYIDFQDLGKWKVH EPKGYFANFSCGCPVLRSDATTHSTVLGLYNTLNPEASASPCCPQDLEPLTILYV GRTPKVEQLSNMVVKCKCS"
40..108
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/note="transforming growth factor beta signal peptide (pot.); putative"
40..93
sig_peptide
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940..1275
mat_peptide
/note="transforming growth factor beta (5' end could be at 109)"
BASE COUNT 525 a 587 c 608 g 467 t
ORIGIN
Query Match 79.7%; Score 270.2; DB 8; Length 2187;
Best Local Similarity 87.3%; Pred. No. 2.2e-64;
Matches 296; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Qy 1 gcttggacacaaattactgctcgcgaacttgaggagaaactgctgtgccccctc 60
Dy 940 GCCCTGGATACCAACTACTGCTTCCGGAACCTGGAGAGAACTGCTGTGCGGCTCTT 999
Qy 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
Dy 1000 TACATTGACTTCGACAGGACCTGGCTGGAATGGTCCATGAGCCTAAAGGCTACTT 1059
Qy 121 gcaactctgctcagggccctggccatacctcgcagtcagtcagacacacacagcag 180
Dy 1060 GCAAACTTCTGTTGGGCGCATGCTCGTACCTCCGAGTGCAGACACCACTCACAGCAG 1119
Qy 181 gtgctggagactgtacaacactgaacctgaagcatctgctgccttgcgtgccc 240
Dy 1120 GTGCTGGGCTTGTACAAACACGCTGAACCCCGAGGCACTGCTTACCCCTGCTGTGCCA 1179
Qy 241 caggacctggagccctgaccatcctgtactatgttggaggagaccccccaaaagtggagcag 300
Dy 1180 CAGGACCTGGAGCCACTGACGATCTTGTACTATGTGGGAGGACACCCCAAGTGGAGCAG 1239
Qy 301 ctctccaaactggtggtagaagcttctgtaaatgtagctga 339
Dy 1240 CTCTCCAATATGGTGGTGAATCTCTGCAAGTGCAGCTGA 1278
RESULT 24
LOCUS A23758 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3(44/45)beta1 hybrid coding region.
ACCESSION A23758
VERSION A23758.1 GI:825592
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 8 19-MAY-1993;
CIBA-GEIGY AG

FEATURES
source Location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 63 a 109 c 98 g 66 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactgtctccgaacttgaggagaaactgtgtggtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
Qy 61 tacattgacttcgcacagagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 61 TACATTGACTTCGCACAGAGATCTGGGCTGGAGTGGTCCATGAACCTTAAGGGCTACTAT 120
Qy 121 gccaactctgtcagagcccttgcccatctacccatccagtcagacacacccacagcag 180
Db 121 GCCAACCTTCTGCTCGGGCCCTGCGCCCTACATTTGGAGCCTTGACACGCGAGTACAGCAAG 180
Qy 181 gtgctggagactgtacaacactgtgaacctgaagcatctgcctcctgtgtggtgcc 240
Db 181 GTCTGGCCCTGTACAACAGCATATAACCGCGGCGCTCGGCGCCGCTGCTGCTGCGCG 240
Qy 241 caggacctggagccctgacctctgtactatgttgaggagaccccaaaagtggagcag 300
Db 241 CAGGCGCTGGAGCCCTGCCCATCTGTACTAGTGGCCGCGCAAGCCAAAGTGGAGCAG 300
Qy 301 ctctccaacatggtggaagtctgttaaatgtagc 336
Db 301 CTGTCCACATGATCGTGGCTGCTGCTGCAAGTGCAGC 336

RESULT 25
A23759
LOCUS A23759 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3(44/45)beta2 hybrid coding region.
ACCESSION A23759
VERSION A23759.1 GI:825593
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 9 19-MAY-1993;
CIBA-GEIGY AG

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactgtctccgaacttgaggagaaactgtgtggtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
Qy 61 tacattgacttcgcacagagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 61 TACATTGACTTCGCACAGAGATCTGGGCTGGAGTGGTCCATGAACCTTAAGGGCTACTAT 120
Qy 121 gccaactctgtcagagcccttgcccatctacccatccagtcagacacacccacagcag 180
Db 121 GCCAACCTTCTGCTCGGGCCCTGCGCCCTACATTTGGAGCCTTGACACGCGAGTACAGCAG 180
Qy 181 gtgctggagactgtacaacactgtgaacctgaagcatctgcctcctgtgtggtgcc 240
Db 181 GTCTGGAGCTTATATATACCATTAATCCAGAAAGCATCTGCTCTCTGCTGCTGCTGCC 240
Qy 241 caggacctggagccctgacctctgtactatgttgaggagaccccaaaagtggagcag 300
Db 241 CAAGATTAGAACCTCTAACCATTTCTACTACATTGGCAAAACACCCAAAGATTGAACAG 300
Qy 301 ctctccaacatggtggaagtctgttaaatgtagc 336
Db 301 CTTTCTAATATGATTGATTAAAGTCTTGCAAAATGCAGC 336

RESULT 26
A48559
LOCUS A48559 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603432.
ACCESSION A48559
VERSION A48559.1 GI:2302329
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEIN
JOURNAL Patent: WO 9603432-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES Location/Qualifiers
source 1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide 1..132
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CDS 1..336
/note="protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HYBRID TGF-BETA3-2"
/protein_id="CAA03118.1"
/db_xref="GI:2302330"
mat_peptide 133..336
/translation="ALDITNYCFRNLEENCVRPLYIDFRODLGKWKVHPKGYANFC
AGAPYLMSSDTQHSRVLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLS
NMIVKSCKS"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactgtctccgaacttgaggagaaactgtgtggtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
Qy 61 tacattgacttcgcacagagatctggctggaagtgggtccatgaacctaaagggtactat 120

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Db 61 TACATTGACITCCAGAGGATCTGGGCTGGAGTGGGTCCTGATGAACCTAAGGGCTACTAT 120
Qy 121 gccaaattctgctagcccttggccataccctccgcagtcagacacacacccagcagc 180
Db 121 GCCAACTTCTGCTGGAGCATGCCGCTATTATGAGGAGTTCAGACATCCACACAGCAGG 180
Qy 181 gtgctggagctgtacaactctgaacccctgaagcatctgctgccttgcgtgctgcc 240
Db 181 GTCTGAGCTTATATAATACATAAATCCAGAGCATCTGCTTCTCTGCTGGGTGTC 240
Qy 241 cagacctgagccctgacatctgactatctgttggagagaccccaagtgagcag 300
Db 241 CAAGATTAGAACCTCTAACCAATCTCTACTACATTCGCAAAACACCCAGATTGAACAG 300
Qy 301 ctctcccaactggtggaagtctgttaaatgtagc 336
Db 301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

RESULT 27
A48573
LOCUS A48573 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603433.
ACCESSION A48573
VERSION A48573.1 GI:2302343
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
COMMENT
FEATURES
source
1. .336
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/db_xref="taxon:32644"
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1. .132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
CDS
1. .336
/notes="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HYBRID TGF-BETA3-2"
/protein_id="CAA03125.1"
/db_xref="GI:2302344"
/translation="ALDTNYCFRNLENCVRLYIDFRQDLGKWWHEPKGYANFC
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NMIVKSKCS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-36;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gcttggacaccaattactcttccgaacttgagaggaactgctgtgcccctc 60
Db 1 GCCTTGGACACCAATTAATCTGCTTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCTC 60
Qy 61 tacattgacttccgacagagctgtgggtggaagtgggtcccatgaacctaagggtactat 120
Db 61 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGTCCATGAACCTAAGGGCTACTAT 120
Qy 121 gccaaattctgctagcccttggccataccctccgcagtcagacacacacccagcagc 180
Db 121 GCCAACTTCTGCTGGAGCATGCCGCTATTATGAGGAGTTCAGACATCCACACAGCAGG 180

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Qy 181 gtgctggagctgtacaacactgtaacctgaacctgaagcatctgcctgccttgcgtgccc 240
Db 181 GTCTGAGCTTATATAATACATAAATCCAGAGCATCTGCTTCTCTGCTGGGTGTC 240
Qy 241 cagacctgagccctgacatctgactatctgttggagagaccccaagtgagcag 300
Db 241 CAAGATTAGAACCTCTAACCAATCTCTACTACATTCGCAAAACACCCAGATTGAACAG 300
Qy 301 ctctcccaactggtggaagtctgttaaatgtagc 336
Db 301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

RESULT 28
AF152592
LOCUS AF152592 244 bp mRNA MAM 28-MAR-2001
DEFINITION Capreolus capreolus transforming growth factor beta 3 (TGF-b3)
mRNA, partial cds.
ACCESSION AF152592
VERSION AF152592.1 GI:8132130
KEYWORDS
SOURCE roe deer.
ORGANISM Capreolus capreolus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
Cervidae; Odocoileinae; Capreolus.
REFERENCE
AUTHORS Wagener,A., Blottner,S., Goeritz,F. and Fickel,J.
TITLE Detection of growth factors in the testis of roe deer (Capreolus
capreolus)
JOURNAL Anim. Reprod. Sci. 64 (1-2), 65-75 (2000)
MEDLINE 20532861
PUBMED 11078967
REFERENCE
AUTHORS Wagener,A. and Fickel,J.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-1999) Evolutionary Genetics, Institute for Zoo
Biology and Wildlife Research, Alfred-Kowalke-Str. 17, Berlin
D-10315, Germany
FEATURES
source
1. .244
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/db_xref="taxon:9858"
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<1..>244
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CDS
<1..>244
/gene="TGF-b3"
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/translation="EENCCVRLYIDFRQDLGKWWHEPKGYANFCGCPYLRSDD
TTHSTVLGLYNTLNPEASAPCCVQDLEPLTILYV"
BASE COUNT 52 a 84 c 57 g 51 t
ORIGIN

Query Match 65.4%; Score 221.6; DB 7; Length 244;
Best Local Similarity 94.3%; Pred. No. 8.2e-51;
Matches 230; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 34 gagagaactctgtgtgcgcccctctacattgacttccgacagatctggctggaag 93
Db 1 GAGGAGAACTCTGTGCGCCCTCTCTATATTCTCCGACAGATCTGGGTGAAA 60
Qy 94 tgggtccatgaactaagggtactatcgcaactctgctcagcgccttgcctacacctc 153
Db 61 TGGGTCCATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCATGCCATACCTC 120
Qy 154 cgcagtcagacacacacccacagcagcgtgctgggactgtacaacactctgaacctgaa 213

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QY 1 gcttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtggtgccccctc 60
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Db 1284 GCCTGGATACCACTACTGCTTCAGCTCCACGGAGAAAGAACTGCTGCGTGGCAGCTC 1343

QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
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Db 1344 TACATTGACTTCCGGAAGGACCTGGCTGGAAGTGGATTTCATGAACCCCAAGGGCTACCAAT 1403

QY 121 gcaaatctctcagggccttgcccatacctcccgagtcgacagacacacccacacagcag 180
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Db 1404 GCCAAATTTCTGCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1463

QY 181 gtgctgggactgtacacactctgaacctgaagcatctgctcgcctgtgctgcccc 240
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Db 1464 GTCCTGGCTCTGTACAACAGACACACCCGGCGCTGCGCGCGCGCTGCTGCGTGGCG 1523

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QY 301 ctctcaacatggtgtgaagtcttgtaaatgtagctga 339
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Db 1584 CTGTCCAACATGATGCTGGGTTCTCTGCAAGTGCAGCTGA 1622

RESULT 31
LOCUS PIGTGFB1A 3206 bp mRNA MAM 31-MAR-1995
DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION M23703
VERSION M23703.1 GI:755044
KEYWORDS transforming growth factor-beta-1.
SOURCE Sus scrofa (strain miniature swine) cDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 3206)
AUTHORS Sporn,M.B. and Roberts,A.B.
TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
JOURNAL Evidence for alternate splicing and polyadenylation
MEDLINE J. Biol. Chem. 263 (34), 18313-18317 (1988)
COMMENT 89054010
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                    RRALDTNYSSTKKNCCVROLYIDFRKDLGNKWIHEPKGYHANFCLGPCPYIWSLDT
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polyA_signal 645 a 1041 c 924 g 596 t
polyA_site
BASE COUNT 645 a 1041 c 924 g 596 t
ORIGIN

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Best Local Similarity 76.1%; Pred. No. 1.4e-47;
Matches 256; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtggtgccccctc 60
  || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1740 GCCTGGATACCACTACTGCTTCAGCTCCACGGAGAAAGAACTGCTGCGTGGCAGCTC 1799

QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
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Db 1800 TACATTGACTTCCGGAAGGACCTGGCTGGAAGTGGATTTCATGAACCCCAAGGGCTACCAT 1859

QY 121 gcaaatctctcagggccttgcccatacctcccgagtcgacagacacacccacagcag 180
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Db 1860 GCCAAATTTCTGCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1919

QY 181 gtgctgggactgtacacactctgaacctgaagcatctgctcgcctgtgctgcccc 240
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Db 1920 GTCTGGCTCTGTACAACAGACACACCCGGCGCTGCGCGCGCTGCTGCGTGGCG 1979

QY 241 caggacctggagccctgacctctgtactatgtgtggagagacccccaaaagtgaagcag 300
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Db 1980 CAGGGCTGGAGCCACTGCCCATGTGTGACTACGTGGGGCGCAAGCCCAAGGTGGAGCAG 2039

QY 301 ctctcaacatggtgtgaagtcttgtaaatgtagctga 339
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Db 2040 CTGTCCAACATGATGCTGGGTTCTCTGCAAGTGCAGCTGA 2078

RESULT 32
LOCUS OCAF000133 339 bp mRNA MAM 06-MAY-1997
DEFINITION Oryctolagus cuniculus transforming growth factor beta-1 mRNA,
partial cds.
ACCESSION AF000133
VERSION AF000133.1 GI:2072531
KEYWORDS rabbit.
SOURCE Oryctolagus cuniculus
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Rabbit transforming growth factor beta-1 active region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Ophthalmology, Med.Univ. S.C., 171 Ashley
Avenue, Charleston, SC 29464, USA
FEATURES
    Location/Qualifiers
        1..339
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                LGPCPYIWSLDTQYSKVALYNQHNPGASAAPCCVPALEPLPIVYVGRKPKVEQLS
                NMIVRSCKS"
BASE COUNT 71 a 114 c 97 g 57 t
ORIGIN

Query Match 60.8%; Score 206.2; DB 7; Length 339;
Best Local Similarity 75.5%; Pred. No. 1.4e-46;
Matches 256; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtggtgccccctc 60
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ORIGIN

Query Match	60.4%	Score	204.6;	DB	10;	Length	862;
Best Local Similarity	75.2%;	Pred.	No. 3.5e-46;				
Matches	255;	Conservative	0;	Mismatches	84;	Indels	0; Gaps
Qy	1	gctttggacaccaattactgtctccgaaccttgaggagagaactcgtgtgtgcgccccc	60				
Db	1	GCCGTGACACCACACTATTGCTTCAGTCTCACGGAGAGAATACTGCTCGTGCGCAGCTG	60				
Qy	61	tacaattgacttcgcacagggatctgggttggaaagtgggtccatgaacctaaagggctactat	120				
Db	61	TACATTGACTTCGCCAAGGACCTCGCGTTGGAACTGGATCCAGAGCCCCAAGGGTACCAT	120				
Qy	121	gcaacttgtctcagggcccttgccccatactccgcagctgcagacacaaccacagcacg	180				
Db	121	GCCAATCTTGCCTCGGGGCCCTGCCTTCATATTTGGAGCCTGGACACGSCAGTACAGCAAG	180				
Qy	181	gtctgggaactgtacaacactctgaacccctgaagcatctgctcgacctgtgtcggtgcc	240				
Db	181	GTCTTGCCCTGTACAACACAGCATAAACCGGGCGCCCTCGGGCGGCCCTGTGCTGGTGGCG	240				
Qy	241	caggacactggagcccttgaccatcctgtactatgttgggagagacccccaaagtggagcag	300				
Db	241	CAGCGCTGGAGCGCTGCCCATCGTACTACTACGTGGGCGCCGAAGCCCAAGGTGGAGCAG	300				
Qy	301	ctctccaacatgggtggtagactttgttaaatgtagtcta	339				
Db	301	CTGTCCAACATGATCTGCGCTCTCTGCAAGTGCAAGCTGA	339				

RESULT 43

BOVTFGB	BOVTFGB	1117 bp	mRNA	MAM	27-APR-1993
LOCUS	Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.				
DEFINITION	Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.				
ACCESSION	M36271				
VERSION	M36271.1	GI:163747			
KEYWORDS	transforming growth factor-beta 1.				
SOURCE	Bovine fibropapilloma, cDNA to mRNA, (library of Okayama and Berg).				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 1117)				
AUTHORS	Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B. and Baker, C.C.				
TITLE	Complementary deoxyribonucleic acid cloning of bovine transforming growth factor-beta-1				
JOURNAL	Mol. Endocrinol. 1, 693-698 (1987)				
MEDLINE	9104252				

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    INFGSSRGDLATIIGMRPPFLMLATPLERAQHLHSSRRRALDINCYFCSSTKKN
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Query Match

60.4%: Score 204.6: DB 7: Length 1117:

Best Local Similarity 75.2%; Pred. No. 3.4e-46;									
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;									
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Db	612	GCCTGGACAC	CAACACTACTGCTTTCAGCTCCACAGAA	AAACTGCTGCTGTTCGTCAGCTC	671				
Qy	61	tacattgacttc	cgacaggatctgggctgggaagtgggtccat	gaacctaagg	gggtactat	120			
Db	672	TACATTGACTTC	CGGAAGGACCTGGGCTGGAAGTGGATTTCAT	GAAACCAACCAAGGGGTACCCAC	731				
Qy	121	gcaactctgtc	tgaagcccttggccatactccgcagtcgagtcag	acacacacacag	cagcag	180			
Db	732	GCCAAATTTCT	CGCTGGGGCCCTGCGCTTACATCTGAGCGCTGGAT	CACATACACATACAGCAAG	791				
Qy	181	gtctggagctg	tacaacactctgaacccctgaacatctgcctcctct	ctgctggtgccc	240				
Db	792	GTCTGGCCCTGT	ACAAACACAGACACCCGGCGCTTCGGCGGCGCGCTG	CTGCTGGTGCCT	851				
Qy	241	cagagctggag	cccttgacatactgtactatgttggaggacccccaa	agtgagcag	300				
Db	852	CAGCGCTGGAG	CCCTTGCCATGCTACTACGTGGCGCACAAGCCAAAGT	GGAGCAG	911				
Qy	301	ctctcaacatg	tgtgtgaagttcttgaatgtagctga	339					
Db	912	TTGTCCAACAT	GATGCTGTGCGCTCTCGCAAGTGCAGCTCA	950					
RESULT 44									
OATGFB1									
LOCUS	O.aries	mRNA	1173 bp	MAM	18-APR-1995				
DEFINITION	O.aries mRNA for transforming growth factor-beta 1.								
ACCESSION	X76916								
VERSION	X76916.1 GI:496648								
KEYWORDS	TGF-beta 1; transforming growth factor-beta 1.								
SOURCE	sheep.								
ORGANISM	Ovis aries								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.								
AUTHORS	1 (bases 1 to 1173)								
TITLE	Woodall,C.J., McLaren,L.J. and Watt,N.J.								
JOURNAL	Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1								
MEDLINE	Gene 150 (2), 371-373 (1994)								
AUTHORS	95121932								
TITLE	2 (bases 1 to 1173)								
JOURNAL	Woodall,C.								
MEDLINE	Direct Submission								
AUTHORS	Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh, Edinburgh EH9 1QH, UK								
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CDS	1. .1173								
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	/db_xref="SWISS-PROT:P50414"								
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BASE COUNT	245 a 378 c 336 g 214 t								
ORIGIN	/product="transforming growth factor-beta 1"								

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Query Match 60.4%; Score 204.6; DB 7; Length 1173;
Best Local Similarity 75.2%; Pred. No. 3.3e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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DB 835 GCCCTGGACACCAACTACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGCTCAGCTC 894

QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 895 TACATTGACTTCCGGAAGACCTGGCTGGAGTGGATTCCAGAACCCCAAGGCTTACCAC 954

QY 121 gccaaacttctgctcagggcccttgcccatatctcccgagtcgagacacacccacagcag 180
DB 955 GCCAATTTCTGCTGGGGCCCTGTCCCTACATCTGGAGCTGGACACACAGTACAGCAAG 1014

QY 181 gtgctggagactgtacacacacttgaaacctgaagctatctgctccttctgtgctgccc 240
DB 1015 GTCTGGGCCCTGTACACACAGCACAAACCCGGCGCATCGCGGCCGCTGCTGCTGCT 1074

QY 241 caggacctggagccctgaccatctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 1075 CAGGCGCTGGAAACCCCTGCCCATCTGTACTACGTGGGCCGCAAGCCCAAGTGGAGCAG 1134

QY 301 ctctccaaactgtgtgaagtcttgtaaatgtagctga 339
DB 1135 TTGTCCAACATGATGTCGCTGCTCTGCAAGTGCAGCTGA 1173

RESULT 45
DOGTGFB1A 1369 bp mRNA MAM 30-OCR-1994
LOCUS DogTFB1A
DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete cds
ACCESSION L34956
VERSION L34956.1 GI:516071
KEYWORDS homologue; transforming growth factor-beta 1.
SOURCE Canis familiaris adult jugular vein endothelial CDNA to mRNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.
TITLE Cloning of a canine cDNA homologous to human transforming growth factor-beta 1 (TGFBeta1)
JOURNAL Unpublished (1994)
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            KLAQEVRLQVNTSNRWYLSNRLPLDTPWLSFDVTGVVQWLSHGGEVEGER
            LSAHSCDSKSDLDQVINGFSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQ
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ORIGIN

Query Match 60.4%; Score 204.6; DB 7; Length 1369;
Best Local Similarity 75.2%; Pred. No. 3.3e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 952 TACATTGACTTCCGGAAGATCTGGCTGGAGTGGATCCATGAGCCCAAGGTTACCAC 1011

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QY 181 gtgctggagactgtacacacacttgaaacctgaagcatcttgccttctgtgctgcccc 240
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QY 241 caggacctggagccctgaccatcttccatctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 1132 CAGGCGCTGGAGCCACTGCCCCATCTGTACTACGTGGGCCGCAAGCCCAAGTGGAGCAG 1191

QY 301 ctctccaaactgtgtgaagtcttgtaaatgtagctga 339
DB 1192 CTGTGCAACATGATGTCGCTCTCTGCAAGTGCAGCTGA 1230

RESULT 46
I08268
LOCUS I08268 1560 bp PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent EP 0373994.
ACCESSION I08268
VERSION I08268.1 GI:589017
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Purchio,A.F., Gentry,L., Twardzik,D. and Brunner,A.M.
TITLE Cloning and expression of simian transforming growth factor-beta 1
JOURNAL Patent: EP 0373994-Al 20-JUN-1990;
FEATURES
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ORIGIN

Query Match 60.4%; Score 204.6; DB 10; Length 1560;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtgccccctc 60
DB 1095 GCCCTGGACACCAACTACTGCTTCAGCTCCACGAGAAAGAACTGCTGCTGCGGAGCTG 1154

QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 1155 TATATTGACTTCCGGAAGACCTTCGCTGGAAGTGGATCCAGAGCCCAAGGCTTACCAC 1214

QY 121 gccaaacttctgctcagggcccttgcccatatctcccgagtcgagacacacccacagcag 180
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Db	1215																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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YKAEVTRVLVMEHTEIYDKFKQSTHYSIMFFENTSELREAVPEPVLSSRAELRLRL
KLKVEHQVELYKQYSNNRWYLSNRLAPSDSPWLSFDVTGTVRQWLSRGEIEGFR
LSAHCSDSDNTLOVDINGFTTGRGLDGLATIHGMNRPFLLLMATPLERAOHLQSSRH
RRALDTNYCFSSSTENKCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDT
QYSKVLALYNQHNPGSAAPCCVQALPELPYIVYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT 341 a 648 c 493 g 298 t
ORIGIN

FEATURES source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:2323 IMAGE:3356605"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
447..1619
/codon_start=1
/product="Similar to transforming growth factor, beta 1"
/protein_id="AAH01180.1"
/db_xref="GI:12654683"
/translation="MPPSGRLRLLLPLLLVLLTPGPAAGLSTCKTIDMELVKRR
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YKAEVTRVLVMEHTEIYDKFKQSTHYSIMFFENTSELREAVPEPVLSSRAELRLRL
KLKVEHQVELYKQYSNNRWYLSNRLAPSDSPWLSFDVTGTVRQWLSRGEIEGFR
LSAHCSDSDNTLOVDINGFTTGRGLDGLATIHGMNRPFLLLMATPLERAOHLQSSRH
RRALDTNYCFSSSTENKCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDT
QYSKVLALYNQHNPGSAAPCCVQALPELPYIVYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT 341 a 648 c 493 g 298 t
ORIGIN

Query Match 60.4%; Score 204.6; DB 91; Length 1780;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttggaggagaactgtgtgtgccccctc 60
Db 1281 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAAGTGTGCTGGCGAGCTG 1340

Qy 61 tacattgacttcgacagatctggctggaagtggctggaactgaacctgaagggctactat 120
Db 1341 TACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATTCACGAGCCCAAGGCTACCAT 1400

Qy 121 gcaacttctgtcagggcccttgcccatcctccgcagtcgagacacacacacagcacg 180
Db 1401 GCAAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGGACACGCGAGTACAGCAAG 1460

Qy 181 gtgtggactgtacacacactctgaacctgaagcactctgctcgtcgtgctgcccc 240
Db 1461 GTCTTGGCCCTGTACAAACGAGCATAAACCGGGCGCTCGGGCGGCGCTGCTGCTGCGCG 1520

Qy 241 caggaacctggagccctgacacactctgtactgttggaggagacccccaaagtggagcag 300
Db 1521 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1580

Qy 301 ctctccaaactgtgtggaagtcttgaagttagctga 339
Db 1581 CTGTCCACATGATCGTGGCTCCTGCAAGTGCAGCTGA 1619

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 6 Row: e Column: 10.

LOCUS BC001180 1780 bp mRNA PRI 16-MAR-2001
DEFINITION Homo sapiens, Similar to transforming growth factor, beta 1, clone
MGC:2323, mRNA, complete cds.
ACCESSION BC001180
VERSION BC001180.1 GI:12654682
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1780)
AUTHORS Shashih, H., Ishii, Y., Miyata, Y., Miyazono, K., Miyagawa, K. and

Query Match 60.4%; Score 204.6; DB 91; Length 1780;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttggaggagaactgtgtgtgccccctc 60
Db 1281 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAAGTGTGCTGGCGAGCTG 1340

Qy 61 tacattgacttcgacagatctggctggaagtggctggaactgaacctgaagggctactat 120
Db 1341 TACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATTCACGAGCCCAAGGCTACCAT 1400

Qy 121 gcaacttctgtcagggcccttgcccatcctccgcagtcgagacacacacacagcacg 180
Db 1401 GCAAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGGACACGCGAGTACAGCAAG 1460

Qy 181 gtgtggactgtacacacactctgaacctgaagcactctgctcgtcgtgctgcccc 240
Db 1461 GTCTTGGCCCTGTACAAACGAGCATAAACCGGGCGCTCGGGCGGCGCTGCTGCTGCGCG 1520

Qy 241 caggaacctggagccctgacacactctgtactgttggaggagacccccaaagtggagcag 300
Db 1521 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1580

Qy 301 ctctccaaactgtgtggaagtcttgaagttagctga 339
Db 1581 CTGTCCACATGATCGTGGCTCCTGCAAGTGCAGCTGA 1619

RESULT 50
LOCUS BC001180 1821 bp RNA PAT 29-SEP-1997
DEFINITION DNA encoding human prepro TGF-beta1.
ACCESSION E03028
VERSION E03028.1 GI:2171250
KEYWORDS JP 19911180192-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1821)
AUTHORS Ohashi, H., Ishii, Y., Miyata, Y., Miyazono, K., Miyagawa, K. and


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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=placenta and glyoblastoma; FH Key
Location/Qualifiers

CDS 842..2014
/locus_start=3
/product="pre TGF-beta"
/mat_peptide
5'UTR 1676..2011
3'UTR 1..841
stem_loop 37..113
stem_loop 2015..2537
polyA_site 2015..2100
2514..2519.
Location/Qualifiers
1..2527
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 472 a 888 c 735 g 432 t
ORIGIN
Query Match 59.9%; Score 203; DB 10; Length 2527;
Best Local Similarity 74.9%; Pred. No. 8.4e-46;
Matches 254; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgcttcgcaacttgaggagaaactgctgtggtgccccctc 60
DB 1676 GCCCTGGACACCAACTATGCTTCAGCTCCACGGAGAGAACTGCTGGCGGAGCTG 1735
QY 61 tacattgactccgacagatctgggtggaagtgggtccatgaacctaaaggtctactat 120
DB 1736 TACATTGATTTCCGACAGAGACTCGGCTGGAAAGTGGATCCACGAGCCCAAGGCTACCAT 1795
QY 121 gccaaattctcagcccttgccatactccgagcagtcgagacacacacacagcag 180
DB 1796 GCCAACTTCTCGCGGCCCTGCCCTTACATTTGGAGCCCTGGACACGAGTACAGCAAG 1855
QY 181 gtgctggagctgacacactctgaacctgaagctgctgctgctgctgctgctgctg 240
DB 1856 GTCTGGCCCTGTACACACGACATACCCGGCGCTCGCGCGCGCTGCTGCTGCTGCG 1915
QY 241 caggacctggagccctgacctctgactatgttggaggagcccccaagtgagcag 300
DB 1916 CAGGCGTGGAGCCGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1975
QY 301 ctctccacatggtggtgaagtcttgaatgtagctga 339
DB 1976 CTGTCCACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2014

RESULT 57
SHPGFB1W SHPGFB1W 334 bp mRNA MAM 11-SEP-1994
LOCUS Ovis aries transforming growth factor-beta 1 mRNA, partial cds.
DEFINITION L36038
ACCESSION L36038
VERSION 1
KEYWORDS transforming growth factor-beta 1.
SOURCE Ovis aries (strain Merino) fetus dorsal skin cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 334)
AUTHORS Sutton,R., Ward,W.G., Raphael,K.A. and Cam,G.R.
TITLE Growth factor expression in skin during wool follicle development
JOURNAL Unpublished (1994)
FEATURES
source
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/organism="Ovis aries"
/strain="Merino"
/db_xref="taxon:9940"
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/dev_stage="fetus"
/tissue_type="dorsal skin"
<1..334
/product="transforming growth factor-beta 1"
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/protein_id="AAA31526.1"
/db_xref="GI:535760"
/translation="DTNYCFSTERNKNCVRLQYIDFRKDLGKWIHPKGYHANFCILG
PCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPQALEPLPIVIVYVGRKPKVEQLSNM
IVRSCKCS"
BASE COUNT 70 a 106 c 94 g 64 t
ORIGIN
Query Match 59.8%; Score 202.8; DB 7; Length 334;
Best Local Similarity 75.4%; Pred. No. 1.2e-45;
Matches 252; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 5 tggacaccaattactgcttcgcaacttgaggagaaactgctgtggtgccccctctaca 64
DB 1 TGGACACCAACTACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGTTGCTCAGCTCTACA 60
QY 65 ttgaacttcgacaggaatctgggtggaagtgggtccatgaacctaaaggtctactatgcca 124
DB 61 TTGACTTCGGAGAACCTGGGCTGGAAAGTGGATTTCATGAACCAAGGGGTACACGCCA 120
QY 125 actctgctcagcccttgcctatactccgagtcgagcagtcgagacacacacacagcagtg 184
DB 121 ATTTCGCTGGGCGCCCTGCCCTTACATCTGGAGCCCTGGACACGAGTACAGCAAGGTTC 180
QY 185 tgggactgtacacactctgaacctgaagctgctgctgctgctgctgctgctgctgctg 244
DB 181 TGGCCCTGTACACACGACACACCCGGCGCATCGGGCGCGCTGCTGCTGCTCAGG 240
QY 245 acttgagccctgacctctgactatgttggaggagcccccaagtgagcagctct 304
DB 241 CGCTGGAACCCCTGCCATCGTGTACTAGCTGGGCGCGCAAGCCAGGTGGAGCAGTTGT 300
QY 305 ccaacatggtggaagtcttgaatgtagctg 338
DB 301 CCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334

RESULT 58
A23754 A23754 336 bp mRNA PAT 25-JAN-1995
LOCUS TGF-beta1(44/45)beta2 hybrid coding region.
DEFINITION A23754
ACCESSION A23754
VERSION A23754.1 GI:825588
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 4 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 90 a 92 c 72 g 82 t
ORIGIN
Query Match 59.5%; Score 201.6; DB 9; Length 336;
Best Local Similarity 75.0%; Pred. No. 2.7e-45;
Matches 252; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
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YAAKEVTRVLVMEKENEYKIVETGSHSIYWFNFNASLRAA VPDPMLLSRALRLRL
LSAQVEHLYQYISNSWYLSNRLITPDSPEWLSFDVTVGVYRQMLSQGMEGLR
LSHCPDSDLVINGIFSSRRGLDITIDGNRPFLLLMATPLERAQQLHSSRH
RRALDTYSSSTEKNCCVRQLYIDFRKDLGWKIHHPKGVHANFCLGCPYIWSLOT
QYSKVLALYNQHNPGASAAAPCCVPQVLEPLPIVYVVGKPKVQLSNMIVRSCKS"
BASE COUNT 230 a 395 c 361 g 201 t
ORIGIN

Query Match 59.4%; Score 201.4; DB 7; Length 1187;
Best Local Similarity 74.6%; Pred. No. 2.6e-45;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
Qy 1 gcttggacacaaattactgttcgcgaacttgaggagaaactgtgtgtgccccctc 60
Db 849 GCTCTGGACACCAACTACTGTCTCCAGCTCCACAGAGAAGAACTGTGCGGTACGGCAGCTG 908
Qy 61 tacattgaacttcagacaggaactgtggctggaagtgggtccatgaacctaaaggctactat 120
Db 909 TACATTGACTTTCGACAGGATCTGGGCTGGAAGTGGATCCACGAGCCCAAGGGCTTACCAC 968
Qy 121 gccaaactctgtcagcgcccttgccataacctccgcagctcagacacacacccacagcagc 180
Db 969 GCCAACTCTGCTGGGCGCTGCCCTTACATTTGGACCTGGACACCCAGTACAGCAAG 1028
Qy 181 gtgtggagactgtacaacactctgaacctgaagcctgactgctgctgtgtgctgcccc 240
Db 1029 GTCCTGGCCCTGTACACACGACCAACCCGGCGCGCTGGCGGCGCGCTGCTGCGTGGCG 1088
Qy 241 caggacactgagcccttgacactctgactatctgtgtggaagagaccccaagtgaggagcag 300
Db 1089 CAGGTGTGGAGCGCTGCCCTCGTACTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1148
Qy 301 ctctccacacatggtggaagtctgtgaaatgtagctga 339
Db 1149 CTGTCCACATGATCGTGGCTCTGCAAGTGCAGCTGA 1187

RESULT 61
AF153013 2796 bp mRNA ROD 24-JUL-2000
LOCUS Rattus norvegicus TGF-beta 2 short form precursor (TGF-beta2) mRNA,
DEFINITION complete cds.
ACCESSION AF153013
VERSION AF153013.1 GI:4929797
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2796)
AUTHORS Koishi,K., Dalzell,K.G. and McLennan,I.S.
TITLE The expression and structure of TGF-beta2 transcripts in rat
muscles
JOURNAL Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000)
MEDLINE 20461836
REFERENCE 2 (bases 1 to 2796)
AUTHORS Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-1999) Anatomy & Structural Biology, University of
Otago, Dunedin PO Box 913, New Zealand
FEATURES Location/Qualifiers
source 1..2796
/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
/tissue_type="muscle"
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308..1552
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/product="TGF-beta 2 short form precursor"
/protein_id="AAD34160.1"
/db_xref="GI:4929798"
/translation="NHCVCLVRLTLLHLPVALSLSTCTLDMDQFMRKRRIEARGOI
LSKLITSPEDYPPDPEVPPVISIYNSTRDLQKASRRRAACERERSDEEYAKE
YKIDMPHSFSENAIPPTFYRPIRVFRDYSTMKNASNLVKAERFVRLQNPKR
VAEQRIELQILKSKDLYTQYIDSKVVKTAEGEWLSFDVDAVHEWLHKKRNL
GFKTLLHLLPSYRLSEQSSRRRRKALDAAYCFRNVDNCCLRPLYIDFKRLGWK
IHEPKGYNAFCAGACPYLWSSDTQHTKVLVLYNTINPEASAPCCVQSODLEPLITY
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1843..1848
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2077..2082
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2752..2757
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BASE COUNT 812 a 659 c 583 g 742 t
ORIGIN

Query Match 59.4%; Score 201.4; DB 94; Length 2796;
Best Local Similarity 74.6%; Pred. No. 2.3e-45;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
Qy 1 gcttggacacaaattactgttcgcgaacttgaggagaaactgtgtgccccctc 60
Db 1214 GCTTGGATGCGCCCTATTGCTTTAGGAATGTGCAGGATAATTGCTGCCCTCGCCCTTT 1273
Qy 61 tacattgaacttcagacaggaactgtggctggaagtgggtccatgaacctaaaggctactat 120
Db 1274 TACATTGATTTTAAAGAGGATCTTGGATGGAATGATCCATGAACCCAAAGATACAAT 1333
Qy 121 gccaaactctgtcagcgcccttgccataacctccgcagctcagacacacacccacagcagc 180
Db 1334 GCTAACTCTGCTGGGCGCATGCCCTTATCTGTGGAGTTCAGACACACACACACAAA 1393
Qy 181 gtgtggagactgtacaacactctgaacctgaagcctgactgctgctgctgctgcccc 240
Db 1394 GTCTTCAGCCTGTACAACACCAACCAACCCGAGCTTCGTCTCCCTTCCTGCTGTGTGTC 1453
Qy 241 caggacactgagcccttgacactctgtactatgttggaggagaccccaagtgaggagcag 300
Db 1454 CAGGATCTGGACACCACTGACCATCTCTACTACATTGGCAATACGCCCAAGATCGAACAG 1513
Qy 301 ctctccacacatggtggaagtctgtgaaatgtagctga 339
Db 1514 CTTTCCAACATGATCGTCAAGTCTTGTAATGACAGCTAA 1552

RESULT 62
AF153012 2880 bp mRNA ROD 24-JUL-2000
LOCUS Rattus norvegicus TGF-beta 2 long form precursor (TGF-beta2) mRNA,
DEFINITION complete cds.
ACCESSION AF153012
VERSION AF153012.2 GI:4980482
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2880)
AUTHORS Koishi,K., Dalzell,K.G. and McLennan,I.S.
TITLE The expression and structure of TGF-beta2 transcripts in rat
muscles
JOURNAL Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000)
MEDLINE 20461836
REFERENCE 2 (bases 1 to 2880)

AUTHORS Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAY-1999) Anatomy & Structural Biology, University of
 Otago, Dunedin PO Box 913, New Zealand
 COMMENT On Jun 3, 1999 this sequence version replaced gi:4929795.
 FEATURES
 source Location/Qualifiers

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 /strain="Wistar"
 /db_xref="taxon:10116"
 /tissue_type="muscle"
 1..2880
 /gene="TGF-beta2"
 308..1636
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 /feature="minor variant"
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 /translation="MHYCVLRTEFLHLPVALSLSTCTSLDMDQFMKRLEAIRGOI
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 KTRAGEWLSFVDVDAHEWHLHDKRNLGFKISLHPCGCTFIPSNNYIIPNKSQLEA
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 2161..2166
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 2836..2842
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 /feature="putative"

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 BASE COUNT
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 Best Local Similarity 74.6%; Pred. No. 2.3e-45;
 Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 QY 1 gctttgacaccaatactgcttcgcaacttgaggagagaactgctgtgtgogccccc 60
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 Db 1358 TACATTGATTTTAAAGAGGATCTTGATGGAATGGATGATGATGATGATGATGAT 1417
 QY 121 gcaactctctcagccctggccatccctccgagtcgagacacacacacacagcag 180
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 Db 1418 GCTAATTCTGCTGGGCGATGCCCTTATCTGTGAGTTCAGACACACACACACAA 1477
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 QY 241 caggactggagccctcgacctctgtactatgttgaggagacccccaaagtggagcag 300
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 Db 1538 CAGGATCTGGACCACTGACCATCTCTACTATGGAATACGCCCAAGATCGAACAG 1597
 QY 301 ctctccacatggtggtgaagcttgtaaatgtagctga 339
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 Db 1598 CTTTCCACATGATGCTCAAGCTTGTGTAATGCAGCTAA 1636

RESULT 63
 AF135598
 LOCUS AF135598 1255 bp mRNA ROD 11-APR-1999

DEFINITION Rattus norvegicus transforming growth factor beta 2 precursor,
 mRNA, complete cds.
 ACCESSION AF135598
 VERSION AF135598.1 GI:4580714
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1255)
 AUTHORS Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
 Perantoni,A.O.
 TITLE Rat transforming growth factor-beta2, complete coding sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1255)
 AUTHORS Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
 Perantoni,A.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1999) Laboratory of Comparative Carcinogenesis,
 National Cancer Institute, FCRDC, Bldg.538, Room 206, Frederick, MD
 21702, USA
 FEATURES
 Location/Qualifiers
 1..1255
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 BASE COUNT 334 a 353 c 299 g 269 t
 ORIGIN
 Query Match 58.9%; Score 199.8; DB 94; Length 1255;
 Best Local Similarity 74.3%; Pred. No. 7e-45;
 Matches 252; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
 QY 1 gctttgacaccaatactgcttcgcaacttgaggagagaactgctgtgtgccccctc 60
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 QY 61 tacattgacttcgacaggatctggctggaagtgggtccatgaacctaaaggctactat 120
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 Db 968 TACATTGATTTTAAAGAGGATCTTGATGGAATGGATGATGATGATGATGATGAT 1027
 QY 121 gcaactctctcagccctggccatccctccgagtcgagacacacacacacagcag 180
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 QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctcgctgtgctgctgccc 240
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 Db 1088 GTCTCAGCGCTGTACAACACCATAAACCCGAGGCTTCTGCTCCCTTGTGTGTGTC 1147
 QY 241 caggactggagccctcgacctctgtactatgttgaggagacccccaaagtggagcag 300
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 Db 1148 CAGGATCTGGACCACTGACCATCTCTACTATGGAATACGCCCAAGATCGAACAA 1207
 QY 301 ctctccacatggtggtgaagcttgtaaatgtagctga 339
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RESULT 64
RN0132718      1274 bp      mRNA      ROD      21-OCT-2000
LOCUS          Rattus norvegicus mRNA for TGF-beta2 protein.
DEFINITION
ACCESSION      AJ132718
VERSION        AJ132718.1 GI:4753895
KEYWORDS       tgf-beta2 gene; TGF-beta2 protein.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
REFERENCE      1 (bases 1 to 1274)
AUTHORS        Konrad, L., Albrecht, M., Renneberg, H. and Amuller, G.
TITLE          Transforming growth factor-beta2 mediates mesenchymal-epithelial
JOURNAL        Interactions of testicular somatic cells
MEDLINE        Endocrinology 141 (10), 3679-3686 (2000)
REFERENCE      2 (bases 1 to 1274)
AUTHORS        Konrad, L.
TITLE          Direct Submission
JOURNAL        Submitted (02-FEB-1999) Konrad L., Anatomy and Cell Biology,
Philipps University, Robert-Koch-Str. 6, 35033 Marburg, GERMANY
FEATURES       Location/Qualifiers
               1..1274
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                /db_xref="GI:4753896"
                /db_xref="SPTREMBL:Q9R2B8"
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                VAQRIELHYILKSLDPTQYIDSKVVKYRAEGWLSFDVTDVHVEWLHKDRNL
                GFKISHPCPTIPNNYIIPNKSELEAFAGIDGTSTYAGDQRTIKSTRKSSG
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BASE COUNT    339 a 354 c 303 g 278 t
ORIGIN

Query Match          58.9%; Score 199.8; DB 95; Length 1274;
Best Local Similarity 74.3%; Pred. No. 7e-45;
Matches 252; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 gctttgacaccaattactgcttcgcgaacttgaggagaactgctgtgctgccccctc 60
Db 922 GCTTTGGATGCCGCTATTGCTTAGGAATGTGCAGGATAATTGCTCGCTCGCCTCTT 981

Qy 61 tacattgacttcgacagatctggctgggaagtgggtgccatgaacctaaagggtactat 120
Db 982 TACATTGATTTTAAGAGGGATCTTGGATGGAATGGATGATGATGATGATGATGATGAT 1041

Qy 121 gcaactctgtcagcccttgccatactcgcagctgagtcagacacacacacagcag 180
Db 1042 GCTAACCTCTGCTGCTGGGATGCCCTTATCTGTGGAGTTCAGACACACACACACAAA 1101

Qy 181 gtgtggagctgtacacactctgaacctgaagctgcatctgcctgcctgctgctccc 240
Db 1102 GTCTAGCTGTACACACACATTAACCCGAGAGCTTCTGCTCCCTTGTGTGTCTCC 1161

Qy 241 caggacctggagccccctgaaccatctgtactatgttggggagggagggagggagcag 300
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Db 1162 CAGGATCTGGAACCACTGACCATCTCTACTACTATTGGTAATACGCCCAAGATGAACAA 1221
Qy 301 ctctccaaatggtggtgaagtctttaaagttagctga 339
Db 1222 CTTTCCAACATGATGTCAGTCAAGTCTTGTAAATGCAGCTAA 1260

RESULT 65
I08275      1561 bp      PAT      02-DEC-1994
LOCUS          I08275
DEFINITION     Sequence 3 from Patent EP 0374044.
ACCESSION      I08275
VERSION        I08275.1 GI:589015
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 1561)
AUTHORS        Purchio, A.F. and Madisen, L.
TITLE          TGF-beta 1 / beta 2 : a novel chimeric transforming growth
JOURNAL        Patent: EP 0374044-A2 3 20-JUN-1990;
FEATURES       Location/Qualifiers
               1..1561
                /organism="unknown"
BASE COUNT     304 a 544 c 442 g 271 t
ORIGIN

Query Match          57.5%; Score 195; DB 10; Length 1561;
Best Local Similarity 73.5%; Pred. No. 1.5e-43;
Matches 249; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1 gctttgacaccaattactgcttcgcgaacttgaggagaactgctgtgctgccccctc 60
Db 1096 GCCCTGGACCACTACTGCTTCAGAAATGTGAGGATAATGCTGCTTACGCTCGCCTT 1155

Qy 61 tacattgacttcgacagatctggctgggaagtgggtgccatgaacctaaagggtactat 120
Db 1156 TACATTGACTTCAAGAGGACCTCGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 1215

Qy 121 gcaactctgtcagcccttgccatactcgcagtcagtcagacacacacacacagcag 180
Db 1216 GCCAACTTCTGCTGGGCGCTGTCCCTACATTGGAGCTGGACAGCAGTACAGCAAG 1275

Qy 181 gtgtggagctgtacacactctgaacctgaacctgaagcattgctcgcctgctgctgccc 240
Db 1276 GTCTGGGCGCTGTACACACAGCATAAACCGGCGCTCGGCGGCGCTGCTGCTGCGCG 1335

Qy 241 caggacctggagccccctgaaccatctgtactatgttggggagggagggagggagcag 300
Db 1336 CAGGGCTGGAGCCACTGCCATGCTGTACTAGTGGGCGCGCAAGCCCAAGGTGGAGCAG 1395

Qy 301 ctctccaaatggtggtgaagtctttaaagttagctga 339
Db 1396 CTGTCCAACATGATGTCGTGCGCTCCGCTCAAAATGCAGCTGA 1434

RESULT 66
MMTGF2      4267 bp      mRNA      ROD      14-JUN-1991
LOCUS          MMTGF2
DEFINITION     Mouse mRNA for transforming growth factor-beta2.
ACCESSION      X57413
VERSION        X57413.1 GI:54772
KEYWORDS       cell proliferation; transforming growth factor-beta2.
SOURCE         Mus musculus.
ORGANISM       Mus musculus.
REFERENCE      1 (bases 1 to 4267)
AUTHORS        Miller, D.A., Lee, A., Pelton, R.W., Chen, E.Y., Moses, H.L. and
Derynck, R.
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TITLE Murine transforming growth factor-beta 2 cDNA sequence and expression in adult tissues and embryos
JOURNAL Mol. Endocrinol. 3 (7), 1108-1114 (1989)
MEDLINE 90014832
FEATURES
source Location/Qualifiers
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/dev_stage="embryonic"
/cell_type="carcinoma"
/cell_lines="PCC3"
1218..2462
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1218..2462
/gene="TGF-beta2"
/codon_start=1
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/protein_id="CAA40672.1"
/db_xref="GI:54773"
/db_xref="SWISS-PROT:P27090"
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/product="transforming growth factor-beta2"
4260
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BASE COUNT 1139 a 1036 c 989 g 1103 t
ORIGIN
Query Match 57.1%; Score 193.4; DB 94; Length 4267;
Best Local Similarity 73.2%; Pred. No. 3.5e-43;
Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgctgtgtgccccctc 60
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QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
Db 2184 TACATTGACTTTAAGAGGATCTGGATGGAATGGATCCATGAACCCAAAGGTACAAT 2243
QY 121 gcaactctgtcagccctggccataacctcccgagtcagacacacacacagcag 180
Db 2244 GCTAACTTCTGTGCTGGGCGATGCCCATATCTATGGAGTTTCAGACACTCAACACCAA 2303
QY 181 gtgctggactgtacacactctgaacctgaagcatctgcctcgcttgcctgtgccc 240
Db 2304 GTCTCAGCTGTACACACCAATAATCCGAGCTTCGCTTCCCTTGCCTGTGTGTC 2363
QY 241 caggacctggagccctgaccactctgtactatgttgggagaccccccagaagtgagcag 300
Db 2364 CAGGACTGTGGAACCACTGACCATCTCTATTACATTGGAATACGCCCAAGATCGAAGCAG 2423
QY 301 ctctcaacatggtggaagtctgtaaatgtactga 339
Db 2424 CTTTCCAATGATGTTCAAGTCTTGTAAATGCAGCTAA 2462
RESULT 67
RNTGFB1 RNTGFB1 1585 bp mRNA ROD 23-MAR-1995
LOCUS Rat mRNA for transforming growth factor-beta 1.
DEFINITION X52498
ACCESSION X52498.1 GI:57341
VERSION growth factor; TGF-beta 1; transforming growth factor-beta 1.
KEYWORDS Norway rat.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Su Wen, Q.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-1990) Su Wen Q., National Cancer Institute NIH,
Bldg 41 Room C629, Laboratory of Chemoprevention, NCI Bethesda MD
20892, U S A
REFERENCE 2 (bases 1 to 1585)
AUTHORS Qian, S.W., Kondaliah, P., Roberts, A.B. and Sporn, M.B.
TITLE cDNA cloning by PCR of rat transforming growth factor beta-1
JOURNAL Nucleic Acids Res. 18 (10), 3059 (1990)
MEDLINE 90272425
FEATURES
source Location/Qualifiers
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413..1585
/note="prepro-TGF-beta 1 (AA -23 to 367)"
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KSTVEOHVELYQYISNNRWYLGNNRLITPTDPELWISFDVTVVVRQMLNODGQGER
FSAHCSDKDNVLHVINGISPKRRDLGTIDHMRPLFLMLLPLERAOHLHSSRH
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482..1582
misc_feature /note="pro-TGF-beta 1 (AA 1 to 367)"
1247..1582
mat_peptide /product="mature TGF-beta 1 (AA 255 to 367)"
BASE COUNT 337 a 538 c 403 g 307 t
ORIGIN
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Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 247; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgctgtgtgccccctc 60
Db 1247 GCCTTGGATACCAACTACTGCTTTCAGCTCCACAGAGAAGAACTGCTGTGTACGCGAGCTG 1306
QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
Db 1307 TACATTGACTTTAAGAGGACCTGGGTGGAAGTGGATCCACGAGCCCAAGGCTTACCAT 1366
QY 121 gcaactctgtcagccctggccataacctcccgagtcagacacacacacacagcag 180
Db 1367 GCCAACTCTGTCTGGGGCCCTGCCCTTACATTGGAGCCTGGACACACACAGTACAGCAAG 1426
QY 181 gtgctggactgtacacactctgaacctgaagcatctgcctcgcttgcctgtgccc 240
Db 1427 GTCTTGGAGGACCTGCCCCATGCTCTACTACGTGGTTCGCAAGCCCAAGTGGAGCAG 1486
QY 241 caggacctggagccctgaccactctgtactatgttgggagaccccccagaagtgagcag 300
Db 1487 CAGCTTGGAGGACCTGCCCCATGCTCTACTACGTGGTTCGCAAGCCCAAGTGGAGCAG 1546
QY 301 ctctcaacatggtggaagtctgtaaatgtactga 339
Db 1547 TTGTCCAACATGATCGTGGCGCTCTCTGTCAAGTGCAGCTGA 1585


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RESULT 70
LOCUS AF097509 358 bp DNA ROD 09-DEC-1998
DEFINITION Cavia porcellus interleukin TGF beta gene, partial cds.
ACCESSION AF097509
VERSION AF097509.1 GI:3983112
KEYWORDS domestic guinea pig.
SOURCE Cavia porcellus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 358)
AUTHORS Wicher,V., Scarozza,A.M., Ramsingh,A.I. and Wicher,K.
TITLE Cytokine gene expression in skin of susceptible guinea-pig infected
with Treponema pallidum
JOURNAL Immunology 95 (2), 242-247 (1998)
MEDLINE 99069279
REFERENCE 2 (bases 1 to 358)
AUTHORS Scarozza,A.M., Ramsingh,A.I., Wicher,V. and Wicher,K.
TITLE Spontaneous cytokine gene expression in normal guinea pig blood and
tissues
JOURNAL Cytokine 10 (11), 851-859 (1998)
MEDLINE 99144670
REFERENCE 3 (bases 1 to 358)
AUTHORS Scarozza,A.M., Ramsingh,A.I., Wicher,V. and Wicher,K.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) New York State Dept of Health, David
Axelrod Institute, Wadsworth Center for Laboratories & Research,
120 New Scotland Ave, Albany, NY 12208, USA
FEATURES
source
1..358
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BASE COUNT 76 a 120 c 103 g 59 t
ORIGIN
Query Match 55.1%; Score 186.8; DB 94; Length 358;
Best Local Similarity 75.2%; Pred. No. 3.3e-41;
Matches 233; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 5 tggacaccaattactgtccgcaacttgaggagaaactgtgtgtgccccctctaca 64
Db 49 TGGACACCAACTATTGCTCCAGCTCCACGAGAGAACTGCTGTGTGGCGGAGCTCTACA 108
QY 65 ttgaattccagacagatctgggtggaagtgggtccatgaacctaaaggctactatgcc 124
Db 109 TTGACTTCGCAAGGACCTTAGGATGGAGTGGATCCACGAGGCCAAGGCTACCAATGCCA 168
QY 125 attctgtcaggcccttgcctacacctccgcagtgagacacacacacacacagcgtgc 184
Db 169 ACTTCGGCTGGGGCCCTGCCCCCTACATTTGGAGCCTGGACACACAGTACAGCAAGTCC 228
QY 185 tgggactgtacacactctgaacctgaagcatctgcctgcgcttgcgtgcgtgccacagg 244
Db 229 TGGCCCTGTACAAACAGCAACACCCGGGGTTTCGGGGCGCTTGTCTGTGTGCCGAGG 288
QY 245 acctggagccctgacctcctgtactatgttgggagagaccccccaaaagtggagcagctct 304
Db 289 CGTTGGAGCACTGGCCACTCGTGTACTAGCTGGGGCGCAAGCAAGGTGGAGCAGCTCT 348
QY 305 ccaacatggt 314
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Db 349 CCAACATGAT 358
RESULT 71
LOCUS PIGTGF2A 1427 bp mRNA MAM 16-JUL-1996
DEFINITION Sus scrofa transforming growth factor beta 2 mRNA, 3' end.
ACCESSION L08375
VERSION L08375.1 GI:1421492
KEYWORDS transforming growth factor beta 2.
SOURCE Sus scrofa (strain crossbreed) male adult Lung cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1427)
AUTHORS Zhou,Y.
TITLE Cloning and expression of porcine transforming growth factor beta 2
in immune cells
JOURNAL Unpublished (1993)
COMMENT On Jul 16, 1996 this sequence version replaced gi:164688.
FEATURES
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/organism="Sus scrofa"
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<1..1305
/feature_start=1
/product="transforming growth factor beta 2"
/protein_id="AA03850.1"
/db_xref="GI:164689"
/translation="HYCVLSAFLLHLVTVALSLSTCIDMDQFMKRRIEARGQIL
SKLKTSPPEYPEPEVPEVPEVSIYVSTRDLLOEKASRRRAAERERSDEEYVKEV
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mat_peptide 904..1302
BASE COUNT 389 a 395 c 336 g 307 t
ORIGIN
Query Match 54.7%; Score 185.6; DB 7; Length 1427;
Best Local Similarity 72.0%; Pred. No. 5.8e-41;
Matches 242; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 1 gctttggacaccaattactgtctccgcaacttgaggagaaactgtgtgtgccccctc 60
Db 904 GCTTTGGATGCACCCCTATTGCTTTAGAAATGTCAGAGATAATTGCTGCTGCGTCCACTT 963
QY 61 tacattgacttcgcagcaggatctgggctggaagtgggtccatgaacctaaagggtactat 120
Db 964 TACATTGATTTCAGAGGGATCTTGGGTGGAATGGATACATGAGCCTAAAGGTACAAT 1023
QY 121 gcaacttctgtcagggcccttgccataacctccgagtcagacacacacacacagcag 180
Db 1024 GCCAACTTCTGTGCGGGGGGTGCCCGTACCTGTGGAGCTCTGACACCCAGCATAGCAGG 1083
QY 181 gtctgggactgtacacactctgaacctgaacctgaacctgaacctgaacctgaacctga 240
Db 1084 GTTCTCAGCTTATATAACACCATAAACCCAGAACTTCTGCTCCCTTGTGCTGTGCTGTC 1143
QY 241 caggacctggagccctgacacactctactatgttgggagagaccccccaaaagtggagcag 300
Db 1144 CAGGATTTAGAACCGCTCACTATCCTCTACTATCATCGCAAAAGCCCAAGATCGAGCAG 1203

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polyergin; transforming factor-beta 2.
African green monkey kidney epithelium, cDNA to mRNA.

SOURCE
ORGANISM Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Cercopithecus.
1 (bases 1 to 1585)
Hanks,S., Armour,R., Baldwin,J.H., Maidonado,F., Spiess,J. and Holley,R.W.

REFERENCE
AUTHORS

TITLE Monomer sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from the nucleotide sequence of the cDNA

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 79-82 (1988)

MEDLINE 88124824

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by S.Hanks, 03-DEC-1987.

FEATURES
SOURCE Location/Qualifiers
1..1585 /organism="Cercopithecus aethiops"
/db_xref="taxon:9534"
<1..>1585 /note="polyergin mRNA"
200..1444 /note="polyergin precursor"
/codon_start=1
/protein_id="AAA35358.1"
/db_xref="GI:176496"
/translation="MHVCLSAFLIHLVTALSLSTCLDMDFMRKRIRAIQSGI
LSKLKITSPPEDYPEPEVPPEVISYINSTRDLLOEKASRRACERERSDEYYAKE
VKIDMPFPFSSNALDPTEYPYRFLRVFDVSAMEKNASNLVKADEFVRQLONPKAR
VPSORLEUILKSOLDTPGTORYIDSXVVKTAEGLWSLFDVDFAEWHLHKDRNS
GFIHSUHCPTCPSPVSNIIIPNKESELEARFAGIDGTSTYTSGDQKI1KSTKKNSG
KTHLLMLLPYSRLSQNTNRKRKALDAAYCFRNQDNCLRLPYIDFKRDLGWKM
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1106..1441 mat_peptide
/note="polyergin"
BASE COUNT 487 a 367 c 334 g 397 t
ORIGIN Unreported.

Query Match	54.2%;	Score 183.8;	DB 89;	Length 1585;
Best Local Similarity	71.4%;	Pred. No. 1.8e-40;		
Matches 242;	Conservative 0;	Mismatches 97;	Indels 0;	Gaps 0;

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Qy      1  gcttggaccaaattactgcttcgcgaaccttgaggagaaactgctgtgcgccccc 60
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Db     1106 GCTTTGGATGGGGCTATTGCTTTAGAAATGTCGAGATAATTGTGCGCTACGTCGCCTT 1165

Qy      61  tacattgactccgcacaggatcggcgtagaagtgggtccatgaacctaaagggctactat 120
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Db     1166 TACATTGATTTCAAGAGGGATCTAGGGTGGAATGGATACACGAACCCAAAGGATACAAT 1225

Qy     121  gccaaactctgctcaggcccttgcccaatacctccgcagtcgacagacaacccccacagcacg 180
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Db     1226 GCCAAACTCTGTGCTGAGCATGCCGCTATTATTATGGAGTTCAGACACTCAGCACAGCAGG 1285

Qy     181  gtctcggactgtacaacctctgaaccctgaagcatctgcctcgccttcgctcgtcgccgccc 240
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Db     1286 GTCTCGAGCTTATATAATACCATAAATCCAGAGACATCTGCTTCTCTCTGCTGGGTGTC 1345

Qy     241  caggacctggagccctcgaccaactctgtactatgtttggggaggaccccccaagtgagcag 300
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Db     1346 CAAGACTTAGAACCTCTAACCATTCCTACTACTATTGGCAAAACACCCAGATTGAACAG 1405

Qy     301  ctctccaacatggtggtgtaagtcttgttaaattagctgta 339
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Db     1406 CTTTTTAATATGATTGTAAAGTCTTGCAAATGCAGCTAA 1444
    
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RESULT 74
CCUG6874
LOCUS CCUG6874 1083 bp mRNA VRT 14-JUL-1997
DEFINITION Cyprinus carpio transforming growth factor-beta 2 mRNA, partial

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cds.
ACCESSION U66874
VERSION 1
KEYWORDS GI:1519488
SOURCE common carp.
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
REFERENCE 1 (bases 1 to 1083)
AUTHORS Sumathy,K., Desai,K.V. and Kondalah,P.
TITLE Isolation of transforming growth factor-beta2 cDNA from a fish,
JOURNAL Cyprinus carpio by RT-PCR
MEDLINE Gene 191 (1), 103-107 (1997)
97354301
REFERENCE 2 (bases 1 to 1083)
AUTHORS Sumathy,K., Desai,K.V. and Kondalah,P.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1996) Center for Reproductive Biology and
Molecular Endocrinology, Indian Institute of Science, Bangalore,
Karnataka 560 012, India
FEATURES
    source
        Location/Qualifiers
            1..1083
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                /db_xref="taxon:7962"
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                /product="transforming growth factor-beta 2"
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                /db_xref="GI:1519488"
BASE COUNT 282 a 310 c 281 g 210 t
ORIGIN
Query Match 53.8%; Score 182.4; DB 8; Length 1083;
Best Local Similarity 74.0%; Pred. No. 4.6e-40;
Matches 231; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgccccctc 60
Db 772 GCTCTGGACGGCGCTTCGCTCAGAAATGTGCAGGACAACTGCTGTTCAGCTCTC 831
QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 832 TACATCGACTTCAAGAAGGATCTGGGTTGGAAGTGTGATCCAGAACCCAGGATATAAC 891
QY 121 gcaactctctcagcccttgccatactccgcagtcgagacacacccacagcag 180
Db 892 GCCAACTTCTGCGGGAGCCCTGCGTATCTGTGGAGTGCAGACACCCAGCAGCAAT 951
QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcttgcctgtgccc 240
Db 952 ATCCCTGGGCTCTACACACCACTTAATCCAGAGCATCTCGCATCTCCTGCTGTGTCT 1011
QY 241 caggacctggagccctgacctctgactatgtttggagagacccccaaagtggagcag 300
Db 1012 CAGGATCTGGAACCCCTTACAATCCTTTACTACATCGGAAAAACGCCCAAAATCGAACAA 1071
QY 301 ctctcaacatg 312
Db 1072 CTGCTCAACATG 1083
RESULT 75
A18279 339 bp mRNA PAT 17-MAY-1994
LOCUS A18279 339 bp mRNA PAT 17-MAY-1994
DEFINITION TGF-beta 2 coding region.
ACCESSION A23752
VERSION A23752.1
KEYWORDS GI:825586
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 3 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
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        Location/Qualifiers
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            1..339
                /note="Protein sequence is in conflict with the conceptual
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                /transl_table=11
                /product="TGF-beta 2"
                /protein_id="CAA01386.1"
                /db_xref="GI:4529904"
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                AGACPYLWSSDTHSRVLSLYNTINPEASPCVSDLEPLTILYIGTKPKIEQLS
                NMIVRSCKCS"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
Query Match 53.7%; Score 182.2; DB 9; Length 339;
Best Local Similarity 71.1%; Pred. No. 6.2e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgccccctc 60
Db 1 GCTTTGGATCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCTACGTCACCTT 60
QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTTGATTTCAAGAGGATCTAGGGTGGAAATGGATACAGAACCCAAAGGGTACAAT 120
QY 121 gcaactctctcagcccttgccatactccgcagtcgagacacacccacagcag 180
Db 121 GCCAACTTCTGCTGGAGCATGCCGTTATTTATGGAGTTCAGACACTCAGCAGCAGG 180
QY 181 gtgctgggactgtacaaactctgaacctgaacctgaagcatctgctcgcttgcctgtgccc 240
Db 181 GTCTTGAGCTTATATAATACCAATAAATCCAGAGCATCTGCTTCTCTCTGCTGTGCTCC 240
QY 241 caggacctggagccctgacctctgactatgtttggagagacccccaaagtggagcag 300
Db 241 CAGATTTAGAACCTCTAACCAATCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctcaacatggtggtggaagtcttgaatgtagctga 339
Db 301 CTTTCTAATATGATGTGTAAGTCTTTGCAATATGCAGCTAA 339
RESULT 76
A23752 339 bp mRNA PAT 25-JAN-1995
LOCUS A23752 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2 coding region.
ACCESSION A23752
VERSION A23752.1
KEYWORDS GI:825586
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)
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CAGACPVLNSSDFQHSRVLSLYNTINPEASAPCCVSQDLEPLTILYIYIKTKPKISQL									
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BASE COUNT	98 a	78 c	71 g	95 t					
ORIGIN									
Query Match 53.7% Score 182.2; DB 9; Length 342;									
Best Local Similarity 71.1%; Pred. No. 6.1e-40;									
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;									
Qy	1	gctttgacacccaattactgtcttcgcgaacttggagagaactgctgtgcgccccctc	60						
Db	4	GCTTTGGATGGCGCTATTGCTTTAGAAATCTGCAGGATAATTGCTCCCTACGTCACATT	63						
Qy	61	tacattgaacttcacagggatctgggtggaagtgggtccatgaacctaaagggctactat	120						
Db	64	TACATTGATTTTCAAGAGGGATCTAGGTGGAAATGGATACACGAACCCAAAGGGTACAAT	123						
Qy	121	gccaaactctgtcagggccttgcgcatactccgcagtcgcagtcgaacacacacccacagcag	180						
Db	124	GCCAACTCTCTGTGTGAGCATGCCGCTATTATTGGAGTTCAGACATCTCAGCACAGCAGG	183						
Qy	181	gtgctgggactgtacaacactctgaacccctgaagcatcttgcctgcctgtgctgctgctccc	240						
Db	184	GTCCTGAGCTTATATAATACCAATAATCCAGAAGCATCTGCTTCTCCTTGTGGTGTCTC	243						
Qy	241	caggacctggagcccttgaccatctgactatgttggggaggaccccccaagtggagcag	300						
Db	244	CAAGATTTAGAACCTCTAAACCATCTCTACTACATTGGCAAAACACCCAAAGATTGAACAG	303						
Qy	301	ctctcccaactggtggggaagctctgttaaattgacttga	339						
Db	304	CTTCTTAATATGATTGATAAGTCTTGCAATGCAAGCTAA	342						
RESULT 82									
All1707									
LOCUS	All1707	342 bp	DNA	PAT	26-NOV-1993				
DEFINITION	mature H.sapiens G-Tsf gene.								
ACCESSION	All1707								
VERSION	All1707.1 GI:490099								
KEYWORDS	human.								
SOURCE	Homo sapiens								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 342)								
AUTHORS	De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.								
TITLE	Production and use of a novel T-cell suppressor factor								
JOURNAL	Patent: EP 0268561-A 6 25-MAY-1988;								
	SANDOZ AG; SANDOZ-PATENT-GBMB; SANDOZ-ERFINDUNGEN								
FEATURES	Verwaltungsgesellschaft m.b.H								
source	Location/Qualifiers								
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BASE COUNT	98 a	78 c	71 g	95 t					
ORIGIN									

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Query Match      53.7%; Score 182.2; DB 9; Length 342;
Best Local Similarity 71.1%; Pred. No. 6.1e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gccttggacaccaattactgctccgcgaacttggaggagaactcgtgtgccccccc 60
Db 4 GCCTTTGATCGGGCCATTCCTTTAGAAATGTCAGAGTAATGTGCGCTTACCTCACT 63

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Qy	61	tacattgactctccagcagatcctggctggaagtgggtccataaaccttaaggcgctactact	120
Db	64	TACATTGATTTTCAAGAGGGGATCTTAGGTGGAAATGGGATACACGAACCCAAAGGGTACAAT	123
Qy	121	gccaaacttctgctcagcccttgcccatactccgcagtcgacacacaaccacagcacg	180
Db	124	GCCAACTTCTTGCTGGAGCAGTCGCCGTATTTATGGAGTTTCAGACACTCAGCACACGAGG	183
Qy	181	gtgctggactgtacaacactctgaacctgaacctgaagcatctgctctgcctgtctgctgctgccc	240
Db	184	GTCTCTGAGCTTATATAATACCATAAATCCAGAAGCATCTGCTTCTCTCTGCTGCGTGCC	243
Qy	241	cagaacctggagccccctgaccatcctctactatgtttgaggagacccccaaaagtggagcag	300
Db	244	CAAGATTTAGAACCTCTAAACCATTTCTCTACTACATTGGCAAACACCCCAAGATTGAACAG	303
Qy	301	ctctccaactgggtgggaagcttgtaaaaatgatgctga	339
Db	304	CTTTCTATATGATTGTAAGTCTTGCAATGCAGCTAA	342
RESULT 83			
A05308	Locus	A05308	1695 bp DNA PAT 07-MAY-1993
DEFINITION	Nucleotide sequence for the human G-Tsf precursor.		
ACCESSION	A05308		
VERSION	A05308.1 GI:345051		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct.		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 1695).		
AUTHORS	Patent: WO 8803807-A 12 02-JUN-1988;		
JOURNAL	Location/Qualifiers		
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	182..1426		
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gene	182..1426		
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	1088..1423		
mat_peptide	/gene="G-Tsf"		
	/product="glioblastoma-derived T-cell suppressor factor"		
BASE COUNT	523 a	386 c	354 g 432 t
ORIGIN			

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Query Match      53.7%; Score 182.2; DB 9; Length 1695;
Best Local Similarity 71.1%; Pred. No. 5e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps

Qy 1 gctttggacaccaatcactgctccgcactggagagaaactgctgtgcgccccct 60
Db 1088 GCATTTGATCGGCCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTAGCTCACTT 114

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Query Match          52.8%; Score 179; DB 8; Length 2724;
Best Local Similarity 70.5%; Pred. No. 3.6e-39;
Matches 239; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Db 982 GCTCTGATGCCGCTACTGCTTTAGGAACTGCCAGGACAATGCTGCTAGTCCCTTA 1041
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Qy 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
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Db 1042 TACATTGACTTTAAAGAGACCTGGTTGGAAGTGATGATACATGAACCCAAAGGTTACAAT 1101
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Qy 121 gcaaatcttctcaggcccttgccatactccgcgaatcgagacacacacccacagcag 180
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Db 1102 GCAAAATTTCTGTGTGGAGCTTGCCGATCTGTGGAGCTCAGATACTCAACATAGCCGG 1161
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Qy 181 gtgctgggactgtacacactctgaacctgaacctgaacctgctgccttgcctgctgccc 240
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Db 1162 GTGCTAAGCTGTACACACCATTAATCCGGAAGCATCTGCTCCCGTGTGCGTGTCT 1221
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Qy 241 caggacctggagcccttgaccatctgtactatgttgggagaccccaagtgagcag 300
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Db 1222 CAAGATTAGACTCTCTTGACCATCTGTACTACATCGGGAATAAGCCAAATAATTGAACAG 1281
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Qy 301 ctctccaaatggtggaagctgtgtaaatgtagctga 339
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Db 1282 CTTTCAAAATATGATTGTAATAATCATGAAGTGCAGCTAA 1320
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RESULT 90
AY007214 1197 bp mRNA ROD 03-SEP-2000
LOCUS Mesocricetus auratus transforming growth factor-beta 2 mRNA,
DEFINITION partial cds.
ACCESSION AY007214 GI:9965485
VERSION AY007214.1
KEYWORDS golden hamster.
SOURCE Mesocricetus auratus
ORGANISM Mesocricetus auratus
REFERENCE 1 (bases 1 to 1197)
AUTHORS Ramesh,G., Kondaiah,P. and Seshagiri,P.B.
TITLE Differential expression and selective localization of transforming
growth factor-beta isoforms in the hamster uterus during estrous
cycle
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1197)
AUTHORS Ramesh,G., Kondaiah,P. and Seshagiri,P.B.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2000) Molecular Reproduction, Development and
Genetics, Indian Institute of science, Bangalore, Karnataka 560
012, India

FEATURES
Source Location/Qualifiers
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CPCTFVPFNNNIIPNKSELEARFAGIDGTSQSHGQOETIKTSKKNKGKTPHLL
MLLPYRLSESQSNRRKRALDAAYCFRNQDNCCLRLPYIDFKRLDGLWKWHEPKGY
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IFQLSNM"
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BASE COUNT 313 a 326 c 291 g 267 t
ORIGIN

Query Match          51.4%; Score 174.4; DB 94; Length 1197;
Best Local Similarity 72.4%; Pred. No. 7.5e-38;
Matches 226; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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Db 886 GCTTTGGATGCTGCCTATTGCTTTAGAAATGTGCAGGATAAATGCTGCCCTCCGCCCTCTT 945
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Qy 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
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Db 946 TACATTGATTTCAGAGGGGATCTTGGTGGAAATGGATCCATGAACCCAAAGGTATAAT 1005
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Qy 121 gcaaatcttctcaggcccttgccatactccgcgaatcgagacacacacccacagcag 180
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Db 1006 GCCAACTTCTGTGCTGGGCAATGCCCGTATCTGTGGAGTTCAGACACTCAGCACCAAG 1065
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Qy 181 gtgctgggactgtacacactctgaacctgaacctgaacctgctgccttgcctgctgccc 240
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Qy 241 caggacctggagcccttgaccatctgtactatgttgggagaccccaagtgagcag 300
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LOCUS Chicken transforming growth factor beta 4 (TGF-beta 4) mRNA,
DEFINITION partial cds.
ACCESSION M31160 X08012 S41706
VERSION M31160.1 GI:1262437
KEYWORDS growth factor; transforming growth factor-beta 4.
SOURCE Chicken cDNA to mRNA.
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 1256)
AUTHORS Jakowlew,S.B., Dillard,P.J., Sporn,M.B. and Roberts,A.B.
TITLE Complementary deoxyribonucleic acid cloning of a messenger
ribonucleic acid encoding transforming growth factor beta 4 from
chicken embryo chondrocytes
JOURNAL Mol. Endocrinol. 2 (12), 1186-1195 (1988)
MEDLINE 89112198
REFERENCE 2 (bases 1 to 1256)
AUTHORS Burt,D.W. and Jakowlew,S.B.
TITLE Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA
JOURNAL Mol. Endocrinol. 6 (6), 989-992 (1992)
MEDLINE 92357039
COMMENT On Apr 12, 1996 this sequence version replaced gi:212760.
The sequence overlaps with that reported by Derynck et al. in
Nature 316:701-705(1985), X02812, and Derynck et al. in Nucl. Acids
Res.15:3187-3187(1987) Y00111, and Van Oberghen et al. in Mol.
Endocrin. 1:693-698(1987).
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Db	1567	CACCTCCNATCATTTATTATTTGGCCCATCTGCTAAAGTAGAGCAGCTCTCTAATATGG	1626
Qy	314	tggtagagctgtgtaaatgtactga	339
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RESULT	96		
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LOCUS	HSTGF37	1676 bp	DNA
DEFINITION	H.sapiens gene for transforming growth factor-beta 3 (TGF-beta 3) exon 7.		
ACCESSION	X14891		
VERSION	X14891.1	GI:37087	
KEYWORDS	growth factor; transforming growth factor; transforming growth factor-beta 3.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Chen, E.Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA		
REFERENCE	2 (bases 1 to 1676)		
AUTHORS	Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L., Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and Chen, E.Y.		
TITLE	A new type of transforming growth factor-beta, TGF-beta 3		
JOURNAL	EMBO J. 7 (12), 3737-3743 (1988)		
MEDLINE	83091120		
COMMENT	See <X14885> to <X14891> for exons 1-7 and also <X14149> for mRNA sequence.		
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RESULT	97		
LOCUS	DJ270M14/c		
DEFINITION	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (VGF-beta 3) gene, complete cds; and unknown genes.		
ACCESSION	AF107885		
VERSION	AF107885.2	GI:5468516	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 192126)		
AUTHORS	Madan,A., Rowen,L., Qin,S., Dickhoff,R., Shaffer,T., James,R., Abbas,I., N., Loretz,C., Madan,A., Dors,M., Dahl,T., Hall,J., Lasky,S. and Hood,L.		
TITLE	Complete genomic sequence of human transforming growth factor-beta 3		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 192126)		
AUTHORS	Madan,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-NOV-1998) Department of Molecular Biotechnology, Box 357730 University of Washington, Seattle, WA 98195, USA		
COMMENT	On Jul 14, 1999 this sequence version replaced gi:3928926. Sequence methodology: High Redundant shotgun sequence using plasmid subclones. Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RM/RepeatMasker.html).		
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LOCUS O.mykiss mRNA for transforming growth factor beta.
DEFINITION X99303
ACCESSION X99303.1 GI:1478246
KEYWORDS TGF-beta; transforming growth factor beta.
VERSION TGF-beta; transforming growth factor beta.
SOURCE rainbow trout.
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Hardie,L.J., Laing,K.J., Daniels,G.D., Grabowski,P.S.,
Cunningham,C. and Secombes,C.J.
TITLE Isolation of the first piscine transforming growth factor B gene:
analysis reveals tissue specific expression and a potential
regulatory sequence in rainbow trout (Oncorhynchus mykiss)
JOURNAL Cytokine In press
REFERENCE 2 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
AB24 2TZ, UK
REMARK revised by [3]
REFERENCE 3 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
AB24 2TZ, UK
COMMENT On Aug 2, 1996 this sequence version replaced gi:1438515.
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2001, 09:13:52 ; Search time 76.31 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	339	100.0	339 17	AAQ15464	Human transforming
5	339	100.0	339 18	AAQ180110	Mature transformin
6	339	100.0	339 18	AAQ15247	TGF active fragmen
7	339	100.0	339 20	AAQ15247	cDNA encoding the
8	339	100.0	339 20	AAQ15247	cDNA encoding a tr
9	339	100.0	609 11	AAQ05774	Sequence encoding
10	339	100.0	2529 13	AAQ20576	Transforming Growt
11	339	100.0	2574 19	AAQ63209	Nucleic acid seque

12	337.4	99.5	2157	15	AAQ56926	Human TGF-beta-3.
13	337.4	99.5	2157	19	AAQ52935	Human transforming
14	337.4	99.5	2158	11	AAQ02820	cDNA sequence enco
15	333	98.2	1239	13	AAQ22229	Mutant transformin
16	332.6	98.1	498	17	AAQ06496	Tissue-derived tum
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18	315	92.9	2676	11	AAQ02819	cDNA sequence enco
19	302.2	89.1	2639	19	AAQ52934	Pig transforming g
20	302.2	89.1	2669	15	AAQ56925	Pig TGF-beta-3. S
21	302.2	89.1	2671	11	AAQ03303	Entire porcine tra
22	297.6	87.8	336	14	AAQ41603	Transforming Growt
23	297.6	87.8	336	17	AAQ17237	Hybrid TGF-beta 1-
24	297.6	87.8	336	17	AAQ15465	cDNA encoding huma
25	291	85.8	4382	22	AAQ55131	Nucleotide sequenc
26	276.8	81.7	336	14	AAQ41605	Transforming Growt
27	276.8	81.7	336	17	AAQ17238	Hybrid TGF-beta 2-
28	276.8	81.7	336	17	AAQ15466	cDNA encoding huma
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30	240	70.8	336	14	AAQ41607	Transforming Growt
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32	240	70.8	336	17	AAQ15467	cDNA encoding huma
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37	204.6	60.4	1303	11	AAQ09317	Monkey transforming
38	204.6	60.4	1559	13	AAQ20289	Sequence encoding
39	204.6	60.4	1560	9	AAQ81084	Sequencing of
40	204.6	60.4	1560	11	AAQ03508	Simian Transformin
41	204.6	60.4	1561	11	AAQ03268	Simian Transformin
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44	204.6	60.4	1821	12	AAQ13392	Human pro-TGF-beta
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49	204.6	60.4	2537	17	AAQ15720	Pre-transforming g
50	204.6	60.4	2537	19	AAQ52933	Human pre-transfor
51	204.6	60.4	2745	16	AAQ05876	cDNA encoding tran
52	204.6	60.4	3541	17	AAQ16516	Collagen AI/TGF-be
53	204.6	60.4	3541	21	AAQ12498	cDNA encoding a ch
54	204.6	60.4	4105	15	AAQ55624	TGFbeta1 5'-UTR-CD
55	203	59.9	339	12	AAQ11993	Transforming Growt
56	203	59.9	339	17	AAQ15462	Human transforming
57	203	59.9	1569	9	AAQ81085	Coding sequence of
58	201.6	59.5	336	14	AAQ41602	Transforming Growt
59	200.4	59.1	345	14	AAQ41599	Mature human Trans
60	195	57.5	1561	11	AAQ04908	Sequence encoding
61	195	57.5	1561	13	AAQ29177	TGF-beta 1/beta 2
62	182.2	53.7	339	12	AAQ11994	Encodes Transformi
63	182.2	53.7	339	14	AAQ41600	Mature human Trans
64	182.2	53.7	339	17	AAQ17236	Human TGF-beta 2 c
65	182.2	53.7	339	17	AAQ15463	Human transforming
66	182.2	53.7	339	18	AAQ42772	TGF active fragmen
67	182.2	53.7	339	20	AAQ15246	cDNA encoding the
68	182.2	53.7	339	20	AAQ93376	cDNA encoding a tr
69	182.2	53.7	1695	16	AAQ05877	cDNA encoding tran
70	182.2	53.7	2208	13	AAQ20291	Sequence encoding
71	182.2	53.7	2568	10	AAQ05767	Sequence of human
72	182.2	53.7	2569	11	AAQ05126	Human TGF-Beta2-44
73	182.2	53.7	2569	13	AAQ20290	Sequence encoding
74	182.2	53.7	2592	16	AAQ41116	Human transforming
75	180.8	53.3	336	14	AAQ41604	Transforming Growt
76	180.6	53.3	2206	11	AAQ03510	Human Transforming
77	180.6	53.3	2207	11	AAQ03511	Hybrid Transformin
78	180.6	53.3	2207	11	AAQ05127	Human TGF-Beta1/TG
79	180.6	53.3	2217	10	AAQ05127	Sequence of human
80	177.4	52.3	2200	16	AAQ04115	Simian-human hybri
81	176.2	52.0	1565	13	AAQ29178	TGF-beta 1. Homo
82	161.2	47.6	2754	21	AAQ63944	cDNA encoding a pa
83	134.2	39.6	852	12	AAQ11774	Encodes Pb-Pb-trun
84	96.8	28.6	975	7	AAQ60973	Genomic sequence e

CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
 XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
 SQ

Query Match 100.0%; Score 339; DB 14; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacacattactgtctcccaacttgagagagaaactgtgtgccccctc 60
 |||||
 DB 1 gctttgacacacattactgtctcccaacttgagagagaaactgtgtgccccctc 60
 |||||
 QY 61 tacattgacttcacagagatctggctggaagtgggtccatgaacctaaagggctactat 120
 |||||
 DB 61 tacattgacttcacagagatctggctggaagtgggtccatgaacctaaagggctactat 120
 |||||
 QY 121 gccaaacttctgctcagcccttgcacatacctccgagtgacagacacaaacacagcag 180
 |||||
 DB 121 gccaaacttctgctcagcccttgcacatacctccgagtgacagacacaaacacagcag 180
 |||||
 QY 181 gtgctgggactgtacacactctgaacctgaacctgaacctgaacctgtcctgcgtgcccc 240
 |||||
 DB 181 gtgctgggactgtacacactctgaacctgaacctgaacctgaacctgtcctgcgtgcccc 240
 |||||
 QY 241 caggacctgagccctgacctgacctgacctgttggaggagcccccaagtggagcag 300
 |||||
 DB 241 caggacctgagccctgacctgacctgacctgttggaggagcccccaagtggagcag 300
 |||||
 QY 301 ctctccaaacatggtggtgaagtctttaaattgactgta 339
 |||||
 DB 301 ctctccaaacatggtggtgaagtctttaaattgactgta 339
 |||||

RESULT 3

AAAT17234
 ID AAT17234 standard; cDNA to mRNA; 339 BP.
 AC
 XX
 AC
 AAT17234;

DT 17-JUL-1996 (first entry)

XX Human TGF-beta 3 cDNA.

DE Transforming growth factor type beta; TGF-beta 3;
 KW protein renaturation; protein folding; ds.
 KW
 XX

OS Homo sapiens.

XX

PN WO9603433-A1.

XX

PD 08-FEB-1996.

XX

PF 12-JUL-1995; 95WO-EP02719.

XX

PR 25-JUL-1994; 94EP-0810439.

XX

PA (CIBA) CIBA GEIGY AG.

XX

PI Cerletti N;

XX

DR WPI; 1996-117000/12.

XX

DR P-PSDB; AAR92772.

XX Prodn. of dimeric biologically active transforming growth factor
 PT by refolding denatured monomer in detergent-free folding buffer
 PT contg. specific organic solvent to improve yield
 XX

PS Example 1B; Page 34; 54pp; English.

XX

CC The coding sequence (AAT17234) of human transforming growth factor

CC TGF-beta 3 (AAR92772) was cloned into plasmid pGEM-52F(+) (Promega)

CC and the construct used to transform E. coli Y1090. Subcloning in

CC pPLMu yielded plasmid pPLMu.hTGF-beta 3. Non-soluble, monomeric
 CC TGF-beta 3 was recovered from E. coli LC 137/pPLMu.hTGF-beta 3 (DSM
 CC 5658) transformants. A biologically active, dimeric form of
 CC TGF-beta 3 was obtd. by refolding this monomer in detergent-free
 CC buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and
 CC TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were
 CC also produced.
 XX

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Query Match 100.0%; Score 339; DB 17; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacacattactgtctcccaacttgagagagaaactgtgtgccccctc 60
 |||||
 DB 1 gctttgacacacattactgtctcccaacttgagagagaaactgtgtgccccctc 60
 |||||
 QY 61 tacattgacttcacagagatctggctggaagtgggtccatgaacctaaagggctactat 120
 |||||
 DB 61 tacattgacttcacagagatctggctggaagtgggtccatgaacctaaagggctactat 120
 |||||
 QY 121 gccaaacttctgctcagcccttgcacatacctccgagtgacagacacaaacacagcag 180
 |||||
 DB 121 gccaaacttctgctcagcccttgcacatacctccgagtgacagacacaaacacagcag 180
 |||||
 QY 181 gtgctgggactgtacacactctgaacctgaacctgaacctgtcctgcgtgcccc 240
 |||||
 DB 181 gtgctgggactgtacacactctgaacctgaacctgaacctgtcctgcgtgcccc 240
 |||||
 QY 241 caggacctgagccctgacctgacctgacctgttggaggagcccccaagtggagcag 300
 |||||
 DB 241 caggacctgagccctgacctgacctgacctgttggaggagcccccaagtggagcag 300
 |||||
 QY 301 ctctccaaacatggtggtgaagtctttaaattgactgta 339
 |||||
 DB 301 ctctccaaacatggtggtgaagtctttaaattgactgta 339
 |||||

RESULT 4

AAAT15464
 ID AAT15464 standard; cDNA to mRNA; 339 BP.
 AC
 XX
 AC
 AAT15464;

DT 10-JUN-1996 (first entry)

XX Human transforming growth factor beta 3 encoding cDNA.

DE Transforming growth factor beta; TGF; regulator; method;
 KW proliferation; differentiation; wound healing; solvent; ds.
 KW
 XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 1..339

FT /*tag= a

FT /product= human_TGF-beta-3

XX

PN WO9603432-A1.

XX

PD 08-FEB-1996.

XX

PF 12-JUL-1995; 95WO-EP02718.

XX

PR 25-JUL-1994; 94EP-0810438.

Db 301 ctctccaacatggtggaagtgtttaaagttagctga 339

RESULT 6

AAT42773

ID AAT42773 standard; cDNA; 339 BP.

XX

AC AAT42773;

XX

DT 26-AUG-1997 (first entry)

XX

DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX

KW Transforming growth factor-beta fusion protein; wound healing;

KW artificial skin; surgery recovery time; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 1..339

FT /*tag= a

FT /function= TGF active fragment

XX

PN W09639430-A1.

XX

PD 12-DEC-1996.

XX

PF 05-JUN-1996; 96WO-US08973.

XX

PR 06-JUN-1995; 95US-0470837.

XX

(CHEU/) CHEUNG D T.

PA

(HALL/) HALL F L.

PA

(NIMN/) NIMNI M E.

PA

(TUAN/) TUAN T.

PA

(WULL/) WU L.

XX

PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX

WPI: 1997-043065/04.

DR

P-PSDB; AAW08175.

XX

Prepn. of transforming growth factor-beta fusion protein - useful to

PT

reduce surgery recovery time and to prepare artificial skin

PT

Disclosure; Page 48; 59pp; English.

XX

CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. The present
 CC sequence encodes a specifically claimed TGF active fragment.
 CC Additionally, the fusion protein may comprise proteinase-sensitive
 CC linker sites and binding domain so the protein sequence may contain
 CC some or all of the following elements: purification tag:proteinase
 CC site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes
 CC wound healing, and the fusion protein can be used to reduce surgery
 CC recovery time and in the preparation of artificial skin. The inclusion
 CC of a purification tag facilitates purification of the fusion protein.
 CC The proteinase site is included to permit cleavage and release of the
 CC purification tag after purification if desired. The extracellular
 CC matrix binding site facilitates delivery of the fusion protein to the
 CC desired site of action. Delivery of the TGF-beta to the site to be
 CC treated reduces the amount of TGF-beta required to be administered to
 CC be effective and reduces the concentration of circulating TGF-beta
 CC which may result in undesirable effects.

XX

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 339; DB 18; Length 339;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttggacaccaattactgtccgcaacttgaggagaactgctgtgtgccccctc 60

Db 1 gctttggacaccaattactgtccgcaacttgaggagaactgctgtgtgccccctc 60
 QY 61 tacattgacttccgacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
 Db 61 tacattgacttccgacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
 QY 121 gccaaacttctgctcaggcccttggcccatatcctccgagtcagacacacacacagcag 180
 Db 121 gccaaacttctgctcaggcccttggcccatatcctccgagtcagacacacacacagcag 180
 QY 181 gtgtgtgactgtacacacactctgaacctgaagcctgacatctgctcgctgtgctgcccc 240
 Db 181 gtgtgtgactgtacacacactctgaacctgaagcctgacatctgctcgctgtgctgcccc 240
 QY 241 caggacctggagccctgacctcctgactatgttggagagaccccaagtggagcag 300
 Db 241 caggacctggagccctgacctcctgactatgttggagagaccccaagtggagcag 300
 QY 301 ctctcccaacatggtgtgaagtctttaaagttagctga 339
 Db 301 ctctcccaacatggtgtgaagtctttaaagttagctga 339

RESULT 7

AAX15247

ID AAX15247 standard; cDNA; 339 BP.

XX

AC AAX15247;

XX

DT 28-APR-1999 (first entry)

XX

DE cDNA encoding the mature form of transforming growth factor-beta-3.

XX

KW Transforming growth factor-beta-3; TGF-beta-like protein;

KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

KW bone repair; tissue repair; bone marrow protective agent;

KW cardioprotection; anti-inflammatory; immunosuppressive;

KW ulcer; bed sore; ds.

XX

OS Homo sapiens.

XX

PN EP891985-A1.

XX

PD 20-JAN-1999.

XX

PF 27-NOV-1990; 90EP-0810922.

XX

PR 06-DEC-1989; 89GB-0027546.

XX

PA (NOVS) NOVARTIS AG.

XX

PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;

XX

WPI: 1999-083520/08.

XX

P-PSDB; AAW97093.

XX

PT Producing biologically active dimeric Transforming Growth

PT Factor-beta - by refolding new monomeric Transforming Growth

PT Factor-beta, useful for treatment of wounds and cancer

XX

PS Example 1; Page 30; 32pp; English.

XX

CC The present sequence encodes the mature form of transforming growth
 CC factor-beta-3. Dimeric, biologically active TGF-beta-like protein
 CC can be produced by subjecting the denatured monomeric form to refolding
 CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
 CC useful for the production of the dimeric, biologically active
 CC TGF-beta-like protein, which is useful for the treatment of wounds
 CC (surface or internal) and cancer in a mammal, in bone and tissue
 CC repair, as a bone marrow protective agent, a mediator of
 CC cardioprotection, for the production of an anti-inflammatory or
 CC immunosuppressive preparation. Treatment is useful for animals,


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XX WPI; 1990-262507/35.
DR P-PSDB; AAR06548.
XX
XX Tissue-derived tumour growth inhibitors - used in diagnosis and
PT treatment of tumours and treatment of proliferative type
PT disorders, burns and wounds
XX
XX Disclosure; Fig 29; 81pp; English.
XX
XX Gene product may be used to inhibit growth of tumour cells, to
CC treat proliferative type disorders, burns and other wounds, and may
CC also be used as an immune modulator. Detection of proteins and of
CC TGF-alpha can indicate presence of a tumour.
CC Proteins may be produced from a bacterial or eukaryotic expression
CC system.
XX
XX Sequence 609 BP; 154 A; 172 C; 158 G; 125 T; 0 other;

Query Match          100.0%; Score 339; DB 11; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcttggacaccaattactctccgcaacttggagagagaactgtgtgccccctc 60
Db 271 gcttggacaccaattactctctccgcaacttggagagagaactgtgtgccccctc 330
Qy 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 331 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 390
Qy 121 gccaaactctgtcagggcccttgcacatactccgcagtcgacagacacacacagcacg 180
Db 391 gccaaactctgtcagggcccttgcacatactccgcagtcgacagacacacacagcacg 450
Qy 181 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 240
Db 451 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 510
Qy 241 caggacctggagccctgacacactcctgtactatgttggaggagaccccccaagtggagcag 300
Db 511 caggacctggagccctgacacactcctgtactatgttggaggagaccccccaagtggagcag 570
Qy 301 ctctccaaactgtgtggaagtcttgaatgtactga 339
Db 571 ctctccaaactgtgtggaagtcttgaatgtactga 609

RESULT 10
AAQ20576
ID AAQ20576 standard; cDNA; 2529 BP.
XX
XX AC AAQ20576;
XX
XX 05-MAY-1992 (first entry)
XX
XX DE Transforming Growth Factor beta 3 coding sequence.
XX
XX DE TGF-beta 3; homodimer; ss.
XX
XX OS Synthetic.
XX
XX PN W09200318-A.
XX
XX PD 09-JAN-1992.
XX
XX PF 25-JUN-1991; 91WO-US04541.
XX
XX PR 25-JUN-1990; 90US-0543348.
XX
XX PA (ONCO-) ONCOGENE SCI INC.
XX

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PI Iwata KK, Foulkes JG, Tendijke P, Haley JD;
XX WPI; 1992-041510/05.
DR P-PSDB; AAR20621.
XX
XX Transforming growth factor beta 3 proteins, precursors and
PT mutants - obt'd. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence
XX
XX Example 2; Fig 1; 107pp; English.
XX
XX This 2529bp full-length TGF-beta3 gene sequence was obtained from
CC three shorter overlapping clones derived from human placental, human
CC umbilical cord and A673 cells cDNA libraries, respectively. The
CC predicted amino acid sequence of the gene encoding TGF-beta3 shows
CC extensive homology to TGF-beta 1 and beta 2.
CC See also AAQ22229 and AAR20622.
XX
XX Sequence 2529 BP; 617 A; 670 C; 661 G; 581 T; 0 other;

Query Match          100.0%; Score 339; DB 13; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.5e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcttggacaccaattactctccgcaacttggagagagaactgtgtgccccctc 60
Db 1163 gcttggacaccaattactctccgcaacttggagagagaactgtgtgccccctc 1222
Qy 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 1223 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 1282
Qy 121 gccaaactctcagggcccttgcacatactccgcagtcgacagacacacacagcacg 180
Db 1283 gccaaactctcagggcccttgcacatactccgcagtcgacagacacacacagcacg 1342
Qy 181 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 240
Db 1343 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 1402
Qy 241 caggacctggagccctgacacactcctgtactatgttggaggagaccccccaagtggagcag 300
Db 1403 caggacctggagccctgacacactcctgtactatgttggaggagaccccccaagtggagcag 1462
Qy 301 ctctccaaactgtgtggaagtcttgaatgtactga 339
Db 1463 ctctccaaactgtgtggaagtcttgaatgtactga 1501

RESULT 11
AAV63209
ID AAV63209 standard; DNA; 2574 BP.
XX
XX AC AAV63209;
XX
XX 14-JAN-1999 (first entry)
XX
XX DE Nucleic acid sequence of human transforming growth factor-beta 3.
XX
XX DE Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; ss.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX CDS 254..1492
XX FT /*tag= a
XX FT /product= TGF-beta3
XX
XX PN W09840747-A1.

```

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XX 17-SEP-1998.
PD
XX
XX 05-MAR-1998; 98WO-CA00180.
PF
XX
XX 07-MAR-1997; 97US-0039919.
PR
XX
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
PA
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
XX Caniggia I, Lye S, Post M;
PI
XX
XX WPI: 1998-520837/44.
DR
XX P-PSDB; AAW80417.
DR
XX Regulation of trophoblast invasion - by, e.g. transforming growth
PT factor-beta3 inhibitor, useful for detecting or treating
PT preeclampsia in pregnant women
PT
XX
XX Disclosure; Fig 1; 59pp; English.
PS
XX
XX The present sequence encodes human transforming growth factor-beta 3
CC (TGF-beta3). The specification describes a composition for regulating
CC trophoblast invasion which comprises an inhibitor of TGF-beta3,
CC TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
CC (HIF-1 alpha) or oxygen tension. The composition is used in methods of
CC diagnosing, monitoring, preventing or treating conditions requiring
CC regulation of trophoblast invasion, especially preeclampsia in pregnant
CC women or choriocarcinomas.
XX
XX Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 other;
SQ
Query Match 100.0%; Score 339; DB 19; Length 2574;
Best Local Similarity 100.0%; Pred. No. 5.5e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgtcttcgcgaacttgaggagaaactgtgtggtgccccctc 60
DB 1154 gctttggacacaaattactgtcttcgcgaacttgaggagaaactgtgtggtgccccctc 1213
QY 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
DB 1214 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 1273
QY 121 gccaaactctcagcccttgcccatacctccgcagtcagacacacacacagcagc 180
DB 1274 gccaaactctcagcccttgcccatacctccgcagtcagacacacacacagcagc 1333
QY 181 gtgctgggactgtacaacacttgaaacctgaagcatctgctcctgtgctgctgccc 240
DB 1334 gtgctgggactgtacaacacttgaaacctgaagcatctgctcctgtgctgctgccc 1393
QY 241 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtgagcag 300
DB 1394 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtgagcag 1453
QY 301 ctctccacatggtggtgaagtcttggtaaatgtagctga 339
DB 1454 ctctccacatggtggtgaagtcttggtaaatgtagctga 1492
RESULT 12
AAQ56926
ID AAQ56926 standard; cDNA; 2157 BP.
XX
XX AAQ56926;
AC
XX
XX 09-JUL-1994 (first entry)
DT
XX Human TGF-beta-3.
DE
XX TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW

```

```

KW transforming growth factor beta-3; recombinant; wound healing;
XX vulnerable; ss.
XX
XX Homo sapiens.
OS
XX
XX US5284763-A.
PN
XX
XX 08-FEB-1994.
PD
XX
XX 22-MAR-1985; 85US-0715142.
PF
XX
XX 22-MAR-1985; 85US-0715142.
PR
XX 13-MAR-1987; 87US-0025423.
PR
XX 04-AUG-1989; 89US-0389929.
PR
XX 04-MAR-1992; 92US-0845893.
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Derynk RMA, Goeddel DV;
PI
XX
XX WPI: 1994-056343/07.
DR
XX P-PSDB; AAR46229.
DR
XX Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
PT
XX Disclosure; Fig 4a-c; 25pp; English.
PS
XX
XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX
XX Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;
SQ
Query Match 99.5%; Score 337.4; DB 15; Length 2157;
Best Local Similarity 99.7%; Pred. No. 1.5e-86;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgtcttcgcgaacttgaggagaaactgtgtggtgccccctc 60
DB 278 gctttggacacaaattactgtcttcgcgaacttgaggagaaactgtgtggtgccccctc 337
QY 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
DB 338 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 397
QY 121 gccaaactctcagcccttgcccatacctccgcagtcagacacacacacagcagc 180
DB 398 gccaaactctcagcccttgcccatacctccgcagtcagacacacacacagcagc 457
QY 181 gtgctgggactgtacaacacttgaaacctgaagcatctgctcctgctgctgctgccc 240
DB 458 gtgctgggactgtacaacacttgaaacctgaagcatctgctcctgctgctgctgccc 517
QY 241 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtgagcag 300
DB 518 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtgagcag 577
QY 301 ctctccacatggtggtgaagtcttggtaaatgtagctga 339
DB 578 ctctccacatggtggtgaagtcttggtaaatgtagctga 616
RESULT 13
AAV52935
ID AAV52935 standard; cDNA; 2157 BP.
XX

```


AC AAV52935;
 XX 21-DEC-1998 (first entry)
 XX Human transforming growth factor-beta 3 cDNA.
 XX Transforming growth factor-beta 3; TGF-beta 3; human; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 2..616
 FT /*tag= a
 FT /transl_except= (pos:50..52, aa:Thr)
 XX
 PN US5801231-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 22-MAR-1985; 85US-0715142.
 XX
 PR 13-MAR-1987; 87US-0025423.
 PR 22-MAR-1985; 85US-0715142.
 PR 04-AUG-1989; 89US-0389929.
 PR 04-MAR-1992; 92US-0845893.
 PR 05-NOV-1993; 93US-0147364.
 PR 30-MAY-1995; 95US-0454468.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Derynck RMA, Goeddel DV;
 PI
 DR WPI; 1998-494840/42.
 DR P-PSDB; AAW78787.
 XX
 XX DNA encoding transforming growth factor-beta precursor sequence -
 PT useful for analysis to perform manipulations to increase yield of
 PT recombinant production of the protein
 PT
 XX Example 6; Fig 4a-c; 26pp; English.
 XX
 CC This nucleotide sequence, hu4, codes for a human partial
 CC transforming growth factor-beta 3 (TGF-beta 3) sequence including
 CC all of the mature sequence. Clone hu4 was isolated from a human
 CC ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934)
 CC as probe. The invention relates to the recombinant production of
 CC TGF-beta. Biologically active TGF-beta is defined as being capable
 CC of inducing EGF-potential anchorage independent growth of target
 CC cell lines and/or growth inhibition of neoplastic cell lines.
 CC Nucleic acids encoding TGF-beta have been isolated and cloned into
 CC vectors which are replicated in bacteria and expressed in
 CC eukaryotic cells. TGF-beta recovered from transformed cells is
 CC used in known therapeutic applications. TGF-beta nucleic acids are
 CC also useful in diagnosis and identification of TGF-beta clones.
 XX
 SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

Query Match 99.5%; Score 337.4; DB 19; Length 2157;
 Best Local Similarity 99.7%; Pred. No. 1.5e-86;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgtgccccctc 60
 DB 278 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgtgccccctc 337
 QY 61 tacattgacttcgcacaggatcgtggctggaagtgggtccatgaacctaaagggtactat 120
 DB 338 tacattgacttcgcacaggatcgtggctggaagtgggtccatgaacctaaagggtactat 397
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgcagtcgagacacacccacagcacg 180
 DB 398 gccaaacttctgctcaggcccttgcccatacctccgcagtcgagacacacccacagcacg 457

QY 181 gtctgggactgtacaaactctgaacccctgaagcatctgctcgcttgcgtgccc 240
 DB 458 gtctgggactgtacaaactctgaacccctgaagcatctgctcgcttgcgtgccc 517
 QY 241 caggacctggagccctgacacatctgtactatcttgggagagaccccaagtggagcag 300
 DB 518 caggacctggagccctgacacatctgtactatcttgggagagaccccaagtggagcag 577
 QY 301 ctctcaacatgtgtggaagtctttaaattgaactga 339
 DB 578 ctctcaacatgtgtggaagtctttaaattgaactga 616
 RESULT 14
 AAQ02820
 ID AAQ02820 standard; DNA; 2158 BP.
 XX
 AC AAQ02820;
 XX
 DT 31-MAY-1989 (first entry)
 XX
 DE cDNA sequence encoding human TGF-beta 3.
 XX
 KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
 KW inhibition.
 XX
 PN W08912101-A.
 XX
 PD 14-DEC-1989.
 XX
 PF 08-JUN-1988; 88WO-US01945.
 XX
 PR 08-JUN-1988; 88WO-U001945.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Derynck RM, Goeddel DV;
 XX
 DR WPI; 1990-007474/01.
 XX
 PT Nucleotide sequence encoding transforming growth factor beta-3 -used as a
 PT probe, or to produce TGF beta 3, for inhibition of growth of normal
 PT and neoplastic cells, eg A549.
 XX
 PS Disclosure; Fig. 4; 61pp; English.
 XX
 CC This sequence encodes human transforming growth factor-beta 3 (TGF-
 CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
 CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
 CC cell growth inhibition.
 XX
 SQ Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0 other;

Query Match 99.5%; Score 337.4; DB 11; Length 2158;
 Best Local Similarity 99.7%; Pred. No. 1.5e-86;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgtgccccctc 60
 DB 278 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgtgccccctc 337
 QY 61 tacattgacttcgcacaggatcgtggctggaagtgggtccatgaacctaaagggtactat 120
 DB 338 tacattgacttcgcacaggatcgtggctggaagtgggtccatgaacctaaagggtactat 397
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgcagtcgagacacacccacagcacg 180
 DB 398 gccaaacttctgctcaggcccttgcccatacctccgcagtcgagacacacccacagcacg 457
 QY 181 gtctgggactgtacaaactctgaacccctgaagcatctgctcgcttgcgtgccc 240
 DB 458 gtctgggactgtacaaactctgaacccctgaagcatctgctcgcttgcgtgccc 517

Db 458 gtgtgggactgtacaacacttgaaacctgaacctgaagcatctgctcgcttgcctgcatgcc 517
 Qy 241 cagacactggagccctgaacctctgtactatgtgtggagagacccccaaagtggagcag 300
 Db 518 caggacctggagccctgaacctctgtactatgtgtggagagacccccaaagtggagcag 577
 Qy 301 ctctccaacatgggtgaagtcttctgtaaatgtagctga 339
 Db 578 ctctccaacatgggtgaagtcttctgtaaatgtagctga 616

RESULT 15
 AAQ22229
 ID AAQ22229 standard; cDNA; 1239 BP.
 XX AC AAQ22229;
 XX DT 05-MAY-1992 (first entry)
 XX DE Mutant transforming growth Factor beta 3 coding sequence.
 XX KW TGF-beta 3; homodimer; ss.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 1..888
 FT /*tag= a
 FT /note= "nucleotides 263-1150 of TGF-beta3"
 FT misc_feature 889..903
 FT /*tag= b
 FT /note= "encodes Factor Xa cleavage site
 followed by a methionine residue"
 FT misc_feature 904..1212
 FT /*tag= c
 FT /note= "nucleotides 1163-1471 of TGF-beta3"
 FT misc_difference 1213..1215
 FT /*tag= d
 FT /note= "wild-type codon = ATG. May be replaced by
 any other codon to give mutant sequence"
 FT misc_feature 1216..1239
 FT /*tag= e
 FT /note= "nucleotides 1475-1498 of TGF-beta3"
 XX WO9200318-A.
 XX 09-JAN-1992.
 XX 25-JUN-1991; 91WO-US04541.
 XX 25-JUN-1990; 90US-0543348.
 XX (ONCO-) ONCOGENE SCI INC.
 PI Iwata KK, Foulkes JG, Tendijke P, Haley JD;
 XX WPI; 1992-041510/05.
 DR P-PSDB; AAR22038.
 XX Transforming growth factor beta 3 proteins, precursors and
 PT mutants - obt'd. from polypeptide and antibodies, with optimal
 PT therapeutic use due to genetic manipulation of coding sequence
 XX Claim 12; Page 66; 107pp; English.
 XX This sequence has been compiled from the description of a mutant TGF-
 CC beta3 contained in the claims. The sequence coding for the Factor Xa
 CC cleavage site may be replaced by one encoding a similar protease
 CC recognition site, e.g. for collagenase. The coding sequence may
 CC also include a region encoding a hydrophobic transmembrane amino
 CC acid sequence, e.g. from c-erbB2 cDNA and a "stop transfer"
 CC sequence. The protease recognition site is located between the
 CC C-terminal of the transmembrane region and the N-terminal of the

CC TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently
 CC cleaved from the membrane. See also AAQ20576 and AAR20622.
 XX Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;
 SQ

Query Match 98.2%; Score 333; DB 13; Length 1239;
 Best Local Similarity 99.1%; Pred. No. 2.3e-85;
 Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 gcttggacaccaaattactgtctccgaacttggagagaaactgtgtgccccctc 60
 Db 904 gcttggacaccaaattactgtctccgaacttggagagaaactgtgtgccccctc 963
 Qy 61 tacattgacttccgacaggaatctgggctggaagtgggtccatgaacctaaagggtactat 120
 Db 964 tacattgacttccgacaggaatctgggctggaagtgggtccatgaacctaaagggtactat 1023
 Qy 121 gcaacttctgtcagggcccttggcccataccctccgcagtcgacacacacccacagcag 180
 Db 1024 gcaacttctgtcagggcccttggcccataccctccgcagtcgacacacacccacagcag 1083
 Qy 181 gtgctggagactgtacaacactctgaacctgaagcatctgcctgccttgcctgcgtgcc 240
 Db 1084 gtgctggagactgtacaacactctgaacctgaagcatctgcctgccttgcctgcgtgcc 1143
 Qy 241 caggacctggagccctgaccatctgtactatgttgggagagacccccaaagtggagcag 300
 Db 1144 caggacctggagccctgaccatctgtactatgttgggagagacccccaaagtggagcag 1203
 Qy 301 ctctccaacatgggtgaagtcttctgtaaatgtagc 336
 Db 1204 ctctccaacnnngtggtagaagtcttgaatgtagc 1239

RESULT 16
 AAT06496
 ID AAT06496 standard; cDNA; 498 BP.
 XX AC AAT06496;
 XX DT 12-JUN-1996 (first entry)
 XX DE Tissue-derived tumour growth inhibitor-1 coding sequence.
 KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
 KW arteriosclerosis; inflammation; psoriasis; therapy; vulneryary;
 XX immunomodulator; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..498
 FT /*tag= a
 FT /product= tumour_growth_inhibitor_precursor
 FT /note= "see AAR86771"
 FT misc_feature 159..160
 FT /*tag= b
 FT /note= "the codons at positions -40 to -1 (i.e. 117
 nucleotides) are not given in the
 specification"
 FT mat_peptide 160..495
 FT /*tag= c
 FT /product= mature_tumour_growth_inhibitor
 FT /note= "see AAR86770"
 XX EP684260-A2.
 XX 29-NOV-1995.
 XX 20-OCT-1987; 87EP-0109866.
 XX 20-OCT-1986; 86US-0922121.

```

XX PA (ONCO-) ONCOGENE SCI INC.
XX PI Gold LI, Iwata KK, Stephenson JR;
XX DR WPI; 1996-000991/01.
XX DR P-PSDB; AAR86770, AAR86771.
XX XX
XX PT Tissue-derived growth inhibitor and corresponding genes - useful for
XX PT detection of tumours, inhibition of tumour growth, treatment of
XX PT proliferative disorders and healing of burns and wounds.
XX PS Claim 6; Fig 29; 83pp; English.
XX XX
XX CC The sequence encodes a 112 amino acid tumor growth inhibitor (TGI)
XX CC (AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an
XX CC additional 93 amino acid residues at the N-terminus. However, the
XX CC nucleotides representing codons -40 to -1 of the precursor TGI are
XX CC not specified in Figure 29, i.e. the cDNA is 498 nucleotides in
XX CC length, but should be 615 nucleotides long. The DNA is used to
XX CC produce the inhibitors by recombinant methods i.e. vector
XX CC expression in bacterium or eukaryotic host cells. The proteins can
XX CC be used to inhibit the growth of human tumour cells, e.g.
XX CC carcinoma, melanoma or leukaemia cells, in the treatment of
XX CC proliferative disorders e.g. arteriosclerosis, inflammation and
XX CC psoriasis, or for the treatment of burns to facilitate wound
XX CC healing. They can also be used as immunomodulators. Although the
XX CC proteins have tumour growth inhibitory activity, they are not
XX CC transforming growth factor-beta-1 or -beta-2.
XX SQ Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;

Query Match          98.1%; Score 332.6; DB 17; Length 498;
Best Local Similarity 98.8%; Pred. No. 2.4e-85;
Matches 335; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gcttggacacaaatctactgtctccgcaacttgaggaggaactgtgtgccccctc 60
DB 160 gcttggacacaaatctactgtctccgcaacttgaggaggaactgtgtgccccctc 219

QY 61 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggctactat 120
DB 220 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggctactat 279

QY 121 gcaacttctgtcagggccttgcctacactcgcgaagtgcagacacacacacagacag 180
DB 280 gcaacttctgtcagggccttgcctacactcgcgaagtgcagacacacacacagacag 339

QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccc 240
DB 340 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccc 399

QY 241 caggacctgagccctgacctcctgtactatgttggaggagaccccaagtggagcag 300
DB 400 caggacctgagccctgacctcctgtactatgttggaggagaccccaagtggagcag 459

QY 301 ctctcaacatgggtgagttcttgaatgttaagtgtactga 339
DB 460 ctctcaacatgggtgagttcttgaatgttaagtgtactga 498

RESULT 17
AAQ06845
ID AAQ06845 standard; cDNA; 2530 BP.
AC AAQ06845;
XX XX
XX DT 05-MAR-1991 (first entry)
XX XX
XX DE Sequence encoding tumour growth inhibitor.
XX XX
XX KW TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;

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KW XX psoriasis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 263..1501
XX FT /tag= a
XX FT polyA_signal 2506..2511
XX FT /tag= b
XX FT polyA_site 2529
XX FT /tag= c
XX PN W09014360-A.
XX PD 29-NOV-1990.
XX PF 17-MAY-1990; 90WO-US02753.
XX PR 17-MAY-1989; 89US-0353410.
XX PR 19-APR-1985; 85US-0725003.
XX PR 07-APR-1986; 86US-0847931.
XX PR 20-OCT-1986; 86US-0992121.
XX PR 20-OCT-1987; 87US-0111022.
XX PR 20-APR-1988; 88US-0183224.
XX PA (ONCO-) ONCOGENE SCI INC.
XX XX Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX DR WPI; 1990-375949/50.
XX DR P-PSDB; AAR08264.
XX PT Tissue-derived tumour growth inhibitors - comprise specified
XX PT protein sequences used to detect, and treat tumours, burns and
XX PT wounds.
XX PS Claim 10; Fig 41; 190pp; English.
XX XX
XX CC The plasmid was isolated from a human cDNA library prepd. from the
XX CC DNA of a chronic myelocytic leukaemia cell line (K562). The
XX CC sequence can be used to produce the tumour growth inhibitor (TGI)
XX CC by recombinant techniques. The protein may also be isolated from
XX CC human umbilical cord and placental tissues. It can be used to
XX CC inhibit tumour cell growth, to treat burns, to facilitate the
XX CC healing of wounds or to treat proliferative disorders. The
XX CC protein and Abs raised to it can be used for detection and typing
XX CC of tumours. The Abs can also be used to inhibit the activity of
XX CC the TGI.
XX SQ Sequence 2530 BP; 619 A; 671 C; 659 G; 581 T; 0 other;

Query Match          96.2%; Score 326.2; DB 11; Length 2530;
Best Local Similarity 97.6%; Pred. No. 2.4e-83;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 gcttggacacaaatctactgtctccgcaacttgaggaggaactgtgtgccccctc 60
DB 1163 gcttggacacaaatctactgtctccgcaacttgaggaggaactgtgtgccccctc 1222

QY 61 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggctactat 120
DB 1223 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggctactat 1282

QY 121 gccaaacttctgtcaggcccttgcctacactcctccagtgagacacacacacagcag 180
DB 1283 gccaaacttctgtcaggcccttgcctacactcctccagtgagacacacacagcag 1342

QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccc 240
DB 1343 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccc 1402

QY 241 caggacctggagccctgacctctgtactatgttggaggagaccccaagtggagcag 300

```

```
Db 1403 caggacctggagcccttgaccatctgtactatgttggaggagccccaagaaggagcaag 1462
|||||
Qy 301 ctctccaacatggtggtgaagctcttgtaaatgtagctga 339
|||||
Db 1463 ctctccaacatggtggtgaagctcttgtaaatgtagctga 1501
|||||

RESULT 18
AAQ02819
ID AAQ02819 standard; DNA; 2676 BP.
XX
AC AAQ02819;
XX
DT 31-MAY-1989 (first entry)
XX
DE cDNA sequence encoding porcine TGF-beta 3.
XX
KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
inhibition.
XX
PN W08912101-A.
XX
PD 14-DEC-1989.
XX
PF 08-JUN-1988; 88WO-US01945.
XX
PR 08-JUN-1988; 88WO-UO01945.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RM, Goeddel DV;
XX
WPI; 1990-007474/01.
DR P-PSDB; AAR04080.
XX
Nucleotide sequence encoding transforming growth factor beta-3 -used as a
probe, or to produce TGF beta 3, for inhibition of growth of normal
and neoplastic cells, eg A549.
XX
PS Disclosure; Fig. 4; 6lpp; English.
XX
This sequence encodes porcine transforming growth factor-beta 3 (TGF-
beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
cell growth inhibition.
XX
SQ Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other;

Query Match 92.9%; Score 315; DB 11; Length 2676;
Best Local Similarity 95.6%; Pred. No. 3.6e-80;
Matches 324; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 gttttgacacaaattactgtctccgcaacttgaggagaaactgtgtgcgccccctc 60
|||||
Db 1175 gccctggacacaaactactctctccgcaatttggaggagaaactgtgtgcgccccctc 1234
|||||

Qy 61 tacattgacttcgcagagatcggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1235 tacattgacttcgcagagatcggtggaagtgggtccatgaacctaaagggtactat 1294
|||||

Qy 121 gccaaacttgcagggcccttgcccatctccagtcagtcagacacaaaccacagcag 180
|||||
Db 1295 gccaaacttgcagggcccttgcccatctccagtcagtcagacacaaaccacagcag 1354
|||||

Qy 181 gtgctggactgtacaacactctgaacctgaagcatctgcctccttgcgtgcgtgcc 240
|||||
Db 1355 gtgctggactgtacaacactctgaacctgaagcatctgcctccttgcgtgcgtgcc 1414
|||||

Qy 241 caggacctggagcccttgaccatctgtactatgttggaggagccccaagaagtggagcag 300
|||||
Db 1415 caggacctggagcccttgaccatctgtactatgttggaggagccccaagaagtggagcag 1474
|||||
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```
Qy 301 ctctccaacatggtggtgaagctcttgtaaatgtagctga 339
|||||
Db 1475 ctctccaacatggtggtgaagctcttgtaaatgtagctga 1513
|||||

RESULT 19
AAV52934
ID AAV52934 standard; cDNA; 2639 BP.
XX
AC AAV52934;
XX
DT 21-DEC-1998 (first entry)
XX
DE Pig transforming growth factor-beta 3 cDNA.
XX
KW Transforming growth factor-beta 3; TGF-beta 3; pig; ss.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 127..1497
FT /*tag= a
FT /transl_except= (pos:481..483, aa:Met)
XX
PN US5801231-A.
XX
PD 01-SEP-1998.
XX
PF 22-MAR-1985; 85US-0715142.
XX
PR 13-MAR-1987; 87US-0025423.
PR 22-MAR-1985; 85US-0715142.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
PR 05-NOV-1993; 93US-0147364.
PR 30-MAY-1995; 95US-0454468.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RMA, Goeddel DV;
XX
WPI; 1998-494840/42.
DR P-PSDB; AAW78786.
XX
DNA encoding transforming growth factor-beta precursor sequence -
useful for analysis to perform manipulations to increase yield of
recombinant production of the protein
XX
Example 6; Fig 4a-c; 26pp; English.
XX
This nucleotide sequence, termed 10+11.3, codes for the porcine
transforming growth factor-beta 3 precursor (prefTGF-beta 3, see
AAW78786). A porcine ovarian cDNA library was screened using human
TGF-beta 1 cDNA (see AAV52933) as probe. A hybridising clone,
designated lambda 11.3, was used to rescreen the library to
identify clone lambda 10. The was combined with clone lambda 11.3
to provide the 10+11.3 sequence. The invention relates to the
recombinant production of TGF-beta. Biologically active TGF-beta
is defined as being capable of inducing EGF-potential anchorage
independent growth of target cell lines and/or growth inhibition of
neoplastic cell lines. Nucleic acids encoding TGF-beta have been
isolated and cloned into vectors which are replicated in bacteria
and expressed in eukaryotic cells. TGF-beta recovered from
transformed cells is used in known therapeutic applications.
CC TGF-beta nucleic acids are also useful in diagnosis and
CC identification of TGF-beta clones.
XX
SQ Sequence 2639 BP; 677 A; 702 C; 697 G; 563 T; 0 other;

Query Match 89.1%; Score 302.2; DB 19; Length 2639;
Best Local Similarity 93.2%; Pred. No. 1.6e-76;
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XX      prodn. of dimeric biologically active transforming growth factor
PT      by refolding denatured monomer in detergent-free folding buffer
PT      contg. specific organic solvent to improve yield
XX
XX      Example 10; Page 36-37; 54pp; English.
XX
XX      A DNA sequence (AAT17237) codes for a recombinant hybrid of human
CC      transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which
CC      the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773)
CC      and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772).
CC      The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
CC      1(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was
CC      recovered from E. coli transformants. A biologically active,
CC      dimeric form of the hybrid was obtd. by refolding the monomer in
CC      detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
CC      TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR92777) were similarly
CC      produced.
XX
XX      Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
SQ
Query Match      87.8%; Score 297.6; DB 17; Length 336;
Best Local Similarity 92.9%; Pred. No. 1.9e-75;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY      1 gcttggacacccaattactgcttcgcgaacttggaggagaactgctgtgccccttc 60
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      1 gccctggacaccaactatgcttcagctccacgagagaactgctgctgcccagctg 60
QY      61 tacattgacttcgcacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      61 tacattgacttcgcgaagacctcgctggaagtggatccacgagcccaggctaccat 120
QY      121 gccaaacttctcagggcccttgcccaactcccgactggaggaactgctgtgccccttc 180
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      121 gccaaacttctcagggcccttgcccaactcccgactggaggaactgctgtgccccttc 180
QY      181 gtgctgggactgtacaacactctgaacctgaagcatctgctcgcttgcctgctgccc 240
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      181 gtgctgggactgtacaacactctgaacctgaagcatctgctcgcttgcctgctgccc 240
QY      241 caggacctggagcccttgaccatctctgtactatgttggaggacccccaaagtggagcag 300
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      241 caggacctggagcccttgaccatctctgtactatgttggaggacccccaaagtggagcag 300
QY      301 ctctccaaatggtgtaagtctgttaattagc 336
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      301 ctctccaaatggtgtaagtctgttaattagc 336
XX
RESULT 24
AAT15465
ID      AAT15465 standard; cDNA to mRNA; 336 BP.
XX
AC      AAT15465;
XX
XX      10-JUN-1996 (first entry)
XX
XX      cDNA encoding human TGF-beta-like protein, TGF-beta-1-3.
XX
XX      Transforming growth factor beta; TGF; regulator; method;
KW      proliferation; differentiation; wound healing; solvent; ds.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      CDS      1..336      a
FT      /*tag=
FT      /product= hybrid_TGF-beta-1-3
FT      1..132
FT      /*tag= b
FT      /note= "encodes N-terminal 44 amino acids of

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FT      mat_peptide      133..336      TGF-beta-1"
FT      /*tag= c
FT      /note= "encodes C-terminal 68 amino acids of
FT      TGF-beta-3"
XX
XX      WO9603432-A1.
XX
XX      08-FEB-1996.
XX
XX      12-JUL-1995;      95WO-EP027118.
XX
XX      25-JUL-1994;      94EP-0810438.
XX
XX      (CIBA ) CIBA GEIGY AG.
XX
XX      Cerletti N;
XX
XX      WPI; 1996-1116999/12.
XX      P-PSDB; AAR91959.
XX
XX      Prodn. of dimeric, biologically active transforming growth factor
PT      beta - by refolding denatured monomer in buffer contg. mild
PT      detergent and specific organic solvents to improve yields
XX
XX      Claim 17; Page 39-40; 59pp; English.
XX
XX      AAT15465 encodes transforming growth factor (TGF) beta-like protein,
CC      TGF-beta-1-3. TGF-beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF-beta
CC      hybrids were made using a new process of producing dimeric,
CC      biologically active TGF beta-like proteins. The new process involves
CC      treating denatured TGF beta monomers with folding buffer contg. a
CC      mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC      solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC      DMF (dimethyl formamide). The detergent allows folding of the monomer
CC      such that, after dimerisation, the TGF beta-like protein retains
CC      biological activity and remains in soluble form. The method allows
CC      relatively high yields of biologically active TGF beta-like proteins
CC      in their native dimeric form. TGF-beta like proteins are multifunctional
CC      regulators of cellular activity and a typical use is to stimulate wound
CC      healing.
XX
XX      Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
SQ
Query Match      87.8%; Score 297.6; DB 17; Length 336;
Best Local Similarity 92.9%; Pred. No. 1.9e-75;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY      1 gcttggacacccaattactgcttcgcgaacttggaggagaactgctgtgccccttc 60
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      1 gccctggacaccaactatgcttcagctccacgagagaactgctgctgcccagctg 60
QY      61 tacattgacttcgcacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      61 tacattgacttcgcgaagacctcgctggaagtggatccacgagcccaggctaccat 120
QY      121 gccaaacttctcagggcccttgcccaactcccgactggaggaactgctgtgccccttc 180
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      121 gccaaacttctcagggcccttgcccaactcccgactggaggaactgctgtgccccttc 180
QY      181 gtgctgggactgtacaacactctgaacctgaagcatctgctcgcttgcctgctgccc 240
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      181 gtgctgggactgtacaacactctgaacctgaagcatctgctcgcttgcctgctgccc 240
QY      241 caggacctggagcccttgaccatctctgtactatgttggaggacccccaaagtggagcag 300
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      241 caggacctggagcccttgaccatctctgtactatgttggaggacccccaaagtggagcag 300
QY      301 ctctccaaatggtgtaagtctgttaattagc 336
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
CC      301 ctctccaaatggtgtaagtctgttaattagc 336
XX

```



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PS Claim 17; Page 42; 59pp; English.
XX
CC AAR15466 encodes transforming growth factor (TGF) beta-like protein,
CC TGF-beta-2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta
CC hybrids were made using a new process of producing dimeric,
CC biologically active TGF beta-like proteins. The new process involves
CC treating denatured TGF beta monomers with folding buffer contg. a
CC mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC DMF (dimethyl formamide). The detergent allows folding of the monomer
CC such that, after dimerisation, the TGF beta-like protein retains
CC biological activity and remains in soluble form. The method allows
CC relatively high yields of biologically active TGF beta-like proteins
CC in their native dimeric form. TGF-beta like proteins are multifunctional
CC regulators of cellular activity and a typical use is to stimulate wound
CC healing.
XX
SQ Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;

Query Match      81.7%; Score 276.8; DB 17; Length 336;
Best Local Similarity 89.0%; Pred. No. 1.5e-69;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 gcttggacacacaaattactgtctccgaacttggaggagaaactgtgtgtgccccctc 60
DB 1 gcttggatgcggcctattgctttgaaatgtgcaggaataattgtgcctacgtccactt 60

QY 61 tacattgacttcgcacaggatctggctggaagtgggtccatgaacctaaaggtactat 120
DB 1 tacattgattccaaggaggtatagggtggaaatggatcacgcagcccaaaagggtacaa 120

QY 121 gccaaacttctgcagggccttgcacatactcccgagtcgagacacacccacagcacg 180
DB 121 gccaaacttctgcagggccttgcacatactcccgagtcgagacacacccacagcacg 180

QY 181 gtgctgggaactgtacaaactgtgaacctgaacctgaagcatctgcctgcctgtgctgcc 240
DB 181 gtgctgggaactgtacaaactgtgaacctgaacctgaagcatctgcctgcctgtgctgcc 240

QY 241 caggacctggagccctgacctctactatgttggaggagaccccaaaagtggagcag 300
DB 241 caggacctggagccctgacctctactatgttggaggagaccccaaaagtggagcag 300

QY 301 ctctccaacatggtgtgaagtcctgtgtaaatgtagc 336
DB 301 ctctccaacatggtgtgaagtcctgtgtaaatgtagc 336

RESULT 29
AAQ41606
ID AAQ41606 standard; cDNA; 336 BP.
XX
AC AAQ41606;
XX
XX 26-AUG-1993 (first entry)
XX
DE Transforming Growth Factor-beta3(44/45)beta1 hybrid.
XX
KW hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
XX cancer treatment; bone repair; growth regulation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
FT /*tag= a
FT /note= "TGF-beta3=1-132, TGF-beta1=133-336"
XX
PN EP542679-A.
XX
PD 19-MAY-1993.
XX
```

```
PF 03-NOV-1992; 92EP-0810845.
XX
PR 11-NOV-1991; 91EP-0810870.
PA (CIBA ) CIBA GEIGY AG.
XX
PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39645.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 8; Page 30-31; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta3(44/45)beta1. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-041607 for the most pref. hybrids.
XX
SQ Sequence 336 BP; 63 A; 109 C; 98 G; 66 T; 0 other;

Query Match      70.8%; Score 240; DB 14; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 gcttggacacacaaattactgtctccgaacttggaggagaaactgtgtgtgccccctc 60
DB 1 gcttggacacacaaattactgtctccgaacttggaggagaaactgtgtgtgccccctc 60

QY 61 tacattgacttcgcacaggatctggctggaagtgggtccatgaacctaaaggtactat 120
DB 61 tacattgacttcgcacaggatctggctggaagtgggtccatgaacctaaaggtactat 120

QY 121 gccaaacttctgcagggccttgcacatactcccgagtcgagacacacccacagcacg 180
DB 121 gccaaacttctgcagggccttgcacatactcccgagtcgagacacacccacagcacg 180

QY 181 gtgctgggaactgtacaaactgtgaacctgtgaacctgtgcctgcctgtgctgcc 240
DB 181 gtgctgggaactgtacaaactgtgaacctgtgaacctgtgcctgcctgtgctgcc 240

QY 241 caggacctggagccctgacctctactatgttggaggagaccccaaaagtggagcag 300
DB 241 caggacctggagccctgacctctactatgttggaggagaccccaaaagtggagcag 300

QY 301 ctctccaacatggtgtgaagtcctgtgtaaatgtagc 336
DB 301 ctctccaacatggtgtgaagtcctgtgtaaatgtagc 336

RESULT 30
AAQ41607
ID AAQ41607 standard; cDNA; 336 BP.
XX
AC AAQ41607;
XX
XX 26-AUG-1993 (first entry)
XX
DE Transforming Growth Factor-beta3(44/45)beta2 hybrid.
XX
KW hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
XX
```

```
KW cancer treatment; bone repair; growth regulation; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
FT FT /*tag= a
FT FT /note= "TGF-beta3=1-132, TGF-beta2=133-336"
XX
XX
PN EP542679-A.
XX
XX 19-MAY-1993.
XX
XX 03-NOV-1992; 92EP-0810845.
XX
XX 11-NOV-1991; 91EP-0810870.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
XX P-PSDB; AAR39646.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 9; Page 32; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred, esp. the hybrid
CC TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-041606 for the other pref. hybrids.
XX
XX Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

Query Match 70.8%; Score 240; DB 14; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttggagagaaactgtgtgccccctc 60
DB 1 gcttggacacaaattactgcttcgcgaacttggagagaaactgtgtgccccctc 60
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
DB 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
QY 121 gccaaactctgtcagggcccttgccatccactccgcagtcgagacacacacagcagc 180
DB 121 gccaaactctgtcagggcccttgccatccactccgcagtcgagacacacacagcagc 180
QY 181 gtcgtggagactgtacaaactgtgaacctgaagcatgacatgctcgtcgtcggtgcc 240
DB 181 gtcgtgagcttataataaccataaataccagaagcatgctcctcgtcgtcggtgcc 240
QY 241 caggacctgagccctgcaccatcctgtactatgtttggaggagcccccaagtggagcag 300
DB 241 caagatttgaaccttaacctctctactacattcgttgcgaaccccccaagattgaacag 300
QY 301 ctctcaacatgtgggtgaagctgttgaatgtacg 336
DB 301 ctttctaataatgtgaagtcttgcaaatgcagc 336
```

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RESULT 31
AAT17239
ID AAT17239 standard; DNA; 336 BP.
XX
AC AAT17239;
XX
DT 17-JUL-1996 (first entry)
XX
DE Hybrid TGF-beta 3-2 DNA.
XX
KW Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;
KW protein renaturation; protein folding; ds.
XX
OS Synthetic.
XX
XX WO9603433-A1.
XX
XX 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02719.
XX
XX 25-JUL-1994; 94EP-0810439.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Cerletti N;
XX
XX WPI; 1996-117000/12.
XX P-PSDB; AAR92777.
XX
XX Prodn. of dimeric biologically active transforming growth factor
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. Specific organic solvent to improve yield
XX
XX Example 10; Page 41-42; 54pp; English.
XX
XX A DNA sequence (AAT17239) codes for a recombinant hybrid of human
CC transforming growth factor-beta, TGF-beta 3-2 (AAR92777), in which
CC the N-terminal 44 amino acids are from TGF-beta 3 (see also AAR92772)
CC and the C-terminal 68 amino acids from TGF-beta 2 (see also AAR92774).
CC The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
CC 3(44/45)beta2. Non-soluble, monomeric hybrid TGF-beta 3-2 was
CC recovered from E. coli LC137 transformants. A biologically active,
CC dimeric form of the hybrid was obtnd. by refolding the monomer in
CC detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
CC TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were similarly
CC produced.
XX
XX Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

Query Match 70.8%; Score 240; DB 17; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttggagagaaactgtgtgccccctc 60
DB 1 gcttggacacaaattactgcttcgcgaacttggagagaaactgtgtgccccctc 60
QY 61 tacattgacttcgcagggcccttgccatccactccgcagtcgagacacacacagcagc 120
DB 61 tacattgacttcgcagggatctggctggaagtgggtccatgaacctaaagggtactat 120
QY 121 gccaaactctgtcagggcccttgccatccactccgcagtcgagacacacacagcagc 180
DB 121 gccaaactctgtcgtggagcatgccgtatttatgtatgagtcacacacagcagcagc 180
QY 181 gtcgtggagactgtacaaactgtgaacctgtgaagcatgctcgtcgtcggtgcc 240
DB 181 gtcctgagcttataataaccataaataccagaagcatgctcctcgtcgtcggtgcc 240
QY 181 gtcctgagcttataataaccataaataccagaagcatgctcctcgtcgtcggtgcc 240
DB 181 gtcctgagcttataataaccataaataccagaagcatgctcctcgtcgtcggtgcc 240
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XX PS Disclosure; Page 44-45; 59pp; English.
XX CC
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. The present
XX CC sequence encodes a specifically claimed TGF active fragment, TGF-beta1.
XX CC Additionally, the fusion protein may comprise proteinase-sensitive
XX CC linker sites and binding domain so the protein sequence may contain
XX CC some or all of the following elements: purification tag; proteinase
XX CC site; ECM binding site; proteinase site; TGF-beta. TGF-beta promotes
XX CC wound healing, and the fusion protein can be used to reduce surgery
XX CC recovery time and in the preparation of artificial skin. The inclusion
XX CC of a purification tag facilitates purification of the fusion protein.
XX CC The proteinase site is included to permit cleavage and release of the
XX CC purification tag after purification if desired. The extracellular
XX CC matrix binding site facilitates delivery of the fusion protein to the
XX CC desired site of action. Delivery of the TGF-beta to the site to be
XX CC treated reduces the amount of TGF-beta required to be administered to
XX CC be effective and reduces the concentration of circulating TGF-beta
XX CC which may result in undesirable effects.
XX CC
XX CC Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

Query Match      60.8%; Score 206.2; DB 18; Length 339;
Best Local Similarity 75.5%; Pred. No. 1.7e-49;
Matches 256; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttgaggagaactgctgtgccccctc 60
   || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1 gccctggacacaaactattgcttcagctccacggagaagaactgctgctggcagctg 60

QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 61 tacattgacttcgcagagactcgctggagtggtccatgagcccaagggtaccat 120

QY 121 gccaaactctgctcaggcccttgcccatacctccgcagtcgacacacacccacagcacg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 121 gccaaactctgctcaggcccttgcccataccttcattggagctggacacgactacagcaag 180

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgtgctgctgcccc 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 181 gtctggccctgtacaaaccagcataaccggcgccctcgccgctgctgctgctgccc 240

QY 241 caggacctgagccctgacctctgtactatgttgaggagaccgcccaaggaggagcag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 241 caggcgctggagccctgacctctgtactatgttgaggagaccgcccaaggaggagcag 300

QY 301 ctctccaaactggtggaagtctttaaattagctga 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 301 ctgtccaaactgatgctgctcctgcaagtgcagctga 339

RESULT 34
AAV9375
ID AAV9375 standard; cDNA; 339 BP.
XX AC AAV9375;
XX CC
XX DT 25-MAR-1999 (first entry)
XX CC
XX DE cDNA encoding a transforming growth factor beta active fragment.
XX KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
XX KW bone morphogenetic protein; transforming growth factor beta;
XX KW active fragment; wound healing; bone growth; purification tag; ds.
XX CC
XX OS Homo sapiens.
XX CC
XX PN W09855137-A1.
XX CC
XX PD 10-DEC-1998.
XX CC

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PF 02-JUN-1998; 98WO-US11189.
XX CC
XX PR 03-JUN-1997; 97US-0868452.
XX CC
XX PA (HALL/) HALL F L.
XX PA (HANE/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX CC
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX CC
XX DR WPI; 1999-059875/05.
XX CC
XX DR P-PSDB; AAW84207.
XX CC
XX XX New bone morphogenetic fusion proteins - comprising a purification
XX PT tag and a bone morphogenetic active fragment, used for enhancing
XX PT wound healing or bone growth
XX CC
XX PS Example 1; Page 41; 64pp; English.
XX CC
XX CC The present sequence encodes a transforming growth factor beta active
XX CC fragment. The protein can be used in place of a bone morphogenetic
XX CC active fragment to create the fusion proteins of the invention. When a
XX CC bone morphogenetic active fragment is used, the fusion proteins are
XX CC designated bone morphogenetic fusion proteins. The bone morphogenetic
XX CC fusion protein may contain some or all of the following elements: a
XX CC purification tag, a proteinase site, an ECM/bone binding site, a second
XX CC proteinase site, and a bone morphogenetic protein active fragment.
XX CC The bone morphogenetic fusion proteins can be used for enhancing wound
XX CC healing or bone growth.
XX CC
XX CC Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

Query Match      60.8%; Score 206.2; DB 20; Length 339;
Best Local Similarity 75.5%; Pred. No. 1.7e-49;
Matches 256; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttgaggagaactgctgtgccccctc 60
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1 gccctggacacaaactattgcttcagctccacggagaagaactgctgctggcagctg 60

QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 61 tacattgacttcgcagagactcgctggagtggtccatgagcccaagggtaccat 120

QY 121 gccaaactctgctcaggcccttgcccatacctccgcagtcgacacacacccacagcacg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 121 gccaaactctgctcaggcccttgcccataccttcattggagctggacacgactacagcaag 180

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgtgctgctgcccc 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 181 gtctggccctgtacaaaccagcataaccggcgccctcgccgctgctgctgctgccc 240

QY 241 caggacctgagccctgacctctgtactatgttgaggagaccgcccaaggaggagcag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 241 caggcgctggagccctgacctctgtactatgttgaggagaccgcccaaggaggagcag 300

QY 301 ctctccaaactggtggaagtctttaaattagctga 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 301 ctgtccaaactgatgctgctcctgcaagtgcagctga 339

RESULT 35
AAT17235
ID AAT17235 standard; cDNA to mRNA; 339 BP.
XX AC AAT17235;
XX CC
XX DT 17-JUL-1996 (first entry)
XX CC
XX DE Human TGF-beta 1 cDNA.

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Db 241 ||||| ||||| || ||||| ||||| || || || ||||| ||||| |||||
Qy 301 ctctcaacatggtggtgaagctgtgtaaatgtagctga 339
Db 301 ctgtccaacatgatgctgctcctgcaagtgcagctga 339

RESULT 37
AAQ09317
ID AAQ09317 standard; cDNA; 1303 BP.
XX
AC AAQ09317;
XX
DT 12-AUG-1990 (first entry)
XX
DE Monkey transforming growth factor-beta cDNA.
XX
KW Transforming growth factor-beta; simian; psoriasis;
KW TGF-beta.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT sig_peptide 22..63
FT mat_peptide 836..1170
FT /tag= a
FT /tag= b
FT /product=monkey transforming growth factor-beta
XX
PN EP353772-A.
XX
PD 07-FEB-1990.
XX
PF 04-AUG-1989; 89EP-0114458.
XX
PR 05-AUG-1988; 88US-0229133.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR WPI; 1990-038499/06.
DR P-PSDB; AAR03743.
XX
PT Inhibition of proliferation of epidermal cells -
PT used to treat psoriasis by contacting cells with compositions
PT containing transforming growth factor-beta.
XX
PS Disclosure; fig 1; 20pp; English.
XX
CC TGF-beta may be used in the treatment of hyperplasia
CC associated with acanthosis-categorised skin diseases, and
CC in alleviating psoriatic symptoms associated with cytokine-
CC induced phenomena. See also AAQ03268 and AAR03750.
XX
SQ Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;

Query Match 60.4%; Score 204.6; DB 11; Length 1303;
Best Local Similarity 75.2%; Pred. No. 6.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 1 gctttggacacaaactactgtctccgcaacttggaggagaactgtgtgtgccccctc 60
|| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 838 gccctggacacaaactactgtctcagctccacgagagaactgtgtgtgccccctg 897
Qy 61 tacattgacttcgacagagatgtggtggaagtgggtccatgaacctaaaggctactat 120
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 898 tatattgacttcgacagagactgtggtggaagtgggtccatgaacctaaaggctaccat 957
Qy 121 gccaaacttctcaggtcccttgcacatccctccgcagtgacacacacacagcacg 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

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Db 958 gccaaacttctcgtgggcccctgtccctacatttggagcctggacacgcagtacagaag 1017
Qy 181 gtctgtggactgtacaacactctgaacctgtgaagcatctgcctgccttgcgtgcgcc 240
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1018 gtctgtggcctgtacaaccagcataaccggggcgctcgggcgccgtgtgcgtgcgcg 1077
Qy 241 caggacctggagccccctgaccatcctgtactatgtttggagagaccccccaagtggagcag 300
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1078 caggcgtggagccactgcccctgtgtactacgtgggcccgaagcccaaggtggagcag 1137
Qy 301 ctctccaacatggtggtgaagctcttgaatgttagctga 339
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 ctgtccaacatgatcgtgcgtcctcctgcaaatgcagctga 1176

RESULT 38
AAQ20289
ID AAQ20289 standard; cDNA; 1559 BP.
XX
AC AAQ20289;
XX
DT 16-APR-1992 (first entry)
XX
DE Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT CDS 262..282
FT /tag= a
FT sig_peptide 283..324
FT /tag= b
FT CDS 325..1098
FT /tag= c
FT mat_peptide 1099..1436
FT /tag= d
XX
PN W09119513-A.
XX
PD 26-DEC-1991.
XX
PF 20-JUN-1991; 91WO-US04449.
XX
PR 20-JUN-1990; 90US-0541221.
XX
PA (BRIM ) BRISTOL-MYERS SQUIB.
XX
PI Oleson FB, Comereski CR;
XX
DR WPI; 1992-024199/03.
DR P-PSDB; AAR20124.
XX
PT Use of transforming growth factor (TGF)-beta and their
PT antagonists - for modulating blood pressure, for treating
PT hypertension and hypotension
XX
PS Disclosure; Fig 1; 42pp; English.
XX
CC A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
XX
SQ Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;

Query Match 60.4%; Score 204.6; DB 13; Length 1559;

```

```

Best Local Similarity   75.2%; Pred. NO. 7e-49;      Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy    1 gcttggacaccaattactgtcttcgcgaacttgaggagaaactgtgtgctgccccctc 60
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1095 gccctggacaccaactactgtcttagctccacggaagaactgtgctgcgagctg 1154
Qy    61 tacattgacttcgcagagatctggctggaaagtggctccatgaacctaaaggctactat 120
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1155 tataattgacttcgaaggacctgctgggaagtggatcccacgagcccaaggctaccat 1214
Qy    121 gccaatcttctcgaagcccttgccccatacctccagtcgacagacacacaacccacagcacg 180
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1215 gccaaactctgctgggcccctgtccctacattggagcctggacacgcagtacagcaag 1274
Qy    181 gtctgggactgtacaaactctgaacctgaacgatctgtcctgccttgcctgctgctgccg 240
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1275 gtctggccctgtacaaacagcataaacccggcgccctcggcgccctgtgctgctgccg 1334
Qy    241 caggacctggagcccttgaccatcctgtactatgtttgggagagacccccaaagtggagcag 300
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1335 caggcgctggagccactgcccatcgttactacgtggcgcaagcccaagtgaggcag 1394
Qy    301 ctctccaacatggtgtgaagtcttgttaaatgtagctga 339
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1395 ctgtccaacatgatcgtgcctcctgcctgcgaatgagctga 1433

RESULT 39
AAN81084
ID AAN81084 standard; cdna; 1560 BP.
XX
AC AAN81084;
XX
DT 09-OCT-1990 (first entry)
XX
DE Coding sequence of simian transforming growth factor-beta 1.
XX
KW Transforming growth factor-beta 1; tumour treatment; ss cdna.
XX
OS Cercopithecus aethiops.
```

CC	expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC	between mature simian and human TGF-beta 1. The plasmid also contains
CC	the SV40 promoter and a selection marker, esp. DHFR.
XX	
SQ	Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
	Query Match 60.4%; Score 204.6; DB 9; Length 1560;
	Best Local Similarity 75.2%; Pred. No. 7e-49; Mismatches 0; Gaps
	Matches 255; Conservative 0; Indels 84; Indels 0;
QY	1 gcttggacaccaataactgcttcgcgaactgtcgagagaacctgctgtgccccccctc 60
Db	1095 gccctggacaccaactactgcttcagctccacggagagaacctgctgctggcagctg 1154
QY	61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db	1155 tatattgacttcgaagacctggctggaagtgatccacgagccaagggtaccat 1214
QY	121 gccaaactctctcaggcccttgccataacctccgcagtcgacacaaccccacgacg 180
Db	1215 gccaaactctcgctggggccctgtccctacatttgagcctggacacgcagtagcaag 1274
QY	181 gtgctgggactgtacaacactctgaacctgaagcatctgcctcgtctgctgcgtgcc 240
Db	1275 gtcttggccctgtacaaccagcataaccggcgcctcggcgcgtgctgctgcgcg 1334
QY	241 caggacctggagccctgaccatcctgtactactgttggagagaccccccaagtggagcag 300
Db	1335 caggcgctggagccactgcccatcgtgtactactgtggcgcgaagcccaaggtggagcag 1394
QY	301 ctctccaacatggtgtgaagtcttgtaaatgactga 339
Db	1395 ctgtccaacatgatcgtgcgtccctgaaaatgcagctga 1433
RESULT	40
AAQ03508	
ID	AAQ03508 standard; DNA; 1560 BP.
XX	
AC	AAQ03508;
XX	
DT	14-AUG-1990 (first entry)
XX	
DE	Simian Transforming growth factor - Betal.
XX	
KW	HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth factors; ds.
XX	
FH	Key Location/Qualifiers
FT	CDS 267..1437
FT	/*tag= a
FT	1103..1437
FT	/*tag= b
PN	
XX	EP356935-A.
XX	
PD	07-MAR-1990.
XX	
PF	25-AUG-1989; 89EP-0115719.
XX	
PR	25-AUG-1988; 88US-0236698.
XX	
PA	(ONCO-) ONCOGEN LTD PARTNER.
XX	
PI	Brankovan V, Lioubin M, Purchio A;
XX	
DR	WPI: 1990-068723/10.
DR	P-FSDB; AAR05663.
XX	
PT	Compsns. contg. transforming growth factor beta -
XX	used for inhibitions of HIV infection and replication in vivo.
XX	

FT		/**tag= C	
FT	mat_peptide	/note= "pro-TGF-beta 1"	
FT		1346..1684	
FT		**tag= e	
XX		/note= "TGF-beta 1"	
PN	JF03180192-A.		
XX			
PD	06-AUG-1991.		
XX			
PF	07-DEC-1989;	89JP-0318243.	
XX			
PR	07-DEC-1989;	89JP-0318243.	
XX	(KIRI) KIRIN BREWERY KK.		
XX			
DR	WPI; 1991-271579/37.		
XX	P-PSDB; AAR13813.		
PT	Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by		
PT	preparing DNA chain contg. base sequence coding for human		
PT	pre:pro-TGF-beta 1, forming expression vector etc.		
XX			
PS	Claim 1; Fig 1; 16pp; Japanese.		
XX			
CC	The DNA sequence encodes human prepro-TGF-beta 1 which can be		
CC	produced by recombinant methods, it has osteogenetic and		
CC	tumoricidal activity.		
XX			
SQ	Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;		
	Query Match	60.4%; Score 204.6; DB 12; Length 1821;	
	Best Local Similarity	75.2%; Pred. No. 7.3e-49;	
	Matches 255; Conservative	0; Mismatches 84; Indels 0; Gaps 0;	
QY	1 gcttggacaccaattactgtcttcgcgaacttgaggagaaactgtgtgccccctc 60		
Db			
QY	1346 gccctggacaccaattgtttcagctccacggagaagaactgtgtgcgagctg 1405		
QY	61 tacattgacttcgcacaggatctgggtggaagtgggtccatgaacctaaaggtactat 120		
Db			
QY	1406 tacattgacttcgcacaggacctggctggaagtggatccacgagcccaagggtaccat 1465		
QY	121 gccaaactctgctcagccccttgccatactccgcagtcgagacacaacccacagcacg 180		
Db			
QY	1466 gccaaactctgctcggccctgccctcatttggagcctggacacgcagtcagacaag 1525		
QY	181 gtgcgtggactgtacaacactctgaaccctgaagcatctgcctgcctgtgctggtgcc 240		
Db			
QY	1526 gtctgcccctgtacaaccagcataaccggcgccctgcgcgcgtgctgctgccc 1585		
QY	241 caggacctgagcccctgaccactctactatgttgggaggacccccaaagtggagcag 300		
Db			
QY	1586 caggcgtggagcgtgcccatcgtactacgtggcgcaagcccaagtgagcag 1645		
QY	301 ctctccaacatgggtggaagtcttgtaaaatgtagctga 339		
Db			
Db	1646 ctgtccaacatgatcgtgctcctctgcaagtgcagctga 1684		
RESULT	45		
AAN60972			
ID	AAN60972 standard; cDNA; 2537 BP.		
XX			
AC	AAN60972;		
XX			
DT	28-OCT-1991 (first entry)		
XX			
DE	Sequence encoding preTGF-beta.		
XX			
KW	Transforming growth factor beta; cancer; wound healing.		
XX			

XX 05-AUG-1990 (first entry)
 XX cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
 DE
 DE
 DE
 XX Transforming growth factor-beta-1 (TGF-beta-1);
 XX neoplastic cell line inhibition;
 KW EGF-potentiated anchorage-independent growth;
 KW
 XX Homo sapiens.
 OS
 XX
 XX
 XX Key Location/Qualifiers
 FT CDS 842..2014
 FT /tag= a
 FT mat_peptide 1676..2011
 FT /tag= b
 FT misc_difference 37..113
 FT /tag= c
 FT /note="stable hairpin loops"
 FT misc_feature 2015..2100
 FT /tag= d
 FT /note="G-C rich sequence
 FT and a downstream TATA-like sequence"
 FT
 XX US4886747-A.
 PN
 XX
 XX 12-DEC-1989.
 XX
 XX 13-MAR-1987; 87US-0025423.
 XX
 XX 13-MAR-1987; 87US-0025423.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Derynck RMA, Goeddel DV;
 PI
 XX WPI; 1990-051338/07.
 DR
 DR P-PSDB; AAR05258.
 XX
 XX Nucleic acid encoding transforming growth factor-beta -
 PT cloned into expression vectors for expression in eukaryotic host
 PT cells for therapeutic use
 PT
 XX
 XX Disclosure; Fig 1b; 28pp; English.
 PS
 XX It was obtained by an analysis of several overlapping cDNAs and gene
 CC fragments, leading to the detn. of a continuous sequence corresp. to the
 CC TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
 CC encode biologically active transforming growth factor (TGF-beta),
 CC operably linked to DNA that encodes a secretory leader (SL). It, or a
 CC nucleic acid capable of hybridising with it, can also be labelled and
 CC used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
 CC proteins.
 XX
 XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 60.4%; Score 204.6; DB 11; Length 2537;
 Best Local Similarity 75.2%; Pred. NO. 7.9e-49;
 Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1 gctttggacacaaataactgttcgcgaacttgaggaggaactgtgtgtgcgccccctc 60
 || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1676 gccctggacacaaataactgttcgcgaacttgaggaggaactgtgtgtgcgagctg 1735
 QY 61 tacattgactccgacagatctggctgggaagtggccatgaacctaaaggtactat 120
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1736 tacattgactccgacagacactcggctgggaagtggatccacagagcccaagggctacat 1795
 QY 121 gccaaactctgtcagggcccttgccacataacctcccgagtcgacagacacacacagcag 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1796 gccaaactctgtcagggcccttgccacataacctcatttgagcctggacacagcagtaagcaag 1855

QY 181 gtctggggaactgtacaacactctgaacccctgaagcatctgcctcgtctgtctgtgctgcc 240
 || |||| ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||
 Db 1856 gtctggcctgtacaacagataaccggcgccctcggcgcgcgtgtctgtctgtgctgccg 1915
 QY 241 caggacactggagccctcgaccatctgtactatgtgtggagagaccccccaagtgagcag 300
 |||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1916 caggcgctggagcgtgccatcgtgtactacgtggcgcaagcccaaggtggagcag 1975
 QY 301 ctctccaacatgtgtgaagtcttgaatgtagctga 339
 || ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 1976 ctgtccaacatgatcgtgcgtcctcctcaagtgaagctga 2014
 RESULT 47
 AAQ02814
 ID AAQ02814 standard; cDNA; 2537 BP.
 XX
 AC AAQ02814;
 XX
 DT 31-MAY-1989 (first entry)
 XX
 XX Sequence of pre-TGF-beta1 cDNA.
 DE
 KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
 KW inhibition.
 XX
 XX Location/Qualifiers
 FH 842..2011
 FT /tag= a
 FT /label=pre-TGF beta 1
 FT CDS 1677..2011
 FT /tag= b
 FT /label=mature TGF-beta 1
 FT GC_signal 2015..2092
 FT /tag= c
 FT misc_feature 2093..2099
 FT /tag= d
 FT /label=TATA-like sequence
 FT stem_loop 37..113
 FT /tag= e
 FT misc_feature 863..911
 FT /tag= f
 FT /label=hydrophobic domain
 FT
 XX WO8912101-A.
 PN
 XX 14-DEC-1989.
 PD
 XX 08-JUN-1988; 88WO-US01945.
 PF
 XX 08-JUN-1988; 88WO-U001945.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Derynck RM, Goeddel DV;
 PI
 XX WPI; 1990-007474/01.
 DR
 DR P-PSDB; AAR04034.
 XX
 XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
 PT probe, or to produce TGF beta 3, for growth inhibition of certain normal
 PT and neoplastic cells, eg A549.
 XX
 PS Disclosure; Fig. 1b; 61pp; English.
 XX
 CC Sequence encodes the 390 amino acid (AA) precursor transforming growth
 CC factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
 CC the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
 CC potential secondary structure. The TATA-like sequence in the 3' untrans-
 CC lated region of the gene is presumably a polyadenylation signal. Mature
 CC TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
 CC cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic

CC acid encoding the second subtype of TGF-beta 3) is useful as a
CC probe or to produce TGF-beta 3 for inhibition of growth of normal and
CC neoplastic cells.
XX
SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other:

Query Match 60.4%; Score 204.6; DB 11; Length 2537;
Best Local Similarity 75.2%; Pred. No. 7.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY	1	gcttggacacaattactgtctccgcgaacttgaggagaactgctgtgtgcgccccc	60
Db	1676	gccttggacacaactattgtctcagttccaccggagaagaactgctgcgtgcggcagt	1735
QY	61	tacattgaccttcgcacaggatctggcttggaaagtgggtcccatgaacctaaagggtc	120
Db	1736	tacattgaccttcgcgaagacctggcttggaaagtggatccacgagccaagggtac	1795
QY	121	gccaaacttgtctcagccccctggccataacctccgcagtcgacagcaaccaagc	180
Db	1796	gccaaacttgtctcgccccctggccatacttggagactggacacgagtcacagc	1855
QY	181	gtctgggactgtacaacacttgaaacctgaagcatctgctcgcttgcgtgcgcc	240
Db	1856	gtctggccctgtacaaccagcatacccccggcgccctgcggcgccgtgctgcgtgc	1915
QY	241	caggacctggagccccctgacctctgtactatgttggagagcccccaagtggagc	300
Db	1916	caggcgctggagcccgctgcccatcgtgtactacgttggccgcgaagcccaaggtg	1975
QY	301	ctctccaacatggttggtgaagctctgttaaatgtagtga	339
Db	1976	ctatccaaatatcgtgcgtccctgcgaagtgcacgtcta	2014

RESULT	48
AAQ56923	
ID	AAQ56923 standard; cDNA; 2537 BP.
XX	
XX	
AC	AAQ56923;
XX	
DT	09-JUL-1994 (first entry)
XX	
DE	Human pre-TGF-beta-1.
XX	
KW	TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW	transforming growth factor beta-3; recombinant; wound healing;
KW	vulnerable; ss.

XX	(GETH) GENENTECH INC.
XX	
XX	Derynk RMA, Goeddel DV;
PI	
XX	
XX	WFI; 1994-056343/07.
DR	P-PSDB; AAR46227.
DR	
XX	
XX	Nucleic acid sequences encoding transforming growth factor-beta -
PT	diagnostic probes, and for use in therapeutics
PT	
XX	
XX	Disclosure; Fig 1b; 25pp; English.
PS	
XX	
XX	cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC	plg TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC	corresponding amino acid sequences were determined (AAR46227-29, and
CC	respectively). A genomic fragment corresponding to a human TGF-
CC	beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC	determined (AAR46230). The sequences have been used in the
CC	construction of vectors for the expression of recombinant TGF-
CC	beta.
XX	
XX	Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
SQ	

Query Match	50.4%	Score	204.6	DB	15	Length	2537
Best Local Similarity	75.2%	Pred. No.	7.9e-49				
Matches	255	Conservative	0	Mismatches	84	Indels	0
Gaps	0						
Qy	1	gctttgacaccaattactgcttcgcgaacttgaggagaaactgctgtgtgcgcccctc	60				
Db	1676	gccctggacccaactattgcttcagctccacggagaaactgctgctgcggcagctg	1735				
Qy	61	tacattgactccgcacaggatctggctggaagtgggtccatgaacctaaaggtctact	120				
Db	1736	tacattgactccgcgaagacctcgctgggaagtggatccacgagccaaaggtaccat	1795				
Qy	121	gccaactctgctcgaaggcccttggccctacatctccgcagtgacacacaacccacgacg	180				
Db	1796	gccaactctgctcggggccctgccctacattggagcctggacacgcagtcagcaag	1855				
Qy	181	gtcctgggaactgtacaacactgtgaacctgaacctgaacatctgctcgccttgcgtgcgc	240				
Db	1856	gtcctggccctgtacaaccagcataaccggggccctcgcgcgcgctgctgctgctg	1915				
Qy	241	caggacctggagccctcgaccactctgactatgttgggagacccccaaagtggagcag	300				
Db	1916	caggcctggagcgcgtgcccatcggtactactcgtgggcgcgaagccaaagtggagcag	1975				
Qy	301	ctctccaacatggtgggtgaagtcttgttaaatgtagtga	339				
Db	1976	ctgtccaacatgatcgtgcgtcctcgaagtgcagctga	2014				

RESULT 49
AAT15720
ID AAT15720 standard; cDNA; 2537 BP.

	Key	Location/Qualifiers
AA		
FH	5'UTR	1..841
FT		
FT		/*tag= a

```

FT misc_feature 37..113
FT /*tag= b
FT /note= "GC-rich region forms stable hairpin loops;
FT similar to structural organisation of c-myc RNA,
FT could play role in mRNA stability or in
FT regulation of transcription"
FT
FT CDS
FT 842..2014
FT /*tag= c
FT /product= pre-TGF_beta_1
FT 1676..2011
FT /*tag= d
FT /product= mature_TGF_beta_1
FT 2015..2100
FT /*tag= e
FT /note= "GC-rich region; possibly responsible for the
FT fact 3'UTR of mRNA could not be cloned as cDNA;
FT may be important for transcription efficiency"
FT
FT repeat_unit 2019..2023
FT /*tag= f
FT TATA_signal 2094..2100
FT /*tag= g
FT /note= "TATA-like sequence; no evidence that this
FT functions a promoter"
FT
FT polyA_signal 2514..2520
FT /*tag= h
FT misc_signal 2529..2536
FT /*tag= i
FT /note= "consensus sequence immediately precedes
FT polyA-tail (Benoist et al)"
FT
XX US5482851-A.
XX
XX 09-JAN-1996.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1996-076891/08.
XX P-PSDB; AAR90827.
XX
XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications
XX or in therapy
XX
XX Example 3; Fig 1; 26pp; English.
XX
XX The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
XX The nucleotide sequence was obtd. by an analysis of several overlapping
XX cDNAs and gene fragments. The DNA is useful for the recombinant
XX production of TGF beta 1, which can be used in, e.g. wound healing.
XX (Revised entry submitted to correct sequence analysis breakdown.)
XX
XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
XX
XX
XX Query Match 60.4%; Score 204.6; DB 17; Length 2537;
XX Best Local Similarity 75.2%; Pred. NO. 7.9e-49;
XX Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
XX
XX 1 gctttggacacaaattactgttcgcgaacttgaggagaactgtgtgtgccccctc 60
XX || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1676 gccctggacacaaattgtctcagctccacgcgagagaactgtgtgtgcccagctg 1735
XX
XX 61 tacattgacttcgcagagatctgggctggaagtgggtccatgaacctaaagggtactat 120
XX

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```

Db 1736 tacattgacttcgcgaagacctcgtgctggaagtgcacacgagcccaagggtacct 1795
Qy 121 gcaacttctgtcagcccttgcctaccatcctcgcagtgacagacacacccacagcacg 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1796 gcaacttctgtcgtcgccctgcctacatttgagcctggacacgcagtacagcaag 1855
Qy 181 gtctgggactgtacaacactgtgaacctgaacctgaagcatctgcctgccttgcgtgccc 240
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1856 gtctggcctgtacaaccagataaccggcgccctcgcgccgctgtgctgctgccc 1915
Qy 241 caggacctggagccctcgaaccatcctgtactatgttggaggagcccccaagtggagcag 300
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1916 caggcctggagcctgcctacatcgtgtactacgtggccgcaagcccaagggtggagcag 1975
Qy 301 ctctcaacatggtgtggaagtcttgaatgtagctga 339
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1976 ctgtccaacatgatctgctgctcctcgaagtgcagctga 2014

RESULT 50
AAV52933
ID AAV52933 standard; cDNA; 2537 BP.
XX
AC AAV52933;
XX
DT 21-DEC-1998 (first entry)
XX
DE Human pre-transforming growth factor-beta 1 cDNA.
XX
KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 842..2014
FT /*tag= a
FT mat_peptide 1676..2011
FT /*tag= b
FT stem_loop 37..113
FT /*tag= b
FT /*note= "putative stable hairpin loop"
FT misc_feature 2015..2100
FT /*tag= c
FT /*note= "GC-rich sequence"
FT polyA_signal 2514..2520
FT /*tag= d
XX
XX US5801231-A.
XX
XX 01-SEP-1998.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX 30-MAY-1995; 95US-0454468.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1998-494840/42.
XX P-PSDB; AAW78785.
XX
XX DNA encoding transforming growth factor-beta precursor sequence -
XX useful for analysis to perform manipulations to increase yield of
XX recombinant production of the protein
XX
XX Example 3; Fig 1B 1-3; 26pp; English.
XX

```

XX This nucleotide sequence codes for the human transforming growth
CC factor-beta 1 precursor (prefTGF-beta 1, see AAW8785). It is a
CC composite of overlapping cDNA clones isolated from different cDNA
CC libraries (placenta, AL72 fibroblastoma, HT1080 fibroblastoma) using
CC TGF-beta exon (see AAU52936) restriction fragments as probes.
CC The 3' region of the sequence was determined using cloned genomic
CC DNA. The invention relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiated anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.

XX
SQ Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

Query Match 60.4%; Score 204.6; DB 19; Length 2537;
Best Local Similarity 75.2%; Pred. No. 7.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gcttgagaccattactgcttcgcgaactggagagaactgtgtgccccccctc 60
DB ||| |
Db 1676 gccctggacaccaactatgttcagctccacggagaaactgtgctgcgcagt 1735

QY 61 tacattgactccgacaggatcggtcggaagtgggtcccatgaacctaaaggctactat 120
DB ||| |
Db 1736 tacattgactccgacaggacctggtggaagtcgatccacgagcccaagggtaccat 1795

QY 121 gccaaccttctgctcaggccccttgcccatactccgcagtgagacacaacccacagcacg 180
DB ||| |
Db 1796 gccaaccttctgctcaggccccttgcccatacttggagctggacacgacgtacagcaag 1855

QY 181 gtgctggagctgtacacactctgaacctgaaacctgcatctgctcgcttgcgtgcc 240
DB ||| |
Db 1856 gtctggccctgtacaaccagcataaccggcgccctcgggcgctgtgctgctgcgcg 1915

QY 241 caggacctgagcccttgaccactctactatattgggagacccccaaagtggagcag 300
DB ||| |
Db 1916 caggcgctggagcgcgtgccatcgtgtactacgtggcgcaaggcccaagttggagcag 1975

QY 301 ctctccaacatggtggtggaagtcttgttaaatgtagctga 339
DB ||| |
Db 1976 ctgtccaacatgatcgtgcgtctcgaagtgcagctga 2014

RESULT 51
AAT05876
ID ID AAT05876 standard; cDNA; 2745 BP.
XX
AC AAT05876;
XX
DT 25-JUN-1996 (first entry)
XX
DE cDNA encoding transforming growth factor-beta 1.
XX
KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW nitric oxide production; hypotension; inflammation; septic shock;
KW treatment; ds.
XX
OS Mammalian sp.
XX
FH Key Location/Qualifiers
FT CDS 842..2017
FT FT /*tag= a
FT FT /product= transforming growth factor-beta 1
XX
PN W09526745-A1.
XX

```

XX FH Key Location/Qualifiers
XX FT CDS 20..3535
XX FT /*tag= a
XX FT /product= collagen IA/TGF-beta-1 fusion protein
XX FT misc_difference 2679
XX FT /*tag= b
XX FT /note= "base 2679 is not identified in the
XX FT specification"
XX FT misc_difference 2688
XX FT /*tag= c
XX FT /note= "base 2688 is not identified in the
XX FT specification"
XX PN CA2151547-A.
XX XX
XX PD 11-DEC-1995.
XX XX
XX PF 12-JUN-1995; 95CA-2151547.
XX XX
XX PR 10-JUN-1994; 94US-0259263.
XX XX
XX PA (USSU ) US SURGICAL CORP.
XX XX
XX PI Espino P, Gruskin EA;
XX XX
XX DR WPI; 1996-140144/15.
XX DR P-PSDB; AAR89470.
XX XX
XX XX Chimaeric DNA encoding protein contg. extracellular matrix protein
XX PT domain - and cellular regulatory factor domain, partic. useful as
XX PT osteogenic agents, also related vectors, transformed cells and
XX PT chimaeric proteins.
XX XX
XX PS Disclosure; Fig 2; 59pp; English.
XX XX
XX CC A chimeric gene (AAR16516) codes for a fusion protein (AAR89470) between
XX CC the helical region of human collagen I(a) and human transforming
XX CC growth factor beta-1 (TGF-beta-1). The collagen moiety was cloned
XX CC from human fibroblast AG02261A cells by PCR amplification. The
XX CC construct was inserted into a pMAL vector for expression in E. coli.
XX CC The fusion protein provides sustained release and delivery of
XX CC TGF-beta-1 to a target tissue. The TGF increases efficacy of
XX CC the body's normal soft tissue repair response and also induces
XX CC osteogenesis.
XX XX
XX SQ Sequence 3541 BP; 504 A; 1143 C; 1188 G; 704 T; 2 other;

Query Match 60.4%; Score 204.6; DB 17; Length 3541;
Best Local Similarity 75.2%; Pred. No. 8.6e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgttcgcgaacttgaggagaaactgtgtgccccctc 60
Db || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3197 gccctggacacaaattgtctcagctccacgcgagaaactgtgctgcgcagctg 3256
Qy 61 tacattgacttcgcagagatgtggtggaagtgggtccatgaacctaaaggtactat 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3257 tacattgacttcgcagagatgtggtggaagtgggtccatgaacctaaaggtactat 3316
Qy 121 gccaaacttctgcagccttgcccatacctcccgagtcagacacacacacagcag 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3317 gccaaacttctgcagccttgcccatacctcccgagtcagacacacacacagcag 3376
Qy 181 gtgtgggactgtacaaactgtgaacctgaagcatctgctccttctgtgctgcccc 240
Db || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3377 gtcttggcctgtacaaaccagataaccggcgctcggcgccgtgctgctgctgcg 3436
Qy 241 caggactggagccctgacctctgtactatgtgttggtgagagacccccaaagtggagag 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3437 caggcgtggagccgctccctgtactactgtgctggtggcgccgaagccccaaagtggagag 3496

```

```

QY 301 ctctccacacatggtggtgaagctctttaaataatgtagctga 339
Db || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
3497 ctgtccacacatgatcgctgcctcctgcaagtgcagctga 3535

RESULT 53
AAAI2498
ID AAAI2498 standard; cDNA; 3541 BP.
XX AC AAAI2498;
XX DT 25-JUL-2000 (first entry)
XX XX
XX DE cDNA encoding a chimeric collagen 1 (alpha1)/TGF-beta1 protein.
XX KW Extracellular matrix protein; self aggregation; hydroxylated proline;
XX KW trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
XX KW collagen; fibronectin; fibronectin; post translational hydroxylation; ss.
XX KW transforming growth factor-beta1; TGF-beta1; chimera; ss.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Unidentified.
XX FH Key Location/Qualifiers
XX FT CDS 20..3535
XX FT /*tag= a
XX FT /product= "chimeric collagen 1 (alpha1)/TGF-beta1
XX FT protein"
XX FT /transl_except= (pos: 2591..2593, aa: Gly)
XX XX
XX PN EP992586-A2.
XX XX
XX PD 12-APR-2000.
XX XX
XX PF 07-OCT-1999; 99EP-0119184.
XX XX
XX PR 09-OCT-1998; 98US-0169768.
XX PA (USSU ) US SURGICAL CORP.
XX XX
XX PI Gruskin EA, Buechter DD, Zhang G, Connolly K;
XX XX
XX DR WPI; 2000-259138/23.
XX DR P-PSDB; AAY84538.
XX XX
XX PT Production of extracellular matrix proteins containing
XX PT 4-trans-hydroxyproline results in native self aggregating proteins,
XX PT useful on medical implants -
XX XX
XX PS Disclosure; Fig 16A-C; 260pp; English.
XX XX
XX CC The specification describes a method for producing an extracellular
XX CC matrix protein or its fragment. The extracellular matrix protein is
XX CC capable of self aggregating in a cell which does not ordinarily
XX CC hydroxylated prolines. The method comprises optimising a nucleic acid
XX CC sequence for expression in the cell by substitution of codons preferred
XX CC by that cell for naturally occurring codons not preferred by the cell;
XX CC incorporating the nucleic acid sequence into the cell; and contacting
XX CC the cell with a hypertonic growth medium containing at least one amino
XX CC acid, selected from the group consisting of trans-4-hydroxyproline and
XX CC 3-hydroxyproline to allow at least one of the amino acids to be
XX CC assimilated into the cell and incorporated into the extracellular matrix
XX CC protein. The method may be used to make host cells assimilate and
XX CC incorporate trans-4-hydroxyproline into proteins. This is especially
XX CC useful in the recombinant production of proteins such as collagen,
XX CC fibrinogen and fibronectin whose ability to self aggregate and produce
XX CC functional proteins depends on the post translational hydroxylation of
XX CC proline. The method is also useful in studying the structure and function
XX CC of polypeptides which do not normally contain trans-4-hydroxyproline.
XX CC The present sequence encodes a chimeric collagen 1 (alpha1)/transforming
XX CC growth factor-beta1 (TGF-beta1) protein, which may be produced using the
XX CC method of the invention.

```



```
SQ Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;

Query Match 60.4%; Score 204.6; DB 21; Length 3541;
Best Local Similarity 75.2%; Pred. No. 8.6e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgaacttggagagaaactgctgtgccccctc 60
   || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3197 gccctggacacaaactattgttcagctccacgagagaagaactgctgctggcgagctg 3256

QY 61 tacattgacttcgcacagatctggctggaagtgggtccatgaacctaaaggctactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3257 tacattgacttcgcgaagacctgcgctggaagtggatccacgagcccaagggtaccat 3316

QY 121 gcaaatcttgcctcagccttgcctacacctccgctgagtcgacagacacacacagcacg 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3317 gcaaatcttgcctcagccttgcctacacctccgctgagtcgagcctgagacagcagtcacagcaag 3376

QY 181 gtgctgggactgtacaaactctgaacctgaacctgaacctgtcctgcctgtgctgctgcc 240
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 3377 gtccctggcctgtacaaaccagataaccggcgctcgcctgcggcgctgctgctgctgccg 3436

QY 241 caggacctggacccctgcacctctgtactatgttggaggaccoccccaagtgaggagcag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3437 caggcctggagccgctgcctcgtgtactacgtggcgcgcaagcccaagtgaggagcag 3496

QY 301 ctctccaaatggtggtgaagcttgaatgttaagtactga 339
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3497 ctgtccaaatgctgctgcctcctgcaagtgcagctga 3535

RESULT 54
AAQ55624
ID AAQ55624 standard; DNA; 4105 BP.
XX AC AAQ55624;
XX DT 12-JUL-1994 (first entry)
XX DE TGFbeta1 5'-UTR-CDS-3'-UTR.
XX KW Transforming Growth Factor beta 1; TGF; non-coding region;
XX KW coding region; resonance; interaction; optimisation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mRNA 1..4105
XX FT /*tag= a
XX FT /note= "the inventor has used T instead of U in
XX FT the TGFbeta1 full-length mRNA"
XX FT 5'UTR 1..2202
XX FT /*tag= b
XX FT enhancer 231..631
XX FT /*tag= c
XX FT misc_RNA 1..230
XX FT /*tag= d
XX FT /note= "N1 region"
XX FT misc_RNA 632..910
XX FT /*tag= e
XX FT /note= "N2 region"
XX FT 911..1039.
XX FT /*tag= f
XX FT /note= "P region"
XX FT CDS 2203..3378
XX FT /*tag= g
XX FT /product= TGFbeta1
XX FT 3'UTR 3379..4105
XX FT /*tag= h
XX FT /note= "the N residues at positions 3464 and
XX FT 3465 each appear as the letter F in
XX FT the specification"
```

```
XX PN FR2692594-A.
XX PD 24-DEC-1993.
XX PF 22-JUN-1992; 92FR-0007571.
XX QY 22-JUN-1992; 92FR-0007571.
XX PA (PERE/) PEREZ J.
XX PI Perez J;
XX QY WPI; 1994-028256/04.
XX PT Application of optimised gene expression - for scientific,
XX PT industrial and therapeutic purposes
XX PS Disclosure; Fig 1; 110pp; French.
XX CC The TGFbeta1 mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and
XX CC 3'-UTR) for various "perturbation" experiments. The relative order
XX CC of the 3 regions was altered, e.g. the 3'-UTR was positioned
XX CC upstream of the CDS and the 5'-UTR was positioned downstream of the
XX CC CDS. The experiments showed that interactions between coding and non-
XX CC coding regions are destroyed by such perturbations.
XX SQ Sequence 4105 BP; 744 A; 1407 C; 1201 G; 751 T; 2 other;

Query Match 60.4%; Score 204.6; DB 15; Length 4105;
Best Local Similarity 75.2%; Pred. No. 8.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgaacttggagagaaactgctgtgccccctc 60
   || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||
Db 3040 gccctggacacaaactattgttcagctccacgagagaagaactgctgctggcgagctg 3099

QY 61 tacattgacttcgcacagatctggctggaagtgggtccatgaacctaaaggctactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3100 tacattgacttcgcgaagacctgcctggtgaagtggatccacgagcccaagggtaccat 3159

QY 121 gcaaatcttgcctcagccttgcctacacctccgctgagtcgacagacacacacagcacg 180
   ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 3160 gcaaatcttgcctcggcgctgcctgcctacatttggagcctggacacagcagtcacagcaag 3219

QY 181 gtgctgggactgtacaaactctgaacctgtgaacctgtgctcgtcctgtgctgctgcc 240
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 3220 gtccctggcctgtacaaaccagataaccggcgctcgcctgcggcgctgctgctgctgccg 3279

QY 241 caggacctggagccctgcacctctgtactatgttggaggaccoccccaagtgaggagcag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3280 caggcctggagccgctgcccactgctactacgtggcgcgcaagcccaagtgaggagcag 3339

QY 301 ctctccaaatggtggtgaagcttgaatgttaagtactga 339
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 3340 ctgtccaaatgatcgtgcctcctgcaagtgcagctga 3378

RESULT 55
AAQ11993
ID AAQ11993 standard; cDNA; 339 BP.
XX AC AAQ11993;
XX DT 29-AUG-1991 (first entry)
XX DE Transforming Growth Factor beta 1.
XX KW TGF-beta1; biologically active protein production; ss.
XX OS Homo sapiens.
XX FT
```



```
XX New chimeric transforming growth factor -
PT with TGF-beta biological activity and increased secretion
PT efficiency.
XX
XX Claim 2; Fig 1; 18pp; English.
XX
CC Chimeric gene has TGF activity and may be more desirable than its
CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
CC from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive
CC than normal. The product is useful in treatment of cancer and wound
CC healing.
CC See also EP-373994.
XX
XX Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 other;
XX
XX
XX Query Match 57.5%; Score 195; DB 11; Length 1561;
XX Best Local Similarity 73.5%; Pred. No. 3.7e-46;
XX Matches 249; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
XX
XX 1 gcttggacacaaattactgctccgcaacttgaggagaaactgctgtgcccctc 60
XX || ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||
XX Db 1096 gccttgacacaaactactgcttcagaaatgtgcaggataattgctcactcgcgtt 1155
XX
XX 61 tacattgacttcgacaggatctgggctggaagtgggtccatgaacctaaaggctactat 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
XX Db 1156 tacattgacttcagaggacctcggtggaagtgtatccacgagcccaaggctaccat 1215
XX
XX 121 gcaacttctgctcagccctgcccatacctcgcagtcgagacacacccacagcaag 180
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
XX Db 1216 gcaacttctgctgggcccctgtccctacatttgagcctggacacgcagtacagcaag 1275
XX
XX 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcctgctgctgccc 240
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
XX Db 1276 gtctggccctgtacaaacagataaccgcgcgcctcgcgcgcgcgtgctgctgccc 1335
XX
XX 241 caggacctggagccctgacctctgtactatgttgaggagaccacccaaagtggagcag 300
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
XX Db 1336 caggcgctggagccactgcccactgctgtactacgtgtggcgccgaagcccaaggaggagcag 1395
XX
XX 301 ctctccaaatggtggtgaagctctgtgtaaatgtagctga 339
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
XX Db 1396 ctgtccaaatgatgtgctgctccgtccgtcaaatgagctga 1434
XX
XX
XX RESULT 61
XX AAQ29177
XX ID AAQ29177 standard; DNA; 1561 BP.
XX
XX AC AAQ29177;
XX
XX DT 10-WAR-1993 (first entry)
XX
XX TGF-beta 1/beta 2 chimeric gene.
XX
XX Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
XX Simian virus 40; SV40; expression vector; Chinese hamster ovary; CHO;
XX vascular endothelial cell; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 262..1434
XX FT /*tag= a
XX FT 1096..1431
XX FT /*tag= b
XX FT /note= "Mature TGF-5 beta"
XX FT sig_peptide 262..348
XX FT /*tag= c
XX FT /note= "TGF-5 beta pre-pro-protein"
XX FT precursor_RNA 349..1095
XX FT /*tag= d
```

```
FT mutation /note= "TGF-5 beta pro-protein"
FT 1120..1122 /*tag= e
FT /label= S9R
FT 1123..1125 /*tag= f
FT /label= S10N
FT 1126..1128 /*tag= g
FT /label= T11V
FT 1129..1131 /*tag= h
FT /label= E12Q
FT 1132..1134 /*tag= i
FT /label= K13D
FT 1144..1146 /*tag= j
FT /label= V17L
FT 1150..1152 /*tag= k
FT /label= Q19P
FT 1168..1170 /*tag= l
FT /label= R25K
FT 1171..1173 /*tag= m
FT /label= K26R
FT 1120..1155 /*tag= n
FT /note= "Mutagenic linker"
FT 179..200 /*tag= o
FT /note= "Feature not labelled in the specification"
XX
XX WO9216228-A.
XX
XX 01-OCT-1992.
XX
XX 13-MAR-1992; 92WO-USO1993.
XX
XX 14-MAR-1991; 91US-0669171.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX Madisen L, Merwin J, Purchio AF;
XX
XX WPI; 1992-348938/42.
XX P-PSDB; AAR27522.
XX
XX Compan. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
XX inhibits proliferation of vascular endothelial cells, useful for
XX treating cancer and to promote wound healing
XX
XX Disclosure; Fig 1; 45pp; English.
XX
XX The sequence given encodes a hybrid transforming growth factor
XX (TGF)-beta termed TGF-beta 1/beta 2 (or TGF-5 beta). The mutations
XX indicated in the features table represent replacements of TGF-beta 1
XX bases with those from the corresponding positions of TGF-beta 2.
XX Simian codon usage was maintained. This DNA sequence could be placed
XX under the control of Simian virus 40 (SV40) expression regulatory
XX region within an expression vector and used to transfect Chinese
XX hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
XX and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
XX effects on the proliferation of vascular endothelial cells equivalent
XX to those produced by TGF-beta 1.
XX
XX Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other;
XX
XX
XX Query Match 57.5%; Score 195; DB 13; Length 1561;
XX Best Local Similarity 73.5%; Pred. No. 3.7e-46;
```

Matches 249; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1 gctttggacacacaaataactgtctccgcaacttggaggagaactgtgtgtgccccctc 60
Dy 1096 gctttggacacacacaaataactgtctccgcaacttggaggagaactgtgtgtgccccctc 60
Qy 61 tacattgtactccgacagatcgtgctggaagtgggtccatgaacctaaagggtactat 120
Dy 1156 tacattgtactccgacagatcgtgctggaagtgggtccatgaacctaaagggtactat 120
Qy 121 gccaaactctgctcagggccctggccatcctccgagtgagacacacacacagcacg 180
Dy 1216 gccaaactctgctcagggccctggccatcctccgagtgagacacacacacagcacg 180
Qy 181 gtgctgggactgtacacactctgaacctctgacatcgtcctgctgctgctgccc 240
Dy 1276 gtgctgggactgtacacactctgacatcgtcctgctgctgctgctgccc 240
Qy 241 caggacctggagccctgacacatcctgtactatgttggaggagaccccccaaaagtggagcag 300
Dy 1336 caggacctggagccctgacacatcctgtactatgttggaggagaccccccaaaagtggagcag 300
Qy 301 ctctccacatggtgtggaagtctgtgaaatgtagctga 339
Dy 1396 ctgctccacatggtgtggaagtctgtgaaatgtagctga 1434

RESULT 62
AAQ11994
ID AAQ11994 standard; DNA; 339 BP.
XX AC AAQ11994;
XX DT 29-AUG-1991 (first entry)
XX DE Encodes Transforming Growth Factor beta 2.
XX KW TGF-beta2; biologically active protein production; ss.
XX OS Homo sapiens.
XX PN EP433225-A.
XX PD 19-JUN-1991.
XX PF 27-NOV-1990; 90EP-0810922.
XX PR 06-DEC-1989; 89GB-0027546.
XX PA (CIBA) CIBA GEIGY AG.
XX PI Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;
XX DR WPI; 1991-180005/25.
XX P-PSDB; AAR12403.
XX PT Prodn. of Transforming Growth Factor type-beta-like proteins - by
XX subjecting denatured monomeric form to refolding conditions
XX Example; Page 27; 35pp; English.
XX This coding sequence was isolated from the CI-215 human glioma cell
XX line. It was incorporated into an appropriate vector to transform
XX Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
XX denatured and glutathione, 1mM oxidised glutathione and 33mM EDTA,
XX 2mM reduced glutathione, 1mM was adjusted to 2.5 and the mixture was
XX After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
XX conc. 10 times. The conc. soln was diluted to the original vol. with
XX 10mM HCl and conc to a final vol of 10 ml. The supernatant from
XX centrifugation at 5000g for 30 min contained disulphide-linked dimeric
XX TGF-beta2.
XX Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

Query Match 53.7%; Score 182.2; DB 12; Length 339;
Best Local Similarity 71.1%; Pred. No. 1.1e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Qy 1 gctttggacacacaaataactgtctccgcaacttggaggagaactgtgtgtgccccctc 60
Dy 1 gctttggatgcgcctattgtcttagaaaatgtcaggataatgtgtcctcactcactt 60
Qy 61 tacattgtactccgacagatcgtgctggaagtgggtccatgaacctaaagggtactat 120
Dy 61 tacattgtattcgaagggtatcctaggtggaatgatacacacacacacacaggtactaa 120
Qy 121 gccaaactctgctcagggccctggccatcctccgagtgagacacacacacagcacg 180
Dy 121 gccaaactctgctgctgagatcctccggtatttattgagttcagacactcagacagcag 180
Qy 181 gtgctgggactgtacacactctgaacctctgacatcgtcctgctgctgctgccc 240
Dy 181 gtgctgagcttatataataaccataaaatccagagcagcatctgtcttctgtcgtgtcc 240
Qy 241 caggacctggagccctgacacatcctgtactatgttggaggagaccccccaaaagtggagcag 300
Dy 241 caagatttagaacctctaacattctctactacattggcaaaacacacacacagattgaacag 300
Qy 301 ctctccacatggtgtggaagtctgtgaaatgtagctga 339
Dy 301 ctctccacatggtgtggaagtctgtgaaatgtagctga 339
RESULT 63
AAQ41600
ID AAQ41600 standard; cDNA; 339 BP.
XX AC AAQ41600;
XX DT 26-AUG-1993 (first entry)
XX DE Mature human Transforming Growth Factor-beta2.
XX KW hTGF-beta2; hybrid protein; wound healing; cancer treatment;
XX KW bone repair; growth regulation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..336
XX FT /*tag= a
XX PN EP542679-A.
XX PD 19-MAY-1993.
XX PF 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX PA (CIBA) CIBA GEIGY AG.
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX DR WPI; 1993-161126/20.
XX P-PSDB; AAR39639.
XX PT New hybrid transforming growth factor-beta molecules - comprise
XX portions of mature TGF-beta isoforms; useful as wound healants,
XX cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX Claim 4; Page 22-23; 48pp; English.
XX The invention covers hybrid TGF-beta molecules consisting of parts
XX of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX CC

XX PA (CIBA) CIBA GEIGY AG.
 XX PI Cerletti N;
 XX DR WPI; 1996-116999/12.
 XX DR P-PSDB; AAR91957.
 XX PT Prodn. of dimeric, biologically active transforming growth factor
 XX PT beta - by refolding denatured monomer in buffer contg. mild
 XX PT detergent and specific organic solvents to improve yields
 XX PS Example 1; Page 34-35; 59pp; English.
 XX CC AAT15462-T15464 encode transforming growth factor (TGF) beta-1,
 CC CC TGF beta-2 and TGF beta-3 which are produced using recombinant
 CC CC DNA technology and used to produce TGF beta-like proteins in
 CC CC dimeric form. The TGF beta-like proteins produced are hybrids of
 CC CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
 CC CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
 CC CC made using a new process of producing dimeric, biologically active
 CC CC TGF beta-like proteins. The new process involves treating denatured
 CC CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
 CC CC CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
 CC CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
 CC CC The detergent allows folding of the monomer such that, after
 CC CC dimerisation, the TGF beta-like protein retains biological activity
 CC CC and remains in soluble form. The method allows relatively high yields
 CC CC of biologically active TGF beta-like proteins in their native dimeric
 CC CC form. TGF-beta like proteins are multifunctional regulators of
 CC CC cellular activity and a typical use is to stimulate wound healing.
 XX SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

Query Match 53.7%; Score 182.2; DB 17; Length 339;
 Best Local Similarity 71.1%; Pred. No. 1.le-42;
 Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
 QY 1 gctttggacacaaattactgtctccgcaactgtgagagaaactgtgtgctgccccctc 60
 DB 1 gctttggatgcccctattgtttagaattgtcaggataattgtcgtcactgctccactt 60
 QY 61 tacattgacttcagacaggtatcgtgggaagtgggtccatgaacctaaaggtactact 120
 DB 61 tacattgatttcaagagggatctagggtggaattgatacagacacccaagggtacaa 120
 QY 121 gccaaactctcagggcccttgccatacctccagtcagtcagacacacccaagcagc 180
 DB 121 gccaaactctgtgtgagcagtcgccgtatttattgagttcagacactcagcacagc 180
 QY 181 gtgctgggactgtacacactctgaacctgaagcatcgtcgtcgtgctgctgccc 240
 DB 181 gctctgagcttatataaccataaataccagaagcatcgtctccttgcgtgctcc 240
 QY 241 caggacctggagccctgacctctgtactatgtgtggaggagcccccacaaagtggagcag 300
 DB 241 caagatttagaacctctaacattctctactacattggtgcaaaacacccaagattgaacag 300
 QY 301 ctctccacatcgttggtgaagtctttgttaattgtactga 339
 DB 301 ctctcctaattgattgtaaaagtcttgcaaatgcagctaa 339
 RESULT 66
 AAT42772
 ID AAT42772 standard; cDNA; 339 BP.
 XX AC AAT42772;
 XX AC
 XX DT 26-AUG-1997 (first entry)
 XX DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX KW Transforming growth factor-beta fusion protein; wound healing;
 XX KW artificial skin; surgery recovery time; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..339
 XX FT /*tag= a
 XX FT /function= TGF active fragment
 XX WO9639430-Al.
 XX PD 12-DEC-1996.
 XX PF 05-JUN-1996; 96WO-US08973.
 XX PR 06-JUN-1995; 95US-0470837.
 XX PA (CHEU/) CHEUNG D T.
 XX PA (HALL/) HALL F L.
 XX PA (NIMN/) NIMNI M E.
 XX PA (TUAN/) TUAN T.
 XX PA (WULL/) WU L.
 XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 XX WPI; 1997-043065/04.
 XX DR P-PSDB; AAW08174.
 XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
 XX PT reduce surgery recovery time and to prepare artificial skin
 XX PS Disclosure; Page 46-47; 59pp; English.
 XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC CC comprises a purification tag and a TGF active fragment. The present
 CC CC sequence encodes a specifically claimed TGF active fragment.
 CC CC Additionally, the fusion protein may comprise proteinase-sensitive
 CC CC linker sites and binding domain so the protein sequence may contain
 CC CC some or all of the following elements: purification tag:proteinase
 CC CC site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes
 CC CC wound healing, and the fusion protein can be used to reduce surgery
 CC CC recovery time and in the preparation of artificial skin. The inclusion
 CC CC of a purification tag facilitates purification of the fusion protein.
 CC CC The proteinase site is included to permit cleavage and release of the
 CC CC purification tag after purification if desired. The extracellular
 CC CC matrix binding site facilitates delivery of the fusion protein to the
 CC CC desired site of action. Delivery of the TGF-beta to the site to be
 CC CC treated reduces the amount of TGF-beta required to be administered to
 CC CC be effective and reduces the concentration of circulating TGF-beta
 CC CC which may result in undesirable effects.
 XX SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

Query Match 53.7%; Score 182.2; DB 18; Length 339;
 Best Local Similarity 71.1%; Pred. No. 1.le-42;
 Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaactgtgagagaaactgtgtgctgccccctc 60
 DB 1 gctttggatgcccctattgtttagaattgtcaggataattgtcgtcactgctccactt 60
 QY 61 tacattgacttcagacaggtatcgtgggaagtgggtccatgaacctaaaggtactact 120
 DB 61 tacattgatttcaagagggatctagggtggaattgatacagacacccaagggtacaa 120
 QY 121 gccaaactctcagggcccttgccatacctccagtcagtcagacacacccaagcagc 180
 DB 121 gccaaactctgtgtgagcagtcgccgtatttattgagttcagacactcagcacagc 180
 QY 181 gtgctgggactgtacacactctgaacctgaagcatcgtcgtcgtcgtgctgctgccc 240

PN W09119513-A.


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XX WPI; 1989-138796/19.
XX P-PSDB; AAP91889.
XX
XX New DNA sequence encoding transforming growth factor beta 2 -
XX used for large scale expression in eucaryotic cells
XX
XX Disclosure; Fig 1a; 27pp; German.
XX
XX PolyA-RNA was isolated from the tamoxifen-treated, human prostatic
XX adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is used
XX for control of the SV40 promoter and expressed in CHO cells. The simian
XX SQ is also claimed.
XX
XX Sequence 2568 BP; 772 A; 597 C; 513 G; 586 T; 0 other;

Query Match      53.7%; Score 182.2; DB 10; Length 2568;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtccgaacttgaggagaaactgtgtgccccctc 60
Db 1456 gcttggatgagccctattgttagaaatgtgcagataattgctgctacgtccactt 1515
Qy 61 tacattgacttcgcacagatgtgggtggaagtgggtccatgaacctaaagggtactat 120
Db 1516 tacattgattccaagaggtactaggtggaatggatcacagaccccaagggtacaat 1575
Qy 121 gccaaactctgtcagcccttgcccataccctccagtcagacacacacacagcag 180
Db 1576 gccaaactctgtcagcagccgtatttatggatcagacactcagcacagcagg 1635
Qy 181 gtgctgggactgtacacactctgaacctgaacctgctgcctgtgctgctgccc 240
Db 1636 gtcctgagcttataataaccataaataccagaagcatctgtctcctgtgctgccc 1695
Qy 241 caggacctgggagccctgacctctgtactatgtgtggaggagcccccaagtggagcag 300
Db 1696 caagatttagaacctctaacattctctactacattggtgcaaaacaccccaagattgaacag 1755
Qy 301 ctctccaacatgggtggaagtcttggtaaatgtagctga 339
Db 1756 ctttctaataatgattgtaaaagcttgcgaatgcagctaa 1794

RESULT 72
AAQ05126
ID AAQ05126 standard; DNA; 2569 BP.
XX AC AAQ05126;
XX
XX 02-NOV-1990 (first entry)
XX
XX Human TGF-Beta2-442 precursor cDNA.
XX
XX Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 467..1792
XX FT /*tag= a
XX mat_peptide 1457..1792
XX FT /*tag= b
XX
XX EP376785-A.
XX
XX 04-JUL-1990.
XX
XX 14-DEC-1989; 89EP-0403480.
XX
XX 16-DEC-1988; 88US-0285140.

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PR 05-DEC-1989; 89US-0446020.
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX WPI; 1990-203127/27.
XX P-PSDB; AAR05748.
XX
XX Cloning and expression of transforming growth factor beta 2 -
XX used for treatment of tumors or for augmenting wound healing.
XX
XX Claim 1; Fig 1a; 58pp; English.
XX
XX TGF-Beta2 may be used in treatment of tumors at effective doses,
XX and may also be useful in augmenting wound healing by stimulating
XX cell proliferation. The growth factor can be produced at high
XX levels from a CHO expression system.
XX
XX Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0 other;

Query Match      53.7%; Score 182.2; DB 11; Length 2569;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtctccgaacttgaggagaaactgtgtgccccctc 60
Db 1457 gcttggatgagccctattgttagaaatgtgcagataattgctgctacgtccactt 1516
Qy 61 tacattgacttcgcacagatgtgggtggaagtgggtccatgaacctaaagggtactat 120
Db 1517 tacattgattccaagaggtactaggtggaatggatcacagaccccaagggtacaat 1576
Qy 121 gccaaactctgtcagcccttgcccataccctccgagtcagacacacacacagcag 180
Db 1577 gccaaactctgtcagcagccgtatttatggatcagacactcagcacagcagg 1636
Qy 181 gtgctgggactgtacacactctgaacctgaacctgctgcctgctgctgctgccc 240
Db 1637 gtccgagcttataataaccataaataccagaagcatctgtctcctgtgctgctgccc 1696
Qy 241 caggacctggagccctgacctctgtactatgtttggaggagcccccaagtggagcag 300
Db 1697 caagatttagaacctctaacattctctatttatgttgcaaaacaccccaagattgaacag 1756
Qy 301 ctctccaacatgggtggaagtcttggtaaatgtagctga 339
Db 1757 ctttctaataatgattgtaaaagcttgcgaatgcagctaa 1795

RESULT 73
AAQ20290
ID AAQ20290 standard; cDNA; 2569 BP.
XX AC AAQ20290;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence encoding human transforming growth factor (TGF) -
XX beta-2-442.
XX
XX Hypertension therapy; hypotensive agent; blood pressure modulator;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 467..475
XX FT /*tag= a
XX sig_peptide 478..525
XX FT /*tag= b
XX CDS 526..1456

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FT mat_peptide /*tag= c
FT 1457..1792
FT /*tag= d
FT 2569
FT polyA_site /*tag= e
XX
XX WO9119513-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
XX 20-JUN-1990; 90US-0541221.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comerreski CR;
XX
XX WPI; 1992-024199/03.
XX P-PSDB; AAR20125.
XX
XX Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX Disclosure; Fig 2; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX complex.
XX
XX Sequence 2569 BP; 772 A; 598 C; 513 G; 686 T; 0 other;

Query Match 53.7%; Score 182.2; DB 13; Length 2569;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgaggagagaactgctgtgctgccccctc 60
Db 1457 gcttggatgcggcctattgcttagaataatgacagataattgctgctacgtccactt 1516

QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 1517 tacattgattcaaggaggatctaggtggaatggatatacagcaacccaaagggtacaat 1576

QY 121 gccaaactctgctcaggcccttgcccatacctccgagtgagacacaccccaagcagc 180
Db 1577 gccaaactctgctcaggagcatgcccgtattatgaggttcagacactcagcagcagc 1636

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcctgtgctgcgtgcc 240
Db 1637 gctcgtgactataataaccataaatcagaagcatctgctctccttgcgtcgtgcc 1696

QY 241 caggacctggagccctgacctctgtactatgttgggagaccctcccaagtgagcag 300
Db 1697 caagatttagaaccttaacctctctactacatctgcaaaacaccccaagattgaacg 1756

QY 301 ctctccaacatgggtggtgaagtcttgtaaatgtagtga 339
Db 1757 cttcttaatatgattgaagtcttgcaaatgcagctaa 1795

RESULT 74
AAR04116
ID AAR04116 standard; cDNA; 2592 BP.
XX
XX AAT04116;
XX

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DT 28-MAY-1996 (first entry)
XX
XX Human transforming growth factor-2 cDNA.
XX
XX TGF-beta1; TGF-beta2; transforming growth factor; protein;
XX cell differentiation; cell proliferation; CHO; Chinese hamster;
XX ovary; COS; monkey kidney; animal; mammal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX sig_peptide 503..550
XX /*tag= a
XX mat_peptide 1484..1819
XX /*tag= b
XX misc_feature 553
XX /*tag= c
XX /*note= "putative signal sequence cleavage site"
XX
XX EP676474-A1.
XX
XX 11-OCT-1995.
XX
XX 14-DEC-1989; 89EP-0104223.
XX
XX 05-DEC-1989; 89US-0446020.
XX 16-DEC-1988; 88US-0285140.
XX
XX (ONCO ) ONCOGEN LP.
XX
XX Madisen L, Purchio AF, Webb N;
XX
XX WPI; 1995-346094/45.
XX P-PSDB; AAR79922.
XX
XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
XX to produce biologically active, mature TGF-beta-2
XX
XX Disclosure; Fig.1a; 52pp; English.
XX
XX This DNA sequence is expressed in a host cell, preferably a
XX COS or CHO cell, containing a recombinant vector encoding this
XX sequence under the control of a 2nd nucleotide sequence that
XX regulates gene expression, preferably the SV40 promoter, so the host
XX cell produces active TGF-beta2. The produced TGF-beta2 protein can
XX be used to regulate cellular differentiation and proliferation.
XX
XX Sequence 2592 BP; 772 A; 613 C; 516 G; 691 T; 0 other;

Query Match 53.7%; Score 182.2; DB 16; Length 2592;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgaggagagaactgctgtgctgccccctc 60
Db 1484 gcttggatgcggcctattgcttagaataatgcaagataattgctgctacgtccactt 1543

QY 61 tacattgactccgacagagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 1544 tacattgattcaaggaggatctaggtggaatggatatacagaaccccaaggtacaat 1603

QY 121 gccaaactctgctcaggcccttgcccatacctccgagtgagacacacaccccaagcag 180
Db 1604 gccaaactctgctcaggagcatgccgtatttatggattcagacactcagcagcagc 1663

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcctgtgctgcgtgcc 240
Db 1664 gtctgagcttatataatcacaataatcagaagcatctgctctccttgcgtgctcc 1723

QY 241 caggacctggagccctgacctctgtactatgttgggagaccctcccaagtgagcagc 300
Db 1724 caagatttagaaccttaacctctctactacatcttgcaaaacaccccaagattgaacg 1783

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Qy	61	tacattgacttcgcagcaggatctggctgggaagtgtccatgaacctaaaggctactat	120
Db	1154	tacattgattccaaggggatctagggaggaaatggtacacgaacccaagggtacaat	1213
Qy	121	gccaaactctgtcagggccctggccatactccgactcgacgaacaaaccacagcag	180
Db	1214	gccaaactctgtctggagcagtcgcggtatttatggagctcagacactcagcacagcag	1273
Qy	181	gtgctggactgtacaaacactctgaacctgaagcatctgcctcgcttgcgtgctgcc	240
Db	1274	gtcctgagcttataataaccataaattccagaagcatctgctctccttgcgtgctgcc	1333
Qy	241	caggacctggagccctgaccactctgtactatgtgtggaggagcccccaagtgagcag	300
Db	1334	caagattagaaccttaacctctctactacattggcgaacacccacagattggaacag	1393
Qy	301	ctctcaacatggtggtagctcttgaatgtagctga	339
Db	1394	ctttctcaatgatgtgaagctcttgcaaaatgcagctaa	1432

RESULT	77
AAQ03511	
ID	AAQ03511 standard; DNA; 2207 BP.
XX	
AC	AAQ03511;
XX	
DT	14-AUG-1990 (first entry)
XX	
DE	Hybrid transforming growth factor TGF-beta1/beta2.
XX	
KW	HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW	factors; ds.
XX	
Key	Location/Qualifiers
PH	267..1437
FT	/*tag= a
FT	1103..1437
FT	/*tag= b
XX	
PN	EP356935-A.
XX	
PD	07-MAR-1990.
XX	
PF	25-AUG-1989; 89EP-0115719.
XX	
PR	25-AUG-1988; 88US-0236698.
XX	
PA	(ONCO-) ONCOGEN LTD PARTNER.
XX	
PI	Brankovan V, Lioubin M, Purchio A;
XX	
DR	WPI; 1990-068723/10.
DR	P-PSDB; AAR05666.
XX	
XX	Compens. contg. transforming growth factor beta -
PT	used for inhibitions of HIV infection and replication in vivo.
XX	
CC	TGF-beta may be used in vivo to prevent formation of syncytia and
CC	inhibit HIV infection. TGF may also be used with other HIV treatments
CC	(AZT, soluble CD4 etc.).
XX	
PS	Disclosure; Fig 3; 20pp; English.
XX	
SQ	Sequence 2207 BP; 600 A; 576 C; 532 G; 499 T; 0 other;

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Query Match      53.3%; Score 180.6; DB 11; Length 2207;
Best Local Similarity 70.8%; Pred. No. 5e-42;
Matches 240; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qv 1 qcttggacaccaattactgtctccgaacttggaggagaactgctgtgtcgcgccctc 60

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[illegible]

RESULT	78
AAQ05127	
ID	AAQ05127 standard; DNA; 2207 BP.
XX	
AC	AAQ05127;
XX	
DT	02-NOV-1990 (first entry)
XX	
DE	Human TGF-Betal/TGF-Beta2 hybrid precursor cDNA expressing
DE	TGF-Beta2.
XX	
KW	Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
CDS	261..1430
FT	/*tag= a
mat_peptide	1092..1430
FT	/*tag= b
FT	
XX	
PN	EP376785-A.
XX	
PD	04-JUL-1990.
XX	
PF	14-DEC-1989; 89EP-0403480.
XX	
PR	16-DEC-1988; 88US-0285140.
PR	05-DEC-1989; 89US-0446020.
XX	
PA	(ONCO-) ONCOGEN LTD PARTNER.
XX	
PI	Purchio AF, Madisen L, Webb N;
XX	
DR	WPI; 1990-203127/27.
DR	P-FSDB; AAR05749.
XX	
PT	Cloning and expression of transforming growth factor beta 2 -
PT	used for treatment of tumors or for augmenting wound healing.
XX	
PS	Claim 15; Fig 1b; 58pp; English.
XX	
CC	TGF-Beta2 may be used in treatment of tumors at effective doses,
CC	and may also be useful in augmenting wound healing by stimulating
CC	cell proliferation. The growth factor can be produced at high
CC	levels from a CHO expression system.
XX	
SQ	Sequence 2207 BP; 600 A; 577 C; 532 G; 498 T; 0 other;


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FT      /*tag= b
FT      /note= "Simian TGF-beta1 precursor"
FT      1085..1423
FT      /*tag= c
FT      /note= "human TGF-beta2 precursor"
FT      278..319
FT      /*tag= d
XX      EP676474-A1.
PN
XX
PD      11-OCT-1995.
XX
PD      14-DEC-1989; 89EP-0104223.
XX
PD      05-DEC-1989; 89US-0446020.
PR      16-DEC-1988; 88US-0285140.
XX
XX      (ONCO ) ONCOGEN LP.
PA
XX      Madisen L, Purchio AF, Webb N;
PI
XX      WPI; 1995-346094/45.
DR      P-PSDB; AAR79921.
XX
XX      Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
PT      to produce biologically active, mature TGF-beta-2
XX
XX      Claim 1, 2 and 3; Fig.1b; 52pp; English.
XX
XX      This hybrid DNA sequence is expressed in a host cell, preferably a
CC      COS or CHO cell, containing a recombinant vector encoding this
CC      sequence under the control of a 2nd nucleotide sequence that
CC      regulates gene expression, preferably the SV40 promoter, so the host
CC      cell produces active TGF-beta2. The produced TGF-beta2 protein can
CC      be used to regulate cellular differentiation and proliferation.
XX
XX      Sequence 2200 BP; 597 A; 588 C; 517 G; 498 T; 0 other;
SQ
      Query Match      52.3%; Score 177.4; DB 16; Length 2200;
      Best Local Similarity 70.2%; Pred. No. 4e-41;
      Matches 238; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
      QY      1 gcttggacacaaataactgctccgcaacttgaggagagaactgctgtgccccctc 60
      DB      1088 gcttgcataccccctattcctttacaaatgycagcataattgctgctcactccact 1147
      QY      61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
      DB      1148 tacattgattcaagacgatctagggtgaaatgatatacagacccaaagggtacaat 1207
      QY      121 gcaacttctgctcaggcccttgcccatcctccagtcagtcagacacaaacccagcaag 180
      DB      1208 gcaacttctgctgagcatgcccgtatttggagtgcagactcagcacagcag 1267
      QY      181 gtgctggagactatacaactctgaacctgaacctgaacctgctcctgctgctgccc 240
      DB      1268 gtcttgagcttataataaccataaataccagaagcatctgctctctgctgctgtcc 1327
      QY      241 caggacctggagcccttgaccatcctctgactatgttgaggaggaccccccagagcgag 300
      DB      1328 caagatttagaaccttaacattctctactatcatattggcaaaccccaagattgaag 1387
      QY      301 ctctccaaatggtggtgaagtctgttaaatgtagtga 339
      DB      1388 ctctctaataatgatgaaagtcttgcaaatgcagctaa 1426
      RESULT 81
      ID      AAQ29178
      XX      AAQ29178 standard; DNA; 1565 BP.
      AC      AAQ29178;

```

```

XX      10-MAR-1993      (first entry)
XX      TGF-beta 1.
XX      Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
KW      Simian virus 40; SV40; expression vector; Chinese Hamster Ovary; CHO;
KW      vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FT      sig_peptide      269..355
FT      /*tag= a
FT      /note= "Signal peptide, pre-pro-protein"
FT      356..1105
FT      /*tag= b
FT      /note= "Pro-protein"
FT      1106..1438
FT      mat_peptide      /*tag= c
XX      WO9216228-A.
XX      01-OCT-1992.
XX      13-MAR-1992; 92WO-US01993.
XX      14-MAR-1991; 91US-0669171.
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      Madisen L, Merwin J, Purchio AF;
XX      WPI; 1992-348938/42.
DR      P-PSDB; AAR29657.
XX
XX      Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
PT      inhibits proliferation of vascular endothelial cells, useful for
PT      treating cancer and to promote wound healing
XX      Disclosure; Fig 1; 45pp; English.
XX      The sequence given encodes the human transforming growth factor
CC      (TGF)-beta 1. This was used within the scope of the invention to
CC      compare to a simian TGF hybrid termed TGF-beta 1/beta 2 (or TGF-5
CC      beta) (see also AAQ29177). the chimeric DNA sequence could be placed
CC      under the control of Simian virus 40 (SV40) expression regulatory
CC      region within an expression vector and used to transfect Chinese
CC      Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
CC      and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
CC      effects on the proliferation of mature TGF-5 beta. TGF-5 beta induces
CC      to those produced by TGF-beta 1.
XX      Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;

```

```

Query Match      52.0%; Score 176.2; DB 13; Length 1565;
Best Local Similarity 72.3%; Pred. No. 8.1e-41;
Matches 245; Conservative 0; Mismatches 88; Indels 6; Gaps 1;
QY      1 gcttggacacaaataactgctccgcaacttgaggagagaactgctgtgccccctc 60
DB      1106 gcttggacacaaataactgctccagaaaatgycaggaataattgctcactgctcgtt 1165
QY      61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
DB      1166 tacattgatttc-----gatctagggtggaaatggtccacgagcccaagggtaccat 1219
QY      121 gcaacttctgctcaggcccttgcccatcctccagtcagtcagacacaaacccagcaag 180
DB      1220 gccaaacttgcctcgggccctgcctcacatttgagcgtgagcagcagtcacagcaag 1279
QY      181 gtgctggagactgtacaacactctgaacctgaacctgaacctgctcctgctgctgccc 240

```


PI	Derynck RMA;
XX	WPI; 1986-326875/50.
XX	TGF-beta prodn. from transformed hosts - useful esp. for treating
XX	wounds (J6 2/9/86).
XX	Disclosure; Fig 2; 26pp; English.
XX	The gene product is known to stimulate cell proliferation and
XX	inhibit anchorage-dependent growth of a variety of human cancer cell
XX	lines, it is esp. useful in treatment of burns and the promotion of
XX	surface and internal wound healing. TGF-beta may be expressed from a
XX	transformed CHO cell line.
XX	See also AAN60972.
XX	Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
XX	
XX	Query Match 28.6%; Score 96.8; DB 7; Length 975;
XX	Best Local Similarity 74.4%; Pred. No. 2.5e-18;
XX	Matches 122; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX	
Qy	21 ctccgcgaacttgagagaaactcgtgtgctgcgccctctacattgacttcacagga 80
Db	341 ctgcagctccacggagaagaactcgtcgtgcggcagctgtacattgacttcgcaagga 400
Qy	81 tctggctggaagtgggtccatgaacctaaaggctactatgccaactctgctcaggccc 140
Db	401 cctcggctggaagtggatccacagagcccaagggtaccatgccaactctgctcgggcc 460
Qy	141 ttgcccatactccgcagtgagacacaaacccacagcacggtgc 184
Db	461 ctgcccatacttgagcctggacacgcagctacgcaagggtac 504
XX	
XX	RESULT 85
XX	AAQ02815
XX	ID AAQ02815 standard; DNA; 975 BP.
XX	AC AAQ02815;
XX	31-MAY-1989 (first entry)
XX	Sequence of genomic fragment encoding a TGF-beta 1 exon.
XX	Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX	inhibition.
XX	Key Location/Qualifiers
XX	CDS 348..500
XX	FT /*tag= a
XX	W08912101-A.
XX	14-DEC-1989.
XX	08-JUN-1988; 88WO-US01945.
XX	08-JUN-1988; 88WO-U001945.
XX	(GETH) GENENTECH INC.
XX	Derynck RM, Goeddel DV;
XX	WPI; 1990-007474/01.
XX	P-PSDB; AAR04075.
XX	Nucleotide sequence encoding transforming growth factor beta-3 -used as a
XX	probe, or to produce TGF beta 3, for inhibition of growth of normal
XX	and neoplastic cells, eg A549.
XX	Disclosure; Fig. 2; 61pp; English.


```

XX PN W09105565-A.
XX PD 02-MAY-1991.
XX PF 18-OCT-1990; 90WO-US06006.
XX PR 18-OCT-1989; 89US-0422962.
XX PA (CREA-) CREATIVE BIOMOLECUL.
XX PI Cohen CM;
XX DR WPI; 1991-148530/20.
XX DR P-PSDB; AAR11957.
XX PT Recombinant truncated transforming growth factor-beta analogues -
XX PT capable of inducing an anti-proliferative effect in mammalian
XX PT epithelial cells in vitro
XX PS Claim 23; Fig 2B; 42pp; English.
XX CC This synthetic gene was designed based on reported sequence data,
XX CC codons inferred from known amino acid sequences and observations of
XX CC partial homology with known genes of the TGF-beta family. It was
XX CC assembled from chemically synthesised oligonucleotides and can be
XX CC expressed in prokaryotic host cells. The sequence is that given in
XX CC the specification, however, 50 bases should be inserted between
XX CC nucleotides 600 and 601 of this sequence; the two "missing" Cys
XX CC codons are presumably contained in the omitted sequence. The
XX CC truncated TGF-beta protein is cleaved from the Fb-Fb domain at the
XX CC hinge region to give the truncated product.
XX CC See also AAQ11774, AAR11942-7 and AAR11954.
XX SQ Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0 other;

Query Match 21.6%; Score 73.2; DB 12; Length 817;
Best Local Similarity 61.6%; Pred. No. 1.2e-11;
Matches 117; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 143 gccataactccgcagtgacagacacacacacagcagcgtgtgtgactgtacacactc 202
Db 615 gtccgtacatctgtctgtgataccagctactccaagtgctgtgtctgtacacacgc 674
Qy 203 tgaacctgaagcatctgcctgccttctgtcgtgtccccaggaacctggagccctgacca 262
Db 675 ataacccggggctagcgcagctcgtgtgtgttccacagccttggaaaccgctgcga 734
Qy 263 tctgtactatgttggaggaccacccaaagtggagcagctctccacacatggtgtgaagt 322
Db 735 tegtattacgtcggccgtaagcctaaggttgaaacagctgtctaactgattgtgcga 794
Qy 323 cttgtaaatg 332
Db 795 gttgcaagtg 804

RESULT 90
AAQ23678
ID AAQ23678 standard; DNA; 894 BP.
XX AC AAQ23678;
XX DT 17-SEP-1992 (first entry)
XX DE Encodes C-terminal portion of bovine BMP-6.
XX KW bovine bone morphogenic protein-6; bone defects; cartilage defects;
XX KW wound healing; bone repair; cartilage formation;
XX KW periodontal disease; ss.
XX OS Synthetic.

```

```

XX FH Key Location/Qualifiers
XX FT CDS 1..669
XX FT /*tag= a
XX FT /product= C-terminal part of bovine BMP-6
XX PN W09205199-A.
XX PD 02-APR-1992.
XX PF 26-SEP-1991; 91WO-US07069.
XX PR 26-SEP-1990; 90US-0588227.
XX PA (GENE-) GENETICS INST INC.
XX PI Celeste A J, Rosen V A, Wang E A, Wozney J M;
XX DR WPI; 1992-132089/16.
XX PT New human bone morphogenic protein-5 derivs. - for treating bone
XX PT and/or cartilage defects, burns, incisions, ulcers, for wound
XX PT healing
XX PS Example 4; Page 25; 54pp; English.
XX CC This sequence was isolated from positive clones in a bovine lambda
XX CC gt10 library isolated with probes AAQ23673-6, which were then screened
XX CC with HEL5. One which hybridised positive was sequenced to yield the
XX CC given sequence. An inframe stop codon indicates it encodes the
XX CC C-terminal part of bovine BMP-6.
XX CC See also AAQ23773-81, and AAR22497-9.
XX SQ Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;

Query Match 16.1%; Score 54.6; DB 13; Length 894;
Best Local Similarity 51.9%; Pred. No. 2.4e-06;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps 2;

Qy 7 gacacaaataactgtctcgcaacttggaggagaaactgtgtgtgccccctctacatt 66
Db 325 gctcagactacaacagcagcagtgagcgctgaagcgctgcggaagcatgagctacgtg 384
Qy 67 gacttcgcacaggaatctggctggaagtgggtccatgaacctaaaggctactatgccaac 126
Db 385 agcttcaggaacctgggtggcgaggtggtggtggtggtggtggtggtggtggtggtggt 444
Qy 127 ttctgtcaggcccttggccataacctcccgagtgacagac-----acaacccacgc 177
Db 445 tactgtgacggagaaatgttcttccctctcaacgcacacatgaacgtaccacacatgcc 504
Qy 178 acggtgtggactgtacaaacctgaaccttgaacctgaagcatctgtcgtcgtcgtcgtg 237
Db 505 atcgtgcagacctgttccacctcatgaaccgcagtgacgtccccaacacgtgtgcgcg 564
Qy 238 cccacgaacctggagccctcgaccatccctgtactatgttggaggagacc-----cccaaatg 294
Db 565 cccacgaacctgaacgcacctctcgtgtctactctgcagcagacacactccaatgtcatctg 624
Qy 295 gacgacgtctccaacatggtgtggaagtcttgaatgttagctga 339
Db 625 aagaagtaccggaacatggtcgtacgagcgtgtgggtgccaatga 669

RESULT 91
AAQ37567
ID AAQ37567 standard; DNA; 894 BP.
XX AC AAQ37567;
XX DT 22-JUN-1993 (first entry)
XX DE

```

```

DE BMP-6 coding sequence.
XX
KW Probe; tryptic peptide; bovine; bone morphogenic protein; BMP-6;
KW BMP-5; carboxy terminal; cartilage; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /tag= a
XX
PN US5187076-A.
XX
PD 16-FEB-1993.
XX
XX 01-JUL-1986; 86US-0880776.
XX
PR 01-JUL-1986; 86US-0880776.
PR 17-DEC-1986; 86US-0943332.
PR 20-MAR-1987; 87US-0028285.
PR 26-MAR-1987; 87US-0031346.
PR 08-APR-1988; 88US-0179100.
PR 08-APR-1988; 88US-0179101.
PR 08-APR-1988; 88US-0179197.
PR 28-MAR-1989; 89US-0329610.
PR 04-MAY-1989; 89US-0347559.
PR 23-JUN-1989; 89US-0370544.
XX
PA (GEMV ) GENETICS INST INC.
XX
XX Celeste AJ, Rosen VA, Wang EA, Wozney JM;
XX
XX WPI; 1993-075724/09.
XX
DR P-PSDB; AAR32903.
XX
XX Isolated DNA sequence encoding bone morphogenic protein (BMP-6) -
PT useful for treating bone and/or cartilage defects and in wound
PT healing and tissue repair
XX
PS Disclosure; Table II; 24pp; English.
XX
XX This sequence was isolated using the probes given in AAQ37557-60. These
CC probes were based on the tryptic peptide fragment from bovine bone
CC morphogenic protein (BMP-6) having the sequence XHELYVSFS. A further
CC clone representing the carboxy terminal part of the bovine BMP-5
CC cartilage/bone protein (see also AAQ37566) was isolated under more
CC stringent conditions.
XX
XX Sequence 894 BP; 169 A; 301 C; 275 G; 149 T; 0 other;
SQ

```

Query Match 16.1%; Score 54.6; DB 14; Length 894;
Best Local Similarity 51.9%; Pred. No. 2.4e-06;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps 2;

```

QY 7 gacacaaattactgtctccgaacttggagagaaactgtgtgtgccccctctacatt 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 325 gctcagactacacagcagcagcagcagcagcagcagcagcagcagcagcagc 384
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 gacttcgacaggaatctgggtggaagtgggtccatgaacctaaaggctactatgccaac 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 385 agcttcacaggaacctgggtggcaggactggatcattgcccccaaggcgtacgtgccaac 444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 ttctgtcaggcccttgcccatccctccgcagtgacagc-----acaacccacagc 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 445 tactgtgacggagaatgttcttcctctcaacgacacacatgaacgtaccacacatgcc 504
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 acggtctgggactgtacacactgtgaacctgaacctgaacctgtcctcgtctgctgggtg 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 505 atcgtgcagacctgtgtacacctcatgaaccccgagtcagctccccaacacgtgtgcgcg 564
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 cccaggaacctgagccctcgaccatccctgtactatgttggaggacc---cccaaaagt 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

565 ccacgaaactgaacgccatctcggtgtctctactctgcagcaacacatccatctcctg 624

295 gacgagctctccacatggtgtgaagtctctgtaaatgtagctga 339
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

625 aagaagtaccggaacatggtgtacgagcgtgtggtgccactga 669
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 92
AAX99261
ID AAX99261 standard; DNA; 894 BP.
XX
AC AAX99261;
XX
DT 04-OCT-1999 (first entry)
XX
DE DNA encoding carboxy-terminal part of bovine BMP-6 bone protein.
XX
KW Bone morphogenic protein; BMP-5; bone formation; cartilage; ulcer;
KW connective tissue; wound healing; burn; incision; tissue repair; BMP-6;
KW periodontal disease; cell differentiation; osteoarthritis; osteoporosis;
KW bone fracture; cosmetic plastic surgery; neuronal survival; ss.
XX
OS Bos sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /tag= a
FT /product= "BMP-6 carboxy terminal fragment"
XX
PN US5939388-A.
XX
XX 17-AUG-1999.
XX
XX 23-JAN-1997; 97US-0788729.
XX
XX 23-JAN-1997; 97US-0788729.
XX 01-JUL-1986; 86US-0880776.
XX 17-DEC-1986; 86US-0943332.
XX 20-MAR-1987; 87US-0028285.
XX 26-MAR-1987; 87US-0031346.
XX 08-APR-1988; 88US-0179100.
XX 08-APR-1988; 88US-0179101.
XX 08-APR-1988; 88US-0179197.
XX 28-MAR-1989; 89US-0329610.
XX 04-MAY-1989; 89US-0347559.
XX 15-NOV-1989; 89US-0437409.
XX 26-SEP-1990; 90US-0588227.
XX 22-DEC-1992; 92US-0995565.
XX 07-SEP-1993; 93US-0116425.
XX 06-JUN-1995; 95US-0469935.
XX
PA (ROSE/) ROSEN V A.
PA (WANG/) WANG E A.
PA (WOZN/) WOZNEY J M.
XX
XX Rosen VA, Wang EA, Wozney JM;
XX
XX WPI; 1999-468410/39.
XX P-PSDB; AAY28984.
XX
XX Bone morphogenic protein composition useful in wound healing and
XX tissue repair
XX
XX Example 4; Columns 19-20; 20pp; English.
XX
XX The invention is related to purified bone morphogenic proteins (BMP).
XX Compositions comprising a matrix, a vehicle and a purified dimeric BMP-5
XX or naturally occurring allelic sequences of BMP-5 are used for inducing
XX bone/and or cartilage or other connective tissue formation in a patient
XX and is useful in wound healing e.g. ulcers, burns and incisions, tissue
XX repair and treating periodontal disease. The composition can be used to
XX treat cell populations e.g. embryonic cells, stem cells to enhance or
XX enrich growth and/or cell differentiation. Tissues that can be treated

CC include epidermis, nerve, muscle, liver, lung, cardiac, pancreas and
CC kidney. Osteoarthritis and osteoporosis can also be treated. It is useful
CC for healing bone fractures and cartilage defects in humans and other
CC animals, particularly domestic animals and thoroughbred horses and also
CC has uses in cosmetic plastic surgery. The composition may increase
CC neuronal survival and be useful in transplantation and the treatment of
CC conditions which exhibit a decrease in neuronal survival. The present
CC sequence represents a DNA encoding the carboxy-terminal part of bovine
CC BMP-6 protein.
XX
SQ Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;

Query Match 16.1%; Score 54.6; DB 20; Length 894;
Best Local Similarity 51.9%; Pred. No. 2.4e-06;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps 2;
QY 7 gacacaattactgtccgcgaacttgagagagaactgtgtgtgccccctctacatt 66
DB 325 gctcagactacaacagcagcagctgagacgacctgctgcggaagcatgagctctacgtg 384
QY 67 gactccgacagagatctggctggagtggtccatgaacctaaagggtctactatgccaac 126
DB 385 agcttcaggaactgggtggcaggactggatcattgcccccaagggtctactgctgccaac 444
QY 127 ttctgtcagggcccttgcccatctccgcagtcagac-----acaacccacagc 177
DB 445 tactgtgacggagaattgttcctctcaacgcacacatgaacgctaccacacatgcc 504
QY 178 acggtgctgggactgtacaacactctgaacctgaagcatctgctcgtctgctgctg 237
DB 505 atcgtgcagacctggttcacctcatgaacctgaccccgagtaoctcccaaacggtgctg 564
QY 238 cccagagacctgagccctgacctcctctactatgttgaggagacc---cccaaatgtg 294
DB 565 cccaggaactgaagccatctcctgctcctactctgacgacacactcccaatgtcatcctg 624
QY 295 gagcagctctcccaacatggtggtgaagtctgttaaatgtagctga 339
DB 625 aagaagtaccggaacatggtctgacgagcgtgtggtgccactga 669

RESULT 93
AAN91769
ID AAN91769 standard; DNA; 454 BP.
AC AAN91769;
XX
DT 22-MAR-1990 (first entry)
XX
DE Consensus gene/probe to osteogenic protein OP1.
XX
KW Periodontal; osteoarthritis
XX
OS Mammal.
XX
PN W08909787-A.
XX
PD 19-OCT-1989.
XX
PF 07-APR-1989; 89WO-US01453.
XX
PR 08-APR-1988; 88US-0179406.
XX
PA (CREA) CREATIVE BIOMOLECUL.
XX
PI Kuberasampath T, Oppermann H, Rueger DC, Ozkaynak E;
XX
DR WPI: 1989-324202/44.
DR P-PSDB; AAP91200.
XX
PT Osteogenic devices comprising matrix contg. osteogenic protein - useful
for inducing endochondral bone growth eg in non-union fractures

XX Disclosure; fig 1B; 104pp; English.
PS This is a synthetic consensus gene sequence, used as a probe to isolate
CC natural genes of proteins that induce endochondral bone formation.
XX
SQ Sequence 454 BP; 101 A; 146 C; 121 G; 86 T; 0 other;
Query Match 15.8%; Score 53.4; DB 10; Length 454;
Best Local Similarity 53.2%; Pred. No. 4.3e-06;
Matches 142; Conservative 0; Mismatches 116; Indels 9; Gaps 1;
QY 51 gcqcccccttaccatgacttcgcagacaggtatctggctggaagtgggtcccatgaacacaa 110
DB 79 gcacgagctgtatgtcagcttcgcagacctggctggcaggactggatcatcgccgtga 138
QY 111 gggtactatgccaactctgtcagggcccttgcccatacctc-----cgcagtg 161
DB 139 agacttcgacgctactactgtcccgagcgtgcagacctggtgaacacatgaaccccggaaggtacc 198
QY 162 agacacaaacccacagcagctgctgggactgtacaacactctgaacctgaagcatctgc 221
DB 199 cagcacaacacgcgcgtggtgcagacctggtgaacacatgaaccccggaaggtacc 258
QY 222 ctgccttctgtgctgcccagacgtgagccctgagccctgacctctgtactatgttgaggag 281
DB 259 caagcctgctgctgcccacagctgtccgcacatgctgtacctggtgacgagaa 318
QY 282 gacccccaaagtggagcagctctccaa 308
DB 319 ttccaccgtggtgctgaagaactacca 345
RESULT 94
AAT11062
ID AAT11062 standard; DNA; 630 BP.
AC AAT11062;
XX
DT 15-APR-1996 (first entry)
XX
DE Murine growth differentiation factor-11 (GDF-11) coding sequence.
XX
KW Growth differentiation factor-11; GDF-11; antibody; detection;
KW disorder; muscle; antisense; suppression; vector; liposome;
KW targeting; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 198..578
FT /*tag= a
FT /product= Murine growth differentiation factor-11.
XX
PN W09601845-A1.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US08543.
XX
PR 08-JUL-1994; 94US-0272763.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI Lee S, Mcpherron AC;
XX
DR WPI: 1996-097589/10.
DR P-PSDB; AAR88554.
XX
PT New Growth Differentiation Factor-11 (GDF-11) - with tissue-specific
expression in muscle, neural and uterine cells, for detecting cell
proliferation disorders

FT XX /note= "the start codon is not indicated"

PN XX WO2000067116-A1.

XX FH 10-FEB-2000.

PD XX

XX PF 28-JUL-1999; 99WO-US17252.

XX FT 28-JUL-1998; 98US-0123929.

XX PR (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PA

XX PI Lee S, McPherron AC;

XX PT WPI: 2000-195289/17.

XX DR P-PSDB; RAY77565.

XX XX

PT Preparation of transgenic animal food product useful for treating renal

PT and muscular disorders, comprises introducing transgene interfering

PT with expression of growth differentiation factor-11 into embryo -

XX

XX Example 3; Fig 1A; 97pp; English.

PS

XX The invention relates to a method for producing animal food products with

XX increased ribs content. The method comprises: (a) introducing a transgene

CC which interferes with expression of growth differentiation factor-11

CC (GDF-11), into an embryo; (b) allowing the embryo to mature; (c) cross-

CC breeding the transgene-positive progeny; (d) processing these progeny to

CC obtain the foodstuff. Modulators of GDF-11 are useful for treating acute

CC or chronic renal disease, and various other muscle associated disorders

CC e.g cancer, AIDS; cell proliferative disorders, neurodegenerative

CC disorders; adipose tissue disorders and immunologic disorders. The animal

CC food product comprises large amounts of muscle and meagre amounts of fats

CC and cholesterol, hence useful in treating obesity and related disorders.

CC The present sequence represents a genomic DNA encoding a partial mouse

CC GDF-11 polypeptide.

XX

SQ Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;

Query Match 15.6%; Score 52.8; DB 21; Length 630;

Best Local Similarity 55.4%; Pred. No. 7e-06;

Matches 102; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 17 actgtctccgaacttgaggagaaactgtgtgtgcgcccctctacattgacttccgac 76

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 262 actcgcgtagaactcgtgagtcgcgcgtgtgtgcgatactctcactcagtggaacttg 321

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 77 aggatctgggtggaagtgggtccatgaaccctaaagggtactatgccaactctgtctcag 136

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 322 aggccttggctgggactggatcatcgacccctaaagcgtacaaaggccaactactgtctcg 381

QY 137 gcccttgcccatcctccgagtcagacacacacccagcagcgtgtgctggactgtaca 196

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 382 gccagtgcgaatacatgttctatgcaaaagtatccacacacccacttgggtgcaacaggcca 441

QY 197 acac 200

Db |||

QY 442 accc 445

Db |||

RESULT 97

AAQ79444

ID AAQ79444 standard; DNA: 789 BP.

XX

XX AAQ79444;

XX

XX 10-AUG-1995 (first entry)

DT

XX Partial bovine bone morphogenetic protein-11 (BMP-11).

DE

XX Bone morphogenetic protein-11; BMP-11; TGF-beta superfamily; ss.

XX

XX

OS Bos taurus.

XX

XX Key Location/Qualifiers

XX CDS 324..704

XX FT /*tag= a

XX FT intron 322..323

XX FT /*tag= b

XX FT /note= "putative 3' end of intron"

XX FT 375..701

XX FT /*tag= c

XX

XX WO9426892-A.

XX

XX PD 24-NOV-1994.

XX

XX PF 12-MAY-1994; 94WO-US05288.

XX

XX PR 12-MAY-1993; 93US-0061464.

XX

XX PA (GENY) GENETICS INST INC.

XX

XX PI Celeste AJ, Wozney JM;

XX

XX WPI: 1995-006788/01.

XX DR P-PSDB; AAR66147.

XX

XX New DNA encoding bone morphogenetic protein 11 - and related

PT vectors, transformed cells and polypeptide(s), including

PT heterodimers, useful e.g. in fertility control bone and tissue

PT repair, etc.

XX

PS Claim 2; Page 40-41; 57pp; English.

XX

XX A bovine genomic library (strain Bovine Activin WC) in lambda EMBL3

CC was screened under low stringency conditions with a 1081-1403 base

CC fragment of human BMP-7 DNA. Positive clones were screened with BMP-

CC 5, -6, and -7 probes under high stringency conditions and one clone

CC reactive in the first screen but not in the second was selected. The

CC hybridisation characteristics were localised to a 0.5 kb fragment.

CC The partial sequence of this clone, lambda 7r-30 (ATCCD 75433) is

CC Q79444. The 5' limit of this exon of the bovine BMP-11 gene is

CC difficult to define. Clone lambda 7r-30 contains at least one exon/

CC intron boundary. BMP-11 polypeptide exists as a dimer comprising two

CC of the mature protein AA sequences or as a heterodimer with one

CC mature sequence from BMP-11 and the other being any of BMP 1-10.

CC The predicted mol. wt. of the mature active species comprising two

CC mature protein sequences is approx. 12,000 daltons. Further active

CC species are contemplated comprising AAs 23-126. Primers C and D

CC are based on clone lambda 7r-30 (see Q79446, Q79447). Nts 375 or

CC 390-704 of Q79444 are claimed. AAs 18-126 of R66147 are claimed.

XX

SQ Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other;

Query Match 15.3%; Score 51.8; DB 16; Length 789;

Best Local Similarity 54.9%; Pred. No. 1.4e-05;

Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgtgtgtgcgcccctctacattgacttccgacagagatctgggtggaagtgg 96

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 408 gagtcccgctgtgcgctacccctcactgtgacttggagctttgtgctggagactgg 467

QY 97 gtccatgaacctaaagggtactatgtccaaacttctctcaggcccttgcccatctccgc 156

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 468 atcatcgtctctaaacgctacaaggccaactactgtctcgcgcagtgagtagatgttt 527

QY 157 agtgcagacacacccacacgacgctgtggtggtgtacacacactctgaacgaagca 216

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 528 atgcaaaagtatccgcacacccacttgggtgcaacaggct-----aacccaagagc 578

QY 217 tctgcctgccttgcgtgcgtgccccaggacgtggagccctgaccatctgact 271

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 579 tctcgggggccctgctgcacacccacacagatgtccccaatcaacatgctctact 633

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 99
 AAV03609
 ID AAV03609 standard; DNA; 789 BP.
 XX
 AC AAV03609;
 XX
 DT 02-APR-1998 (first entry)
 XX
 DE Bovine BMP-11 coding sequence.
 XX
 KW Bone-morphogenetic protein-11; BMP-11; inhibin-beta; inhibin-alpha;
 KW bone formation; cartilage repair; wound healing; periodontal disease;
 KW follicle stimulating hormone regulator; contraception; haematopoiesis;
 KW gonal tumour suppressor; therapy; cow; bovine; ds.
 XX
 OS Bos sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 324..704
 FT /*tag= a
 FT sig_peptide 324..374
 FT /*tag= b
 FT mat_peptide 375..701
 FT /*tag= c
 XX
 PN US5700911-A.
 XX
 XX 23-DEC-1997.
 XX
 XX 30-MAY-1995; 95US-0452772.
 XX
 XX 20-MAY-1994; 94US-0247907.
 PR 12-MAY-1993; 93US-0061464.
 PR 30-MAY-1995; 95US-0452772.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Celeste AJ, Wozney JM;
 XX
 XX WPI; 1998-062433/06.
 DR P-PSDB; AAW40816.
 XX
 XX Human and bovine bone morphogenetic protein 11 - useful for inducing
 PT bone and cartilage formation
 PT
 XX
 XX Claim 4; Column 23-26; 19pp; English.
 XX
 CC This sequence represents the coding sequence for the bovine bone
 CC morphogenetic protein-11 (BMP-11) of the invention. The human BMP-11
 CC polypeptide (see AAW40817), mature human BMP-11, or its dimers with
 CC other inhibin-beta, inhibin-alpha or bone morphogenetic proteins are
 CC useful for inducing bone and/or cartilage formation, e.g. for bone,
 CC ligament or cartilage repair, wound healing or treatment of periodontal
 CC disease. BMP-11 may also be useful for regulating the production of
 CC follicle stimulating hormone, for contraception, to stimulate
 CC haematopoiesis, and to suppress the development of gonadal tumours.
 XX
 SQ Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other;

Db 468 atcatgctcctaaacgctacaagccaactactgctccggccagtgcgagtacatgttt 527
QY 157 agtgacagacacacccacagcagtgctgggactgtacaacactctgaacctgaagca 216
Db 528 atgcaaaagtatccgcacacccacttggtgcaacaggct-----aacccaagaggc 578
QY 217 tctgctcgccttgctgctgccccagcactggagccccctgacctctgtact 271
Db 579 tctgcgggccctgctgacacccccacccaagaagtgcgcccaatcaacatgctctact 633

RESULT 100

AAx58652
ID AAx58652 standard; DNA; 789 BP.

XX AC AAx58652;

XX 16-AUG-1999 (first entry)

XX DE Bovine activin WC (BMP-11) partial DNA sequence.

XX KW Activin WC; bone morphogenetic protein 11; BMP-11; cattle; bovine;
KW bone; cartilage; connective tissue; neuronal tissue;
KW wound healing; tissue repair; vulnery; contraceptive;
KW transforming growth factor-beta; ds.

XX OS Bos taurus.

XX FH Key Location/Qualifiers
FT intron 322..323
FT /*tag= a

FT FT /partial
FT FT /note= "putative 3' end of intron"
FT CDS 324..704
FT FT /*tag= b

FT mat_peptide 375..701
FT FT /*tag= c

XX WO9924058-A2.

XX PN 20-MAY-1999.

XX PD 06-NOV-1998; 98WO-US23827.

XX PF 07-NOV-1997; 97US-0966297.

XX PR (GENY) GENETICS INST INC.

XX PA Celeste AJ, Thies SR, Wozney JM;

XX PI WPI; 1999-327207/27.

XX DR P-PSDB; AAY06096.

XX PT Administration of human or bovine bone morphogenetic protein 11

XX PS Example 1; Page 55; 62pp; English.

CC This is a partial nucleotide sequence of bovine activin WC, or
CC bone morphogenetic protein 11 (BMP-11). The DNA was isolated by
CC screening a bovine genomic library with a fragment of human BMP-7
CC DNA probe and with a mixed BMP-5, BMP-6 and BMP-7 probe; the
CC recombinant hybridised positively to the BMP-7 probe under reduced
CC stringency conditions and exhibited weak or no hybridisation to the
CC mixed probe under high stringency conditions. The clone includes
CC an open reading frame encoding at least 126 amino acids (see
CC AAY06096) of the C-terminal portion of bovine BMP-11 protein. This
CC is an example of a novel family of proteins of the transforming
CC growth factor beta superfamily. BMP-11 proteins may be useful to
CC induce bone and/or cartilage formation and in wound healing and
CC tissue repair, or for augmenting the activity of other BMP
CC proteins. BMP-11 may also be useful for regulating the production
CC of follicle stimulating hormone (e.g. for contraception), to

CC stimulate haematopoiesis, to suppress the development of gonadal
CC tumours, and especially (claimed) to induce neuronal cell
CC formation, growth differentiation, proliferation and maintenance.
XX
SQ Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other;

Query Match 15.3%; Score 51.8; DB 20; Length 789;
Best Local Similarity 54.9%; Pred. No. 1.4e-05;
Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgctgtgtggcccccctctacattgacttcgcagacaggatctctggctggaagtgg 96
Db 408 gagtccgcgtgttgcgcgtaccctcctcactgtgactttgaggcttttggctgggactgg 467

QY 97 gtccatgaacctaaagggtactatgccaaactctgtctcaggcccttggccatactccgc 156
Db 468 atcatgctcctaaacgctacaaggccaactactgctcccgccagtgcgagtacatgttt 527

QY 157 agtgacagacacacccacagcagtggtgctgggactgtacaacactctgaacctgaagca 216
Db 528 atgcaaaagtatccgcacacccacttggtgcaacaggct-----aacccaagaggc 578

QY 217 tctgctcgccttgctgctgccccagcactggagccccctgacctctgtact 271
Db 579 tctgcgggccctgctgacacccccacccaagaagtgcgcccaatcaacatgctctact 633

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Perfect score: 339
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Scoring table: IDENTITY_NUC
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Searched: 324599 seqs, 94655562 residues
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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8	302.2	89.1	2671	6 5168051-9
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15	204.6	60.4	339	3 US-09-123-233-1
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81	51	15.0	1822	1	US-08-480-528A-3	Sequence 3, Appli
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85	51	15.0	1822	1	US-08-643-563A-16	Sequence 16, Appl
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99	51	15.0	1822	3	US-08-278-730A-16	Sequence 16, Appl
100	51	15.0	1822	3	US-08-458-811-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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 ; Sequence 3B, Application US/08486057B
 ; Patent No. 5650494
 ; GENERAL INFORMATION:
 ; APPLICANT: Cerletti, Nico
 ; APPLICANT: McMaster, Gary K.
 ; APPLICANT: Cox, David
 ; APPLICANT: Schmitz, Albert
 ; APPLICANT: Meyhack, Bernd
 ; TITLE OF INVENTION: Process for Refolding Recombinantly
 ; Produced TGF-beta-like Proteins
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Henry P. No. 5650494ak
 ; STREET: 520 White Plains Road, P.O. Box 2005
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-9005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,057B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/201,703
 ; FILING DATE: 25-FEB-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/960,309
 ; FILING DATE: 13-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/621,502
 ; FILING DATE: 03-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 8927546.5
 ; FILING DATE: 06-DEC-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5650494ak, Henry P.
 ; REGISTRATION NUMBER: 33200
 ; REFERENCE/DOCKET NUMBER: 4-17861+/Cont3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 277-5110
 ; TELEFAX: (908) 277-4306
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 339 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..339
 ; US-08-486-057B-3

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Db	121	GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGTGCAGACACACACCCACGACG	180
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Db	181	GTGCTGGGACTGTACAACACTCTGAACCCCTGAAGCATCTGCCTCGCCTGCTGCGTGCCC	240
Qy	241	cagacactggagccctcgaccactctgtactatgttgggaggacccccaaagtggagcag	300
Db	241	CAGGACCTGGAGCCCTCGACCATCCTCTACTATGTGTTGGGAGGACCCCAAAAGTGGAGCAG	300
Qy	301	ctctccaaactgggtggaagtcttgtaaaatgagtga	339
Db	301	CTCTCCAACTGGTGGTGAAGACTCTTGTAAATGTAGCTGA	339
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	; Sequence 33, Application US/08470837		
	; Patent No. 5800811		
	; GENERAL INFORMATION:		
	; APPLICANT: Nimmi, Marcel E.		
	; APPLICANT: Hall, Frederick L.		
	; APPLICANT: Tuan, Tai-Lan		
	; APPLICANT: Wu, Lingtao		
	; APPLICANT: Cheung, David T.		
	; TITLE OF INVENTION: Transforming Growth Factor B Fusion		
	; TITLE OF INVENTION: and		
	; TITLE OF INVENTION: Their Use in Wound Healing		
	; NUMBER OF SEQUENCES: 34		
	; CORRESPONDENCE ADDRESS:		
	; ADDRESSEE: Merchant & Gould		
	; STREET: 11150 Santa Monica Boulevard, Suite 400		
	; CITY: Los Angeles		
	; STATE: California		
	; COUNTRY: USA		
	; ZIP: 90025-3395		
	; COMPUTER READABLE FORM:		
	; MEDIUM TYPE: Floppy disk		
	; COMPUTER: IBM PC compatible		
	; OPERATING SYSTEM: PC-DOS/MS-DOS		
	; SOFTWARE: PatentIn Release #1.0, Version #1.30		
	; CURRENT APPLICATION DATA:		
	; APPLICATION NUMBER: US/08/470,837		
	; FILING DATE:		
	; CLASSIFICATION: 424		
	; ATTORNEY/AGENT INFORMATION:		
	; NAME: Sharp, Janice A.		
	; REGISTRATION NUMBER: 34,051		
	; REFERENCE/DOCKET NUMBER: 30630-1US01		
	; TELECOMMUNICATION INFORMATION:		
	; TELEPHONE: 310-445-1140		
	; TELEFAX: 310-445-9031		
	; INFORMATION FOR SEQ ID NO: 33:		
	; SEQUENCE CHARACTERISTICS:		
	; LENGTH: 339 base pairs		
	; TYPE: nucleic acid		
	; STRANDEDNESS: double		
	; TOPOLOGY: linear		
	; MOLECULE TYPE: cdna		
	; FEATURE:		
	; NAME/KEY: CDS		
	; LOCATION: 1..336		
	; FEATURE:		
	; NAME/KEY: mat_peptide		
	; LOCATION: 1		
	US-08-470-837-33		

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Query Match      100.0%; Score 339; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgagcccccctc 60
   |||||||
Db 1 GCTTTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCTC 60
   |||||||

QY 61 tacattgactccgacagatgctggctggaagtgggtccatgaacctaaaggtactat 120
   |||||||
Db 61 TACATTGACTCCGACAGGATCGGCTGGAAGTGGTCCATGAACCTTAAGGGCTACTAT 120
   |||||||

QY 121 gcaaatctgtcagagcccttgccatcactccgcagtcgagacacaaacccacagcag 180
   |||||||
Db 121 GCCAACTTCTGCTAGGCGCTTGCCCATACCTCCGAGTGCAGACACAACCCACAGCAG 180
   |||||||

QY 181 gtgctgggactgtacaaactctgaacctgaacctgaacctgacctgctgctgctgccc 240
   |||||||
Db 181 GTGCTGGGACTGTACAACTCTGAACCTCGAAGCATCTGCCCTCGCCTTGCTGCGTGCC 240
   |||||||

QY 241 caggacctggagccctgacctcctgtactatgttggaggagcccccacaaagtggagcag 300
   |||||||
Db 241 CAGGACCTGGAGCCCTGACCATCTCTGTACTATGTGGGAGGAGACCCCAAGTGGAGCAG 300
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QY 301 ctctccaaactggtgagtgaaagtctgttaaatgtagctga 339
Db 301 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 3
US-08-789-588-3
; Sequence 3, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5

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; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; US-08-789-588-3

Query Match      100.0%; Score 339; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgagcccccctc 60
   |||||||
Db 1 GCTTTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCTC 60
   |||||||

QY 61 tacattgactccgacagatgctggctggaagtgggtccatgaacctaaaggtactat 120
   |||||||
Db 61 TACATTGACTCCGACAGGATCGGCTGGAAGTGGTCCATGAACCTTAAGGGCTACTAT 120
   |||||||

QY 121 gcaaatctgtcagagcccttgccatcactccgcagtcgagacacaaacccacagcag 180
   |||||||
Db 121 GCCAACTTCTGCTAGGCGCTTGCCCATACCTCCGAGTGCAGACACAACCCACAGCAG 180
   |||||||

QY 181 gtgctgggactgtacaaactctgaacctgaacctgaacctgacctgctgctgccc 240
   |||||||
Db 181 GTGCTGGGACTGTACAACTCTGAACCTCGAAGCATCTGCCCTCGCCTTGCTGCGTGCC 240
   |||||||

QY 241 caggacctggagccctgacctcctgtactatgttggaggagcccccacaaagtggagcag 300
   |||||||
Db 241 CAGGACCTGGAGCCCTGACCATCTCTGTACTATGTGGGAGGAGACCCCAAGTGGAGCAG 300
   |||||||

QY 301 ctctccaaactggtgagtgaaagtctgttaaatgtagctga 339
Db 301 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 4
US-09-123-233-5
; Sequence 5, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLu.m.hTGF-beta3 (DSM 5658)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta3"
US-09-123-233-5

Query Match 100.0%; Score 339; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactctccgaacttgagagagaactgctgtgccccctc 60
DB 1 GCTTTGGACACAAATTACTGCTTCGCAACTTGGAGGAGAAGTGTGTGCGCCCCCTC 60
QY 61 tacattgactccacagagatctggctggaagtgggtcccatgaacctaaaggctactat 120
DB 61 TACATTGACTTCCGACAGAGACTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaaactctgctcaggcccttgcccatctccgagctgcagacacacacacagcagc 180
DB 121 GCCAAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGTGCAGACACAAACCCACAGCAG 180
QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgctgcgcttgcgtgccc 240
DB 181 GTGCTGGGACTGTACAACACTCTGAACCTGAACCATCTGCTCGCCCTGTGCTGCGTGC 240
QY 241 cagacctggagccctgaacctctgactatgttggagagaccccaaaagtggagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTCTGACTATGTGGGAGAGACCCCAAAAGTGGAGCAG 300
QY 301 ctctccaacatggtggaagtcttggtaaatgtagctga 339
DB 301 CTCTCCAACATGGTGGTGAAGTCTTGTGTAATGTAGCTGA 339

METHODS OF PR
; Sequence 1, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2529 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Transforming Growth Factor-Beta 3
; IMMEDIATE SOURCE:
; CLONE: TGF-B3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 263..1498
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 263..1498
; OTHER INFORMATION:
PCT-US91-04541-1

Query Match 100.0%; Score 339; DB 5; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.2e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactctccgaacttgagagagaactgctgtgccccctc 60
DB 1163 GCTTTGGACACAAATTACTGCTTCGCAACTTGGAGGAGAAGTGTGTGCGCCCCCTC 1222
QY 61 tacattgactccgacagatctggctggaagtgggtcccatgaacctaaaggctactat 120
DB 1223 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 1282
QY 121 gccaaactctgctcaggcccttgcccatctccgagctgcagacacacacacagcagc 180
DB 1283 GCCAAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGTGCAGACACAAACCCACAGCAG 1342
QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgctgcgctgctgcccc 240
DB 1343 GTGCTGGGACTGTACAACACTCTGAACCTGAACCATCTGCTCGCCCTGTGCTGCGTGC 1402
QY 241 cagacctggagccctgacctctgactatgttggagagaccccaaaagtggagcag 300
DB 1403 CAGGACCTGGAGCCCTTGACCATCTCTGACTATGTGGGAGGAGACCCCAAAAGTGGAGCAG 1462
QY 301 ctctccaacatggtggaagtcttggtaaatgtagctga 339
DB 1463 CTCTCCAACATGGTGGTGAAGTCTTGTGTAATGTAGCTGA 1501

RESULT 6
5262319-1
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931

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; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO:1:
; LENGTH: 2529
; 5262319-1

Query Match 100.0%; Score 339; DB 6; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.2e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 60
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Db 1163 gcttggacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 1222
QY 61 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1223 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat 1282
QY 121 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagcacg 180
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Db 1283 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagcacg 1342
QY 181 gtctgggactgtacaacactctgaaccttgaaacctgaagcatctgcctgccttgcgtgcc 240
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Db 1343 gtctgggactgtacaacactctgaaccttgaaacctgaagcatctgcctgccttgcgtgcc 1402
QY 241 caggacctggagccctgacctctgtactatgttgaggagaccctcaagtgagcacg 300
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Db 1403 caggacctggagccctgacctctgtactatgttgaggagaccctcaagtgagcacg 1462
QY 301 ctctccaaacatggtggtgaagtcttgtaaatgtagctga 339
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RESULT 7
5168051-10
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:10:
; LENGTH: 2233
5168051-10

Query Match 96.0%; Score 325.4; DB 6; Length 2173;
Best Local Similarity 99.4%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 gcttggacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 60
|||||
Db 278 gcttggacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 337
QY 61 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 338 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat - 396
QY 121 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagcacg 180
|||||
Db 397 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagcacg 456
QY 181 gtctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgcc 240
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Db 457 gtctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgcc 516
QY 241 caggacctggagccctgacctctgtactatgttgaggagaccctcaagtgagcacg 300
|||||

Db 517 caggacctggagccctgacctatctgtactatgttggaggaccccccaagtggagcacg 576
QY 301 ctctccaaacatggtggtgaagtcttgaatgttagctga 339
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Db 577 ctctccaaacatggtggtgaagtcttgaatgttagctga 615

RESULT 8
5168051-9
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:9:
; LENGTH: 2671
5168051-9

Query Match 89.1%; Score 302.2; DB 6; Length 2671;
Best Local Similarity 93.2%; Pred. No. 1.3e-76;
Matches 316; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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Db 1159 gccctggacacaaactactgtctccgaacttgagagaaactgtgtgccccctc 1218
QY 61 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1219 tacattgacttcgcacaggaatcgggtggaagtgggtccatgaacctaaagggtactat 1278
QY 121 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagcacg 180
|||||
Db 1279 gccaaattctgtcaggcccttgccataacctccgcagtcgagacacaaaccacagctcg 1338
QY 181 gtctgggactgtacaacactctgaacctgaagcatctgcctgccttgcgtgcc 240
|||||
Db 1339 gtctgggactgtacaacactctgaacctgaagcatctgcctgcgtgcc 1398
QY 241 caggacctggagccctgacctctgtactatgttggaggaccccccaagtggagcacg 300
|||||
Db 1399 caggacctggagccctgacctctgtactacgtcgaggagaccgcccaagtggagcacg 1458
QY 301 ctctccaaacatggtggtgaagtcttgtaaatgttagctga 339
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Db 1459 ctctccaaacatggtggtgaagtcttgcagtgtagctga 1497

RESULT 9
US-09-123-233-7
; Sequence 7, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA of
DESCRIPTION: TGF-beta1 and TGF-beta3 DNA"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino
OTHER INFORMATION: acids of human TGF-beta1"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino
OTHER INFORMATION: acids of human TGF-beta3"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta named
TGF-beta1-3"
US-09-123-233-7

Query Match 87.8%; Score 297.6; DB 3; Length 336;
Best Local Similarity 92.9%; Pred. No. 1.4e-75;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgttcgcgaacttgaggaggaactgtgtgtgccccctc 60
DB 1 GCCCTGGACACCACTATTGCTTACGCTCCACGGAGAAAGAACTGCTGCGCGAGCTG 60
QY 61 tacattgacttcgcagacatctggctgggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGACTTCCGCAAGAGACCTCGGCTGGAAAGTCCACAGACCCCAAGGGCTACCAT 120
QY 121 gccaaactctgtcagggcccttgccatacctccgcagtgagacacacacacagcag 180
DB 121 GCCAACTTCTGCTCAGGCCCCITGCCCATACCTCCGAGTGAGACACACACAGCAGC 180
QY 181 gtgctggagactgtacacacactgtgaacctgaagcatctgctccttgcgtgccc 240
DB 181 GTGCTGGAGCTGTACACACTGTGAACCTTGAAGCATCTGCCCTGCTGCGTGCCTC 240
QY 241 cagaacctggagccctgaacctctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTTGGGAGGAGCCCCCAAAAGTGGAGCAG 300
QY 301 ctctccacatggtggtgaagtctgtgtaaatgtagc 336
DB 301 CTCTCCACATGGTGGTGAAGTCTGTGTAATGTAGC 336

RESULT 10
US-09-123-233-9
Sequence 9, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta2-3"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino
OTHER INFORMATION: acids of human TGF-beta2"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino
OTHER INFORMATION: acids of human TGF-beta3"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta2-3"
US-09-123-233-9

Query Match 81.7%; Score 276.8; DB 3; Length 336;
Best Local Similarity 89.0%; Pred. No. 1.1e-59;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgttcgcgaacttgaggaggaactgtgtgtgccccctc 60
DB 1 GCTTTGGATGCGGCCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCTACGTCCACTT 60
QY 61 taacttgacttcgcagcagatctgggtgggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCCAAGGGTACAAT 120
QY 121 gccaaactctgtcagggcccttgccatacctccgcagtgagacacacacacagcag 180
DB 121 GCCAACTTCTGCTCAGGCCCCITGCCCATACCTCCGAGTGAGACACACACAGCAGC 180
QY 181 gtgctggagactgtacacacactgtgaacctgaagcatctgctccttgcgtgccc 240
DB 181 GTGCTGGAGCTGTACACACTGTGAACCTTGAAGCATCTGCCCTGCTGCGTGCCTC 240
QY 241 caggacctggagccctgacctctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTTGGGAGGAGCCCCCAAAAGTGGAGCAG 300
QY 301 ctctccacatggtggtgaagtctgtgtaaatgtagc 336
DB 301 CTCTCCACATGGTGGTGAAGTCTGTGTAATGTAGC 336

RESULT 11
US-09-123-233-11
Sequence 11, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta3-2"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLu.M.TGF-beta3(44/45)beta2
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino
OTHER INFORMATION: acids of human TGF-beta3"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino
OTHER INFORMATION: acids of human TGF-beta2"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta3-2"
US-09-123-233-11

Query Match 70.8%; Score 240; DB 3; Length 336;
Best Local Similarity 82.1%; Pred. No. 2.7e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgccccctc 60
DB 1 GCTTGGACACAAATTACTGCTCCGCACTGGAGAGAACTGCTGTGCCCCCTC 60
QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGACTCCGACAGGATCTGGCTGGAGTGGGTCCATGAACCTTAAGGGCTACTAT 120
QY 121 gcaacttctgctcagcccttgccatacctcgcgagtcagacacacacacagcag 180
DB 121 GCCAATTCTGCTGGAGCATGCCGATATTATGAGTTCAGACACTCAGACACAGCAGG 180
QY 181 gtctggagactgtacacactctgaacctgaagcagctgctgcctgtctgctgccc 240
DB 181 GTCTGGAGCTTATATAATACCAATAATCCAGAAAGCATCTGCTTCTCTGCTGCGGTCC 240
QY 241 caggacctggagcccttgacctctgtactatgttggaggagagcccccacaaagtggagcag 300
DB 241 CAAGATTAGAACCTTAACCAATTCTACTACTATGCGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctccacatggtggtgaagtcttgaatatgtacg 336
DB 301 CTCTCTAATATGATTGATAAAGTCTTGCAAAATGCAGC 336

RESULT 12
US-08-470-837-29
Sequence 29, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould

STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30630-10501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1
US-08-470-837-29

Query Match 60.8%; Score 206.2; DB 1; Length 339;
Best Local Similarity 75.5%; Pred. No. 9.7e-50;
Matches 256; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgccccctc 60
DB 1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAAGAACTGCTGCTGGCAGCTG 60
QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCCATGAGCCCAAGGGCTACCAT 120
QY 121 gcaacttctgctcagcccttgccatacctcgcgagtcagacacacacacagcag 180
DB 121 GCCAATTCTGCTGGAGCATGCCGCTTACATTTGGAGCCTGGACACGACGACGACGAG 180
QY 181 gtctggagactgtacacactctgaacctgaagcagctgctgcctgtctgctgccc 240
DB 181 GTCTGGCCTGTACAAACACAGCATAAACCGGGCGCTCGGGCGGCCGCTGCTGCGTGGCG 240
QY 241 caggacctggagcccttgacctctgtactatgttggaggagagcccccacaaagtggagcag 300
DB 241 CAGCGCTGGAGCGCTGCCCATCTGTACTGTACTGTGGCCCGCAGCCCAAGGTGGAGCAG 300
QY 301 ctctccacatggtggtgaagtcttgaatatgtactga 339
DB 301 CTGTCCAAACATGATGCTGCGCTCTCTGCAAGTGCAGCTGA 339

RESULT 13
US-08-486-057B-1
Sequence 1, Application US/08486057B
Patent No. 5650494

GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-4306
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-486-057B-1

Query Match 60.4%; Score 204.6; DB 1; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttgaggagaactgtgtgtgccccctc 60
Db 1 GCCCTGGACACAACTATTGCTTACGCTCCACGGAGAGAAGTGTGCTGGCGAGCTG 60
Qy 61 tacattgacttcgcagacagatctgggtgggaagtgggtccatgaacctaaagggctactat 120
Db 61 TACATTGACTTCCGACGAGACTCGGCTGGAAGTGGATCCACAGACCCCAAGGGCTTACCAT 120
Qy 121 gccaaactctgctcaggcccttgccataacctccgcaagtgcagacacacaccacagcagc 180

Db 121 GCCAACTTCTGCTGGGCCCTGCCCCCTACATTTGAGGCTTGACACGCGAGTACAGCAAG 180
Qy 181 gtgctgggagctgtacaacactctgaacctctgaacctctgaacctctgctgtgctgctgccc 240
Db 181 GTCTGGCCCTGTACACACGAGCATAAACCGGGGCGCTCGGGCGCGCTGCTGCTGCTGCGGCGG 240
Qy 241 caggacctggagccctcgaccatcctgtactatgttggaggagaccccccaagtgagcag 300
Db 241 CAGGCGCTGGAGCGCTGCCCATCGTGTACTAGTGTGGCGGCAAGCCCAAGGTGGAGCAG 300
Qy 301 ctctccacatgtgtggtgaagtcttgttaataatgtagtga 339
Db 301 CTGTCCACATGATGTGGCTCTCTGCAAGTGCAGCTGA 339
RESULT 14
US-08-789-588-1
Sequence 1, Application US/08789588
Patent No. 5922846
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..339
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..339
US-08-789-588-1

Query Match 60.4%; Score 204.6; DB 2; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttggacaccaattactgtctccgaacttgaggagaactgtgtgtgccccctc 60
DB 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGTGTGCGTGGCGAGCTG 60

QY 61 tacattgacttcgcagagatctggctgggaagtgggtccatgaacctaaaggctactat 120
DB 61 TACATTGACTTCCGCAAGGACCTCGCTGGAAGTGATCCAGGACCCCAAGGCTACCAT 120

QY 121 gccaactctgtcaggcccttgccatcacctccgcagtcgagacacacccacagcag 180
DB 121 GCAACTTCTGCTCGGGCCCTGCCCTTACATTTGGAGCTGGACACGAGTACAGCAAG 180

QY 181 gtctgggactgtacaacactctgaacctgaacctgaacctgaacctgaacctgaacctga 240
DB 181 GTCTGGCCCTGTACAACACCAAGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 120

QY 121 gccaactctgtcaggcccttgccatcacctccgcagtcgagacacacccacagcag 180
DB 121 GCAACTTCTGCTCGGGCCCTGCCCTTACATTTGGAGCTGGACACGAGTACAGCAAG 180

QY 181 gtctgggactgtacaacactctgaacctgaacctgaacctgaacctgaacctgaacctga 240
DB 181 GTCTGGCCCTGTACAACACCAAGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 120

QY 241 caggacttgagccctgaccatctgtactatgttgaggagaccccaaaagtggagcag 300
DB 241 CAGGCGCTGGAGCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300

QY 301 ctctcaacatggtggaagtcttgaatatgtactga 339
DB 301 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGACGTGA 339

RESULT 15
US-09-123-233-1
Sequence 1, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE: 19910314
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.htGF-beta1 (DSM 5656)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta1"
US-09-123-233-1

Query Match 60.4%; Score 204.6; DB 3; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttggacaccaattactgtctccgaacttgaggagaactgtgtgtgccccctc 60
DB 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGTGTGCGTGGCGAGCTG 60

QY 61 tacattgacttcgcagagatctggctgggaagtgggtccatgaacctaaaggctactat 120
DB 61 TACATTGACTTCCGCAAGGACCTCGCTGGAAGTGATCCAGGACCCCAAGGCTACCAT 120

QY 121 gccaactctgtcaggcccttgccatcacctccgcagtcgagacacacccacagcag 180
DB 121 GCAACTTCTGCTCGGGCCCTGCCCTTACATTTGGAGCTGGACACGAGTACAGCAAG 180

QY 181 gtctgggactgtacaacactctgaacctgaacctgaacctgaacctgaacctgaacctga 240
DB 181 GTCTGGCCCTGTACAACACCAAGCTGGAAGTGGATCCACGAGCCCGCTGCTGGCGCG 240

QY 241 caggacttgagccctgaccatctgtactatgttgaggagaccccaaaagtggagcag 300
DB 241 CAGGCGCTGGAGCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300

QY 301 ctctcaacatggtggaagtcttgaatatgtactga 339
DB 301 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGACGTGA 339

RESULT 16
US-07-669-171-1
Sequence 1, Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669,171
FILING DATE: 19910314
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-159-999
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

Db 1919 CAGGGCGTGGAGCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGTTGGACGAG 1978
QY 301 ctctccaaacatggtggtgaagtctttaaataatgtagctga 339
Db 1979 CTGTCCAACATGATCGTGGCGCTCCTGCAAGTGCAGCTGA 2017
RESULT 19
US-07-669-171-3
; Sequence 3, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/D2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-669-171-3
Query Match 58.0%; Score 196.6; DB 1; Length 1569;
Best Local Similarity 73.7%; Pred. No. 7.9e-47;
Matches 250; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 1 qcttggacacaaataactgcttcgcaactggaggaactgctgtgagccccctc 60
Db 1104 GCCCTGGACACCAACTATTGCTCAGAAATGTCCAGGAAATGCTGCCTACGCTCGCCT 1163
QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaacctaaaggctactat 120
Db 1164 TACATTGATTTCAAGAGGATCTAGCTGGAAGTGTGATCCACGAGCCCAAGGCTACCAT 1223
QY 121 gccaaattctgctagggcccttgccatccatcccgagtcgagacacacccacagcaag 180
Db 1224 GCCAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGGACACGACGATACAGCAAG 1283
QY 181 gtgctgggactgtacaaactctgaacctgaacctgaagcatctgctctgctgctgccc 240
Db 1284 GTCCCTGGCCCTTACAAACAGATAACCCGGCGCTCGCGGCGCTGCTGCTGCGCG 1343
QY 241 caggacctggagccccctgacctctctgtactatgtgtgggagggaccccccaagtgagcag 300

Db 1344 CAGGGCTGGAGCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGTTGGACGAG 1403
QY 301 ctctccaaacatggtggtgaagtctttaaataatgtagctga 339
Db 1404 CTGTCCAACATGATCGTGGCGCTCCTGCAAGTGCAGCTGA 1442
RESULT 20
US-08-486-057B-2
; Sequence 2, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-486-057B-2
Query Match 53.7%; Score 182.2; DB 1; Length 339;
Best Local Similarity 71.1%; Pred. No. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;


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QY 1 gctttggacacaaattactgttccgcaacttggaggaagaactgtgtgtgccccctc 60
Db 1 GCTTTGGATGCGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTCAGTCCACTT 60
QY 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGTTGGAATGGATACAGAACCCCAAGGGTACAAT 120
QY 121 gcaacttctgtcagggccctgcccatactcccgagtcgacagacacacccacagcacg 180
Db 121 GCAAACTTCTGTGCTGGAGCATGCGCGTATTATGGAGTTCAGACACTCAGCACAGCAGG 180
QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcccc 240
Db 181 GTCTTGAGCTTATATAATACCAATAATCAGAAGCATCTGCTTCTCTGCTGCGTGTCC 240
QY 241 caggacctggagccctgacctctgtactatgttgaggagaccccaaaagtggagcag 300
Db 241 CAAGATTTAGAACCTCTACCAATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctccaaatggtggtgaagtcttctaataatgtagctga 339
Db 301 CTTTCTAATATGATTGTTAAAGTCTTGCAAAATGCAGCTAA 339
RESULT 21
US-08-470-837-31
; Sequence 31, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; FEATURE:
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; NAME/KEY: mat_peptide
; LOCATION: 1
; US-08-470-837-31
Query Match 53.7%; Score 182.2; DB 1; Length 339;
Best Local Similarity 71.1%; Pred. No. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 gctttgacacaaattactgttccgcaacttggaggaagaactgtgtgtgccccctc 60
Db 1 GCTTTGGATGCGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTCAGTCCACTT 60
QY 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGTTGGAATGGATACAGAACCCCAAGGGTACAAT 120
QY 121 gcaacttctgtcagggccctgcccatactcccgagtcgacagacacacccacagcacg 180
Db 121 GCAAACTTCTGTGCTGGAGCATGCGCGTATTATGGAGTTCAGACACTCAGCACAGCAGG 180
QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcccc 240
Db 181 GTCTTGAGCTTATATAATACCAATAATCAGAAGCATCTGCTTCTCTGCTGCGTGTCC 240
QY 241 caggacctggagccctgacctctgtactatgttgaggagaccccaaaagtggagcag 300
Db 241 CAAGATTTAGAACCTCTACCAATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctccaaatggtggtgaagtcttctaataatgtagctga 339
Db 301 CTTTCTAATATGATTGTTAAAGTCTTGCAAAATGCAGCTAA 339
RESULT 22
US-08-789-588-2
; Sequence 2, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
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; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; OTHER INFORMATION: /product= "human TGF-beta2"
US-08-789-588-2

Query Match 53.7%; Score 182.2; DB 2; Length 339;
Best Local Similarity 71.1%; Pred. No. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgaacttgaggagaactgctgtgtgcgccccctc 60
Db 1 GCTTTGGATGCGGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCACATT 60

QY 61 tacattgactccgacagatctggctgaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGGTGAATGGATACACGAACCCAAAGGGTACAAT 120

QY 121 gcaactctgctcagccctgcccatacctccgagtcagacacacacacacagcagc 180
Db 121 GCCAACTTCTGCTGAGCATGCCGCTATTATGAGGTTCAGACACTCAGACAGG 180

QY 181 gtgctgggactgtacaaactctgaacctgaagcactgctgcctgctgcctgctgcgc 240
Db 181 GTCCTGAGCTTATATAATACCAATAATCCAGAGCATCTGCTTCTCTCTGCTGCTGCC 240

QY 241 caggacctgagccccctgacctctgactatgttggaggagcccccaaaagtggagcag 300
Db 241 CAAGATTAGAACCTTAACCATTTCTTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300

QY 301 ctctcccaactggtggaagtctttaaagttagctga 339
Db 301 CTTTCTAATATGATGTTAAAGTCTTGCAAAATGCAGCTAA 339

RESULT 24
PCT-US94-03705-4
; Sequence 4, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; TITLE OF INVENTION: TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; OTHER INFORMATION: /product= "human TGF-beta2"
US-09-123-233-3

Query Match 53.7%; Score 182.2; DB 2; Length 339;
Best Local Similarity 71.1%; Pred. No. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgaacttgaggagaactgctgtgtgcgccccctc 60
Db 1 GCTTTGGATGCGGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCACATT 60

QY 61 tacattgactccgacagatctggctgaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGGTGAATGGATACACGAACCCAAAGGGTACAAT 120

QY 121 gcaactctgctcagccctgcccatacctccgagtcagacacacacacacagcagc 180
Db 121 GCCAACTTCTGCTGAGCATGCCGCTATTATGAGGTTCAGACACTCAGACAGG 180

QY 181 gtgctgggactgtacaaactctgaacctgaagcactgctgcctgctgcctgctgcgc 240
Db 181 GTCCTGAGCTTATATAATACCAATAATCCAGAGCATCTGCTTCTCTCTGCTGCTGCC 240

QY 241 caggacctgagccccctgacctctgactatgttggaggagcccccaaaagtggagcag 300
Db 241 CAAGATTAGAACCTTAACCATTTCTTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300

QY 301 ctctcccaactggtggaagtctttaaagttagctga 339
Db 301 CTTTCTAATATGATGTTAAAGTCTTGCAAAATGCAGCTAA 339

RESULT 23
US-09-123-233-3
; Sequence 3, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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Matches	241;	Conservative	0;	Mismatches	98;	Indels	0;	Gaps	0;
Qy	1	gctttggacacccaattactgtcttcgcgaacttgagagagaactgctgtgtgcgccccctc	60						
Db	1457	gctttggatcgggccctattgtttagaataatgcaggataattgctgctcagctccact	1516						
Qy	61	tacattgacttcgcacagatctggctgggaatgggtccatgaacctaaagggtactat	120						
Db	1517	tacattgattcaagaggatctagggtggaaatgatacagaacccaagggtacaat	1576						
Qy	121	gccaaactctgctcaggcccttgcccatacctccgcagtgacagacaacccacagacg	180						
Db	1577	gccaaactctgtgctggagcatgccgtatttatggagttcagacactcagcacagcag	1636						
Qy	181	gtcgtggagactgaacaacactgaacacctgaagcatctgctgcctgtgtcggtgcc	240						
Db	1637	gtcctgagcttatataacaccataatccagaagcatctgtctctctgtcggtgcc	1696						
Qy	241	caggacctggagccctgaccatctctgtactatgttggagagaccccaaatgtgagcag	300						
Db	1697	caagatttagaacctctaaccatctctctattattgtggcaaaacccaagaatgaacag	1756						
Qy	301	ctctccacaatcgtgtggtgaagtcttgttaaatgtagctga	339						
Db	1757	ctttctaataatgattgtaaagtcttgcaaatgcagctaa	1795						
RESULT	26								
	5221620-3								
	;Patent No. 5221620								
	;APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY								
	;TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING								
	;GROWTH FACTOR BETA-2								
	;NUMBER OF SEQUENCES: 16								
	;CURRENT APPLICATION DATA:								
	;APPLICATION NUMBER: US/07/446,020								
	;FILING DATE: 05-DEC-1989								
	;PRIOR APPLICATION DATA:								
	;APPLICATION NUMBER: 285,140								
	;FILING DATE: 16-DEC-1988								
	;APPLICATION NUMBER: 234,065								
	;FILING DATE: 18-AUG-1988								
	;APPLICATION NUMBER: 148,267								
	;FILING DATE: 25-JAN-1988								
	;APPLICATION NUMBER: 106,752								
	;FILING DATE: 06-OCT-1987								
	;SEQ ID NO:3								
	;LENGTH: 2207								
	5221620-3								
Query Match	53.3%;	Score	180.6;	DB	6;	Length	2207;		
Best Local Similarity	70.8%;	Pred. No.	2.9e-42;						
Matches	240;	Conservative	0;	Mismatches	99;	Indels	0;	Gaps	0;
Qy	1	gctttggacacccaattactgtcttcgcgaacttgagagagaactgctgtgtgcgccccctc	60						
Db	1095	gctttgatacggcctattgtttagaataatgcagataattgctgctcagctccact	1154						
Qy	61	tacattgacttcgcacagatctggctgggaatgggtccatgaacctaaagggtactat	120						
Db	1155	tacattgattccaagaggatctagggtggaaatgatacagaacccaagggtacaat	1214						
Qy	121	gccaaactctgctcaggcccttgcccatacctccgcagtgacagacaacccacagacg	180						
Db	1215	gccaaactctgtgctggagcatgccgtatttatggagttcagacactcagcacagcag	1274						
Qy	181	gtcgtggagactgaacaacacttgaaacctgaagcatctgctcgctgcgtgcgtgcc	240						
Db	1275	gtcctgagcttatataacaccataaacccagaagcatctgctctctgtgcgtgcc	1334						
Qy	241	caggacctggagccctgaccatctctactatgttgggagaccccaaatgtgagcag	300						


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; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
;
US-07-841-646-33

Query Match 15.2%; Score 51.6; DB 1; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 ctctacattgacttcgcagcagatctgggctgg---aagtgggtccatgaacctaaagggc 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 CTGTAGTGGACTTCAGCGCAGCTGGGCTGGGAGCTGGATCATCGCCCGCTCGAC 72

Qy 115 tactatgccaattctgtcagggcccttgccatactc-----cgacgtgcagc 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 TTCGAGCGCTACTACTGCTCCGAGGCTGCGAGTCCCTCTCGGGATCACTTCAACAGC 132

Qy 166 acaacccacagcagctgtgctgggactgtgtaaacacactctgaacccctgaagcatctgctcg 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 ACCAACCCAGCGCTGGTGGAGACCTCTGGTGAACACATGAACCCCGCAAGGTACCCAG 192

Qy 226 cctgtctgctgccccagacacctggagccctgaccatctgtactatgttgagagacc 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 CCCTGCTGGTGCCACCGAGCTGTCCGCCATCAGCATCTGTGTACCTGGACGAGAATTCC 252

Qy 286 cccaaagtggagcagctctcccaacatgggtg 315
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Db 253 ACCGTGGTGTGAAGAACTACCCAGGAGATG 282

RESULT 36
US-08-147-023-33
; Sequence 33, Application US/08147023
; Patent No. 5468845
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,023
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
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Db 133 ACCAACCCGCGTGTGTGAGACCCCTGTGTGAACATGAACCCCGGCAAGGTACCCAAG 192
Qy 226 ccttctgctgtccccagagactgagccctgaccatccttactatatttggggagacc 285
Db 193 CCTGTGCTGTCGCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGACGAGAATTCC 252
Qy 286 cccaagtggagcagctctcccaatggg 315
Db 253 ACCGTGGTGTGAAGAACTACCAAGGAGATG 282

RESULT 39
US-08-449-699A-33
; Sequence 33, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.-L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,699A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
; US-08-449-699A-33

Query Match 15.2%; Score 51.6; DB 2; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 cctcacatgtctccgacagatctggctgg--aagtgggtccatgaacctaaagggc 114
Db 13 CTGTACGTGGACTTCCAGCGCGAGCTGGGCTGGGACGACTGGATCATCGCCCGCTCGAC 72

Qy 115 tactatgccaacttctgctcaggcccttgccataacctc-----cgagtgagac 165
Db 73 TTGGAGCGCCTACTACTACTCTCCGAGCGTGCAGTTCCCTCTCGGGATCACTTCAACAGC 132
Qy 166 acaaccacagcagctgctgggactgtacaacactctgaacctgaagcatctgctcg 225
Db 133 ACCAACCCGCGTGTGTGAGACCCCTGTGTGAACATGAACCCCGGCAAGGTACCCAAG 192
Qy 226 ccttctgctgtccccagagactgagccctgaccatccttactatgttggggagacc 285
Db 193 CCTGTGCTGTCGCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGACGAGAATTCC 252
Qy 286 cccaagtggagcagctctcccaatggg 315
Db 253 ACCGTGGTGTGAAGAACTACCAAGGAGATG 282

RESULT 40
5496552-1
; Patent No. 5496552
; APPLICANT: KUBERASAMPATH, THANGAVEL; RUEGER, DAVID C.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,252
; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO: 1:
; LENGTH: 315
5496552-1

Query Match 15.2%; Score 51.6; DB 6; Length 315;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 cctcacatgtctccgacagatctggctgg--aagtgggtccatgaacctaaagggc 114
Db 13 ctgtacgtggacttccagcgcagctgggctgggacgtggtatcgcccccgtcgac 72
Qy 115 tactatgccaacttctgctcaggcccttgccataacctc-----cgagtgagac 165
Db 73 ttcgagcgtctactgtctccgagcgtccagttccctctgcggtatcattcaacagc 132
Qy 166 acaaccacagcagctgctgggactgtacaacactctgaacctgaagcatctgctcg 225
Db 133 accaaccacgcgtgtgagaccctgtgaaacacatgaaccccggaaggtacccaag 192
Qy 226 ccttctgctgtccccagagactgagccctgaccatccttactatgttggggagacc 285
Db 193 ccttctgctgtccccacagcgtgtccgccatcagcatgctgtacctgtgacctgacgagaattcc 252
Qy 286 cccaagtggagcagctctcccaatggg 315
Db 253 accgtgtgtgtgaagaactaccaggagatg 282

RESULT 41
US-07-718-274A-1
; Sequence 1, Application US/07718274A
; Patent No. 5284756
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia

```

; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/718,274A
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
; US-07-718-274A-1

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Query Match      15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

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QY 17 actgttcgcgaacttggaggagaactgtgtgtgccccctctacattgaacttcgac 76
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Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145
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QY 77 aggatctggctggaagtgggtccatgaacctgaaggctactatgcaactctgtctcag 136
   || || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGCTGGCAGGACTGGATCATCGCGCTGAAGCCTACGCCGCTACTACTGTGAGG 205
   || || || || || || || || || || || || || || || || || || || ||

QY 137 gcccttggccat-----acctccgcagtgacacacacccacagcacggtgtctgg 187
   || || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTATGATGAACGCCACCAACCGCCATCGTGAGG 265
   || || || || || || || || || || || || || || || || || || || ||

QY 188 gactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccccagacc 247
   || || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 325
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QY 248 tggagccctgaccatcctgtactatgttgggagggaccccccaagtggagcagctctcca 307
   || || || || || || || || || || || || || || || || || || || ||
Db 326 TCAATGCCATCTCCGCTCTACTTCCGATGACAGCTCCAACGCTCATCTCTGAAGAAATACA 385
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QY 308 acatggtgtg 318
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Db 386 GAAACATGGTG 396
RESULT 42
; Sequence 9, Application US/08163877
; Patent No. 5399677
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Murray, Beth
; APPLICANT: Wolfman, Neil
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/163,877
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170 x 8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
; US-08-163-877-9

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Query Match      15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

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QY 17 actgttcgcgaacttggaggagaactgtgtgtgccccctctacattgaacttcgac 76
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Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145
   || || || || || || || || || || || || || || || || || || || ||

QY 77 aggatctggctggaagtgggtccatgaacctgaaggctactatgcaactctgtctcag 136
   || || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGCTGGCAGGACTGGATCATCGCGCTGAAGCCTACGCCGCTACTACTGTGAGG 205
   || || || || || || || || || || || || || || || || || || || ||

QY 137 gcccttggccat-----acctccgcagtgacacacacccacagcacggtgtctgg 187
   || || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTATGATGAACGCCACCAACCGCCATCGTGAGG 265
   || || || || || || || || || || || || || || || || || || || ||

QY 188 gactgtacaacactctgaacctgaagcatctgcctgccttgcgtgccccagacc 247
   || || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 325
   || || || || || || || || || || || || || || || || || || || ||

QY 248 tggagccctgaccatcctgtactatgttgggagggaccccccaagtggagcagctctcca 307
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```

Db 326 TCAATGCCATCTCCGTCCTACTTCCATGATGACAGCTCCAAAGCTCATCTCTGAAGAAATACA 385
QY 308 acatggtggtg 318
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Db 386 GAAACATGGTG 396

RESULT 43

US-08-149-106-1
; Sequence 1, Application US/08149106
; Patent No. 5411941
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,106
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417

US-08-149-106-1

Query Match 15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
QY 17 actgtccgcacactggagggaactgctgtgctgcgccctctacattgacttcgcac 76
| | | | |
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145
| | | | |
QY 77 aggatctgggtggaagtgggtccatgaacctaagggtactatgccaaactctgtcag 136
| | | | |
Db 146 ACCTGGGTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCGCCTACTACTGTGAGG 205
| | | | |

QY 137 gccttgcccat-----acctccgcagtgagacacacacacacacagcagtgctg 187
| | | | |
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAAGCCACCAACACGCCATCGTGAGA 265
| | | | |
QY 188 gactgtacacactctgaaccctgaagcatctgcctcgccttctgctgctgccccagacc 247
| | | | |
Db 266 CGTGTGCCACTTCATCAACCCGAAACGGTGGCCCAAGCCCTGCTGTGCGCCACGAGC 325
| | | | |
QY 248 tggagccctgaccatccctgctactatgttgaggagaccccccaaaagtggagcagctctcca 307
| | | | |
Db 326 TCAATGCCATCTCCGTCCTACTTCCATGATGACAGCTCCAAAGCTCATCTCTGAAGAAATACA 385
| | | | |
QY 308 acatggtggtg 318
| | | | |
Db 386 GAAACATGGTG 396

RESULT 44

US-08-298-021-1
; Sequence 1, Application US/08298021
; Patent No. 5508263
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Heterodimeric Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-64023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,021
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,106
; FILING DATE: 11-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/718,274
; FILING DATE: 20-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 1..417
; US-08-298-021-1

Query Match 15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgagagaaactgctgtgtgcccctctacatgacttcgac 76
   || || || || || || || || || || || || || || || || || || ||
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctggctggaagtgggtccatgaacctaaaggtctactatgccaacttctgctcag 136
   || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGGCGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctccgagtgacagacacacccacagcagtgctgg 187
   || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAACGCCACCAACCCAGCCCATCGTGAGAGA 265

QY 188 gactgtacaaactctgaacccctgaagcatctgctcgccttgctgctgctgctgctgctgctg 247
   || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGCGAGC 325

QY 248 tggagccctgaccatctactatgtttggggagaccccccaagtgagcagctctcca 307
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Db 326 TCAATGCCATCTCCGCTCTACTTCGATGACAGCTCCAACGCTCATCTGAAGAAATACA 385

QY 308 acatggtggtg 318
   || || || || || || || || || || || || || || || || || || ||
Db 386 GAAACATGGTG 396

RESULT 45
US-08-360-914B-9
; Sequence 9, Application US/08360914B
; Patent No. 5756308
; GENERAL INFORMATION:
; APPLICANT: Neil M. WOLFMAN and John McCOY
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,914B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; LOCATION: 1..417
; US-08-298-021-1

Query Match 15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgagagaactgctgtgtgccccctctacatgacttcgac 76
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Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctggctggaagtgggtccatgaacctaaaggtctactatgccaacttctgctcag 136
   || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctccgagtgacagacacacccacagcagtgctgg 187
   || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAACGCCACCAACCGCCATCGTGCGAGA 265

QY 188 gactgtacaaactctgaacccctgaagcatctgctcgtcctgtgctgccccagacc 247
   || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGCGAGC 325

QY 248 tggagccctgaccatctctactatgtttggggagaccccccaagtggagcagctctcca 307
   || || || || || || || || || || || || || || || || || || ||
Db 326 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGCTCATCTGAAGAAATACA 385

QY 308 acatggtggtg 318
   || || || || || || || || || || || || || || || || || || ||
Db 386 GAAACATGGTG 396

RESULT 45
US-08-360-914B-9
; Sequence 9, Application US/08360914B
; Patent No. 5756308
; GENERAL INFORMATION:
; APPLICANT: Neil M. WOLFMAN and John McCOY
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,914B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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> REGISTRATION NUMBER: 25,447
> REFERENCE/DOCKET NUMBER: 27129/33199
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 312/474-6300
> TELEFAX: 312/474-0448
> TELEX: 25-3856
> INFORMATION FOR SEQ ID NO: 248:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 557 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: protein
> ORIGINAL SOURCE:
> ORGANISM:
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 66..548
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: residues 1-65
> OTHER INFORMATION: /label=EcoRI
> OTHER INFORMATION: /note="residues 1-65 comprise EcoRI site to beginning of pel
> OTHER INFORMATION: B."
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: AA 1-22
> OTHER INFORMATION: /label=pel B
> OTHER INFORMATION: /note="pel B is the leader sequence from the pectate lyase
> OTHER INFORMATION: gene of Erwinia carotovora."
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: AA 23-161
> OTHER INFORMATION: /label="Bone D"
> OTHER INFORMATION: /note="Bone D is the subunit of human osteogenic protein (see
> OTHER INFORMATION: U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, S
> OTHER INFORMATION: ID Nos: 1 and 2."
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: residues 549-557
> OTHER INFORMATION: /label=XhoI
> OTHER INFORMATION: /note="residues 549-557 comprise stop codon and XhoI site."
>
> US-08-621-803-248

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Query Match	15.0%;	Score 51;	DB 2;	Length 557;
Best Local Similarity	50.5%;	Pred. No.	8.2e-06;	
Matches 157;	Conservative	0;	Mismatches 145;	Indels 9;
Gaps	1;			
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Db	217	ACAGCAGCAGGACCAGGCGAGCCCTGTAAAGACGACGACTGTATGTCNAGCTTCCGAG	276	
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Qy	77	aggtatcgggctggaaagtgggtgccatgaacctaaaggctactatgccaaactttctgtctcag	136	
Db	277	ACCTGGGCTGCAGGACTGGATCATCGCGCTGAAGGCTAGCGCGCCTACTACTTGTAGG	336	
<hr/>				
Qy	137	gccctttgccoat-----acctcgcagtgcgagacacaacccccacgacggtgtgtg	187	
Db	337	GGGAGTGTGCCTTCCCCTCTGAACCTCTACATGAACGCCACCAACACGCGCATCGTCAGA	396	
<hr/>				
Qy	188	gactgtacaaactctgaacctgaacatctgctcgtccttgcgtgcgcccaagacc	247	
Db	397	CGCTGGTCCACTTCATCAACCCGGAAACGGGTGCCAAGCCCTGCTGTGGCCCCACGCAGC	456	
<hr/>				
Qy	248	tggagcccctgacctactgtacttatgttggaaggagacccccaaaagtggagcagctctcca	307	
Db	457	TCAATGCCATCTCCGTCTCTACTTCGATGACACTCCAAGCTCATCTCTGAAGAAATACA	516	
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Qy	308	acatgttgtgtg	318	
Db	517	GAACATGGTG	527	

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RESULT 49
US-09-271-970-1
: Sequence 1, Application US/09271970
: Patent No. 6242219
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Gavitt, Patrick D.
: TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
: FILE REFERENCE: 1103/11041US01
: CURRENT APPLICATION NUMBER: US/09/271,970
: CURRENT FILING DATE: 1999-03-18
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO 1
: LENGTH: 557
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (66)..(548)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(65)
: OTHER INFORMATION: /label= EcoRI /note="residues 1-65 comprise EcoRI
: OTHER INFORMATION: site to beginning of pel B."
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(22)
: OTHER INFORMATION: /label=pel B /note="pel B is the leader sequence
: OTHER INFORMATION: from the pectate lyase gene of Erwinia
: OTHER INFORMATION: carotovora."
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (23)..(161)
: OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
: OTHER INFORMATION: human osteogenic protein (see, U.S. Patent No. 6242219
: OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID No. 6242219
: OTHER INFORMATION: and 2."
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (549)..(557)
: OTHER INFORMATION: /label=xhoI /note="residues 549-557 comprise stop
: OTHER INFORMATION: codon and xhoI site."
: US-09-271-970-1

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[illegible]

*** TELETYPE NUMBER: 03 000,024

860 TCAATGCCATCTCCGTCTCTACTTCGATGACAGCTCCAAAGTCATCCTCA

860 TCAATGCCATCTCCG

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QY 308 acatggtggtg 318
Db 920 GAAACATGGTG 930

RESULT 57
US-08-147-023-10
; Sequence 10, Application US/08147023
; Patent No. 546845
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,023
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1004 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "OpIb"
; OTHER INFORMATION: /note= "OpIb - FUSION"
; US-08-147-023-10

Query Match 15.0%; Score 51; DB 1; Length 1004;
Best Local Similarity 50.5%; Pred No. 9.8e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttgaggagaaactgtgtgccccctctacattgacttcgcag 76
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Db 620 ACAGCAGCAGCGACGAGGAGGAGGCTGTGAAGAAGCAGCAGCTGTATGTGAGCTCCGAG 679

QY 77 aggtatctgggtggaagtgggtccatgaacctaaagggtactatgccaacttctgcag 136
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 ACCTGGGCTGGCAGGACTGGATCATCGGCGCTGAAGGCTACGCCGCTACTACTGTGAGG 739

QY 137 gcccttgcccat-----acctcccgagtgagacacacacacacagcaggtgctgg 187
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 740 GGGAGTGTGCCTTCCTCTGAACCTCTACATGAACGCCACCAACGCCCATCGTGCAGA 799

QY 188 gactgtacaacactctgaacctgaagcatctgccttgcctgctgctgccccagacc 247
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QY 248 tggagccctgaccatcctgtactatgttgggagagacccccaaagtggagcagctcca 307
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QY 308 acatggtggtg 318
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Db 920 GAAACATGGTG 930

RESULT 58
US-08-447-570-10
; Sequence 10, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1004 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cdna
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "OPIB"
; OTHER INFORMATION: /note= "OPIB - FUSION"
; US-08-447-570-10

Query Match 15.0%; Score 51; DB 1; Length 1004;
Best Local Similarity 50.5%; Pred. No. 9.8e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgcaacttggaggagaactgtgtgtgagcccccctctacattgacttcgac 76
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Db 620 ACAGCAGCAGCGACGAGGCGCTGTAAAGACGACGAGCTGTATGTCTCAGCTTCCGAG 679
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Db 680 ACCTGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTAGCGCGCTACTACTGTGAGG 739
QY 137 gcccttgcccat-----acctcgcgagtgagacacacacccacgacggtgtgg 187
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Db 740 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAAGGCCACCAACACGCCATCGTCAGA 799
QY 188 gactgtacaacactctgaacctgaagcatctgcctgcgcttctgtgcgtgccccagacc 247
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Db 800 CGCTGTGTCACCTTCATCAACCCGGAACGGTGGCCCAAGCCCTGCTGTGCGCCACGAGC 859
QY 248 tggagccctgaccatctgtactgtgtgtggagagaccccccaagtgagcagctctcca 307
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QY 308 acatggtgtg 318
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Db 920 GAAACATGGTG 930

RESULT 59
US-08-449-700-10
; Sequence 10, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
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; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1004 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "OPLB"
; OTHER INFORMATION: /note= "OPLB - FUSION"
;
US-08-449-700-10

Query Match 15.0%; Score 51; DB 2; Length 1004;
Best Local Similarity 50.5%; Pred. No. 9.8e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

Qy 17 actgtctccgcaacttgaggagaactgtgtgctgccccctctacattgacttcogac 76
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Db 620 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 679

77 aggatctctgggtggaagtgtccatgaacctaaagggtactactatgtccaaacttctctcag 136
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Db 680 ACCTGGGCTGGCAGGACTGGATCATCGGCCCTGAAGGCTACGCCGCTACTACTGTGAGG 739

137 gcccttgcccat-----acctccgcagtgcaagacacacacacacagcaggtgtctgg 187
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188 gactgtacaacactctgaacctgaagcatctgcctcgccttgcgtgctgccccagagacc 247
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248 tggagcccttgaccatcctgtactatgttgggagagaccccccaagtggagcagctctcca 307
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Db 860 TCAATGCCATCTCGTCTCTACTTCTGATGACAGCTCCAACAGCTCATCTCTGAAGAAATACA 919

308 acatggtggtg 318
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Db 920 GAAACATGGTG 930

RESULT 60
US-08-449-699A-10
; Sequence 10, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,699A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1004 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
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; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1224
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Op1d"
; OTHER INFORMATION: /note= "Op1d - FUSION"
;
; US-08-447-570-14

Query Match 15.0%; Score 51; DB 1; Length 1277;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 137; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaactgtgtgtgcccctctacatgaacttcgac 76
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Db 893 ACAGCAGCAGCGACGAGCGCCTGTGAAGAGCAGCAGCTGTATGTGAGCTTCCGAG 952

QY 77 agaatctgggtggaagtgggtccatgaacctaaagggtactatgccaactctgtcag 136
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QY 137 gcccttgccat-----acctcgcagtgagacacacacacacacagtggtg 187
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QY 188 gactgtacaacactctgaacccctgaagcatctgctcgcctctgtgctgcccagacc 247
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Db 1073 CGTGTCTCACTTCATCAACCCGGAACCGTGCCCAAGCCTGCTGTGCGCCACGAGC 1132

QY 248 tggagcccttgaccatctctactatgttggaggagaccccaagtggagcagctccca 307
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QY 308 acatggtggtg 318
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Db 1193 GAAACATGGTG 1203

RESULT 65
US-08-449-700-14
; Sequence 14, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; TELECOMMUNICATION INFORMATION:
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; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,023
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
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; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
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; APPLICATION NUMBER: US 422,613
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: FITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1452 /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Op1c"
; OTHER INFORMATION: /note= "Op1c - FUSION"
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US-08-147-023-12

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Query Match          15.0%; Score 51; DB 1; Length 1505;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgcaactggaggagaactgctgtgtgcccctctacattgacttcgcac 76
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Db 1121 ACAGCAGCAGCAGCAGCAGCAGCCTGTAAAGACGACGAGCTGTATGTACAGCTTCGAG 1180

QY 77 aggatctgggctggaagtgggtccatgaacctaaaggctactatgccaactctctcag 136
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Db 1181 ACCTGGCTGGCAGAGCTGGATCATCGCGCTGAAGCTACGCGCGCTACTACTGTGAGG 1240

QY 137 gcccttggccat-----acctcgcagtgacagacacacacacacagcagtgctgg 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1241 GGGAGTGTGCTTCCTCCCTCTGAACCTCTTACATGAACGACCAACGACGCTCGTGAGA 1300

QY 188 gactgtacaacactctgaaccctgaagcatctgcctgccttgcctgctgccccagacc 247
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Db 1301 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGACG 1360

QY 248 tggagccccctgaccatctctactatgttggaggagcccccaaaagtggagcagctccca 307
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Db 1361 TCAATGCCATCTCGTCTCTACTTCTGATGACAGCTCCAACGTCATCTGAAGAAATACA 1420

QY 308 acatggtggtg 318
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Db 1421 GAAACATGGTG 1431

RESULT 73
US-08-447-570-12
; Sequence 12, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
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> APPLICATION NUMBER: US 621,849
> FILING DATE: 04-DEC-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 616,374
> FILING DATE: 21-NOV-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 600,024
> FILING DATE: 18-OCT-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 599,543
> FILING DATE: 18-OCT-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 579,865
> FILING DATE: 07-SEP-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 569,920
> FILING DATE: 20-AUG-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 483,913
> FILING DATE: 22-FEB-1990
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 422,613
> FILING DATE: 17-OCT-1989
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 315,342
> FILING DATE: 23-FEB-1989
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 232,630
> FILING DATE: 15-AUG-1988
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 179,460
> FILING DATE: 08-APR-1988
> ATTORNEY/AGENT INFORMATION:
> NAME: PITCHER, EDMUND R.
> REGISTRATION NUMBER: 27,829
> REFERENCE/DOCKET NUMBER: CRP-001CP6
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 617/248-7000
> TELEFAX: 617/248-7100
> INFORMATION FOR SEQ ID NO: 12:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 1505 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: cDNA
> HYPOTHETICAL: YES
> ANTI-SENSE: NO
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 1..1452
> OTHER INFORMATION: /function="OSTER
> OTHER INFORMATION: /product="OPIC"
> OTHER INFORMATION: /note="OPIC - 12
US-08-447-570-12

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	Query Match	15.0%	Score 51;	DB 1;	Length 1505;
	Best Local Similarity	50.5%;	Pred. No. 1.1e-05;		
	Matches 157;	Conservative 0;	Mismatches 145;	Indels 9;	Gaps 1;
Qy 17	actcttccgcacacttgagagagaactgctgtgtgcgccccctctacattgaacttcagac	76			
Db 1121	ACAGCAGGCGCACGAGGCGGCTGTAAAGACGACGAGCTGTATCTCAGCTTCCGAG	1180			
Qy 77	aggatctgggctggaagtgggtcccatgaactaaagggtctactatgccaaactctctgctcaag	136			
Db 1181	ACCTGGGCTGCGAGGACTGGATCATCGCGCCTGAAGGCTACGCCGCTACTACTGTGAGG	1240			
Qy 137	gcccttggccat-----acctccgcagctgcagacacacacccacagcagcgtgctcgg	187			
Db 1241	GGGAGTGTGCCTTCCTCTGAACTCCCTACATGAAGCGCCACCAACACGCCCATCTGTCGAGA	1300			

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Qy 188 gactgtacaacactgaacctgaagcattctgcctctgccttgcctgctgcctgaagc 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1301 CGCTGGTCCACCTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCACGCAGC 1360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 248 tggagcccttgaccatctctgttactatgttggaggagacccccaaaagtggagcagctctcca 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1361 TCAATGCCATCTCCGCTCTCTACTTCGTATGACAGCTCCCAACGTCATCTCTGAAGAAATACA 1420
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Qy 308 acatggtggtg 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1421 GAAACATGGTG 1431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 74
US-08-449-700-12
; Sequence 12, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 18-OCT-1990

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; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1452
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "OPIC"
; OTHER INFORMATION: /note= "OPIC - FUSION"
;
US-08-449-700-12

Query Match 15.0%; Score 51; DB 2; Length 1505;
Best Local Similarity 50.5%; Pred. No. 1.le-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

Qy 17 actgtctcgcaacttgaggagaaactctgtgctgccccctctacattgacttccgac 76
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Db 1121 ACAGCAGCGGACGAGGAGGCGCTGTAGAGACGACGAGCTGTATGTCAGCTTCCGAG 1180

Qy 77 aggtatctgggctggaagtgggtccatgaacctaaaggctactatgccaaacttctgctcag 136
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Db 1181 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGGCTACTACTGTGAGG 1240

Qy 137 gcccttgcccat-----acctccgcagtcagacacaaacccacagcagtgctg 187
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Db 1241 GGGAGTGTGCTTCCCTGTGAACCTCTACATGAACGCCACCAACGCCCATCGTGCGAGA 1300

Qy 188 gactgtcaaacactctgaacctgaagcatctgctgcctctgtgctgccccagagacc 247
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Db 1301 CGCTGGTCCATTTCATCAACCCGGAACGGTGGCCAAAGCCCTGCTGTGCGGCCACGAGC 1360

Qy 248 tggagccctgaccatctgtactatgttggaggagacccccaaaagtggagcagctctcca 307
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Db 1361 TCAATGCCATCTCGTCTCTACTTCGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 1420

Qy 308 acatggtggtg 318
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Db 1421 GAAACATGGTG 1431

RESULT 75
US-08-449-699A-12
; Sequence 12, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN

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APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE, 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901.703
FILING DATE: 19920616
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "Op1"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Op1"
US-07-901-703-1

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
Qy 17 actgtccgcaacttgagagaactctgtgtgcccctctacattgaactccgac 76
Db 1010 ACAGCAGCAGGACGACGAGGAGGCGCTAGAGAGCAGAGCTGTATGTACAGCTTCCGAG 1069
Qy 77 aggatctgggtggaagtgggtccatgaacctaaagggctactatgccaaactctgctcag 136
Db 1070 ACTTGGGCTGGCAGACTGGATCATCGGCGCTGAAGGCTAGCCGCTACTACTGTGAGG 1129
Qy 137 gcccttgcccat-----acctccagctgcagacacacccacagcaggtgctgg 187
Db 1130 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAAGCGCCACCAACCCAGCCCTCGTGCAGA 1189
Qy 188 gactgtacaacacttgaaacctgaagatctgctcgttgctgctgccccagacc 247
Db 1190 CGTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGTGTGCGCCACGACG 1249
Qy 248 tggagccctgaccatctctgactatgttggaggagaccccaagtgagcagctctcca 307
Db 1250 TCAATGCCATCTCGTCTCTACTTCGATGACAGCTCAACGTCATCTCTGAAGAAATACA 1309

Qy 308 acatggtggtg 318
Db 1310 GAAACATGGTG 1320
RESULT 78
US-08-147-023-1
Sequence 1, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:


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; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "hOpl-pp"
; OTHER INFORMATION: /note= "hOpl cDNA"
;
US-08-479-666-3

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps

QY 17 actgttcgcgaacttgagagagaactgctgtgccccctctacattgaattccgac 76
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Db 1010 ACAGCAGCAGCAGCAGAGGCGGCTTAAGAAAGCAGCAGCTGTATGTCTCCGAG 1069
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QY 77 aggatctggctggaagtgggtccatgaacctaaaggtcactatgccaaactctgctcag 136
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QY 137 gaccttgcccat-----acctccgcagtgagacacacccacagcacggtgctgg 187
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QY 188 gactgtacaacactctgaacctgaagcatctgctcgcttgcgttgcgtgccccaggacc 247
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QY 248 tggagcccttgaccatcctgtactactgttggggaggacccccaaagtggagcagctctcca 307
   || || || || || || || || || || || || || || || || || || ||
Db 1250 TCAATGCCATCTCCGCTCTACTTCGATGATGACGTCCAACGTCATCTTGAAGAAATACA 1309
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QY 308 acatggtggtg 318
   || || || || || || || || || || || || || || || || || || ||
Db 1310 GAAACATGGTG 1320
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RESULT 83
US-08-155-343A-16
; Sequence 16, Application US/08155343A
; Patent No. 5656593
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: FANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
; TITLE OF INVENTION: REGENERATION.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,343A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100

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; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-155-343A-16

Query Match          15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

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QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaactctctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCGCCTACTACTGTGAGG 1129

QY 137 gcccttgcccat-----acctccgcagtgccagacacacacacacacaggtgctgg 187
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QY 188 gactgtacaaactctgaacctgaacctgaacctgaacctgaacctgaacctgaacctga 247
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Db 1190 CGCTGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGGCGCCACGCGAG 1249

QY 248 tggagccctgaccatctgtactatgttggaggagaccccccaaaagtggagcagctctcca 307
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QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 85
US-08-643-563A-16
; Sequence 16, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 752,857
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 667,274
; FILING DATE: 11-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-060CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-406-672-16

Query Match          15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaactggagggaactgctgtgtgcgccccctctacattgacttcgcac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCGCCTACTACTGTGAGG 1129

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Db 1130 GGGAGTGTGCTTCCTCTGAACCTCTACATGAACGCCACCAACCGCATCGTGCAGA 1189

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Db 1190 CGCTGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGGCGCCACGCGAG 1249

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QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 85
US-08-643-563A-16
; Sequence 16, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
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; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "hOPI-PP"
; OTHER INFORMATION: /note= "hOPI cDNA"
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US-08-901-200A-3

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps

QY 17 actgtcttcgcgaacttgaggagaaactgtgtgtcgccccctctacattgacttcgcag 76
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QY 77 aggatctggctggaagtgtgtccatgaacctaaagggtactactatgccaacttctgctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCCTGAAGGTCACGCCGCTTACTGTGAGG 1129

QY 137 gcecttgccat-----acctccgcagtgccagacacccacagcacggtgctgg 187
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Db 1130 GGGAGTGTGCCTTCCTCTGAACCTCTACATGAACGCCACCAACGCCATCTGTGAGA 1189

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Db 1190 CGCTGGTGCACCTTCATCAACCCGGAACGGTGCCCAAGCCCTGTGTGCGCCACGCAGC 1249

QY 248 tggagccctgaccatcctgtactatgttgggagagacccccaaagtgagcagctctcca 307
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Db 1250 TCAATGCCATCTCCGCTCTTACTTCGATGACAGCTCCAAGCTCATCTCTGAAGAAATACA 1309

QY 308 acatggtggtg 318
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Db 1310 GAACATGGTG 1320

RESULT 93
US-08-481-337A-9
; Sequence 9, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: SAMPATH, Kuber T.
;
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; TITLE OF INVENTION: Surface Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.

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; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
;
US-08-481-337A-9

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttgaggagaaactgtgtgtgcgccccctctacattgacttcgcac 76
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DB 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaactcttctcag 136
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DB 1070 ACCTGGGTGGCAGGACTGGATCATCGCGCCTGAAGCTACGCCGCTACTACTGTGAGG 1129
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QY 137 gcccttgccat-----acctcgcagtcgcagacacacacacacacacacacacac 187
   | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1130 GGGAGTGTGCCTTCCCTCTGTGAACCTCTATGAACGCCCAACCAACCAACCAACCA 1189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 188 gactgtacacactctgaacctgaagcatctgcctcgctgtcgtgcgtgcgtgcgtgcgt 247
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DB 1190 CGCTGGTCCACTTCATCAACCGCGGAACGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1249
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QY 248 tggagccctgaccatcctgtactattgtggaggagcccccccaagtgagcagcgtctcca 307
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DB 1250 TCAATGCCATCTCCGTCCTTACTTCGATGACAGCTCCAACGCTCATCTCTGAAGAAATACA 1309
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QY 308 acatggtggtg 318
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DB 1310 GAAACATGGTG 1320

RESULT 94
US-08-449-700-1
; Sequence 1, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKANAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
; US-08-449-700-1

Query Match          15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaactgtgtgctgcgccctctacattgacttcgac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctgggtggaagtgggtccatgaacctaaaggctactatgcaacttctgctcag 136
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Db 1070 ACCTGGCTGGCAGGACTGGATCATCGCGCTGAAGCCTAGCGCGCTACTACTGTGAGG 1129

QY 137 qccttgcctccat-----acctccgcagtgacacacacccacacagcgtgtcg 187
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Db 1130 GGGAGTGTGCTTCCCTCTGAACTCTACATGACGCGCCACCAACCGCCATCGTGCGAGA 1189

QY 188 gactgtacaacactctgaacctctgaagcatctgctcgccttgcgtgcgccaggacc 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCTGCTGTGCGCCACGCGAGC 1249

QY 248 tggagccctgacctctctgtactatgttggaggagacccccaaagtggagcagctctcca 307
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Db 1250 TCAATGCCATCTCCGCTCTACTTCTGATGACAGCTCCAAAGTCTCAAGTCTCAAGAAATACA 1309

QY 308 acatggtgtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 96
US-08-449-699A-1
; Sequence 1, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,699A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
; US-08-449-699A-1

Query Match          15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaactgtgtgctgcgccctctacattgacttcgac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctgggtggaagtgggtccatgaacctaaaggctactatgcaacttctgctcag 136
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Db 1070 ACCTGGCTGGCAGGACTGGATCATCGCGCTGAAGCCTAGCGCGCTACTACTGTGAGG 1129

QY 137 qccttgcctccat-----acctccgcagtgacacacacccacacagcgtgtcg 187
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Db 1130 GGGAGTGTGCTTCCCTCTGAACTCTACATGACGCGCCACCAACCGCCATCGTGCGAGA 1189

QY 188 gactgtacaacactctgaacctctgaagcatctgctcgccttgcgtgcgccaggacc 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCTGCTGTGCGCCACGCGAGC 1249

QY 248 tggagccctgacctctctgtactatgttggaggagacccccaaagtggagcagctctcca 307
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Db 1250 TCAATGCCATCTCCGCTCTACTTCTGATGACAGCTCCAAAGTCTCAAGTCTCAAGAAATACA 1309

QY 308 acatggtgtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 96
US-08-696-268B-3
; Sequence 3, Application US/08696268B
; Patent No. 5968752
; GENERAL INFORMATION:
; APPLICANT: ICHIJIO, HIDENORI
; APPLICANT: NISHITOH, HIDEKI
; APPLICANT: SAMPATH, KUBER T.
; TITLE OF INVENTION: NOVEL SIGNALING RECEPTOR FOR
; TITLE OF INVENTION: MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,268B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "Osteogenic Protein"
; OTHER INFORMATION: /product= "Op1"
; OTHER INFORMATION: /standard_name= "Op1"
;
US-08-696-268B-3

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttggaggagaactgtgtgtgccccctctacattgacttcgcac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctggctgggaagtgggtccatgaacctaaagggtactatgccaacttctgctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCGCGCTGAAGGCTACGCGCTACTACTGTGAGG 1129

QY 137 gcccttgcccat-----acctccgagtgagacacacacacacacagcgtgtctgg 187
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Db 1130 GGGAGTGTGCTTCCTCCCTCTGAACCTCTACATGAACGCCACCAACACGCTATGTCGAGA 1189

QY 188 gactgtacacactctgaacctgaagcactctgcctgccttgcgtgctgccccagacc 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 1249

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Db 1250 TCAATGCCATCTCCGCTCTACTTCGATGACAGCTCCAAAGCTACCTCTGAAGAAATACA 1309

QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 97
US-08-461-397A-16
; Sequence 16, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; Sequence 15, Application US/08912088
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; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
;
US-08-461-397A-16

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

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QY 77 aggatctggctgggaagtgggtccatgaacctaaagggtactatgccaacttctgctcag 136
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QY 137 gcccttgcccat-----acctccgagtgagacacacacacacacagcgtgtctgg 187
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 1249

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RESULT 98
US-08-912-088-16
; Sequence 16, Application US/08912088
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	Best Local Similarity	50.5%;	Pred. No. 1.2e-05;		
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QY	77	aggatctgggctggaagtgggtccatgaacctaaagggtctactatgccaaactcttgcctcag	136		
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QY	137	gcctctggccat-----acctccgagtcgagacacaaacccacagacggtgctgg	187		
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	Query Match	15.0%;	Score 51;	DB 3;	Length 1822;
	Best Local Similarity	50.5%;	Pred. No. 1.2e-05;		
	Matches 157;	Conservative 0;	Mismatches 145;	Indels 9;	Gaps 1;
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Qy 308 acatggtggtg 318
Db 1310 GAAACATGGTG 1320

RESULT 100
US-08-458-811-1
; Sequence 1, Application US/08458811
; Patent No. 6027743
; GENERAL INFORMATION:
; APPLICANT: KHOURI, ROGER K.
; APPLICANT: SAMPATH, KUBER T.
; APPLICANT: RUEGER, DAVID C.
; TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT
; TITLE OF INVENTION: BODY PARTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,811
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
US-08-458-811-1

Query Match 15.0%; Score 51; DB 3; Length 1822;

Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
Qy 17 actgtctccgcaacttgaggagaaactgctgtgtgcgccccctctacattgacttccgac 76
Db 1010 ACAGCAGCAGCGACGACGAGCGCCTGTAAGAAGCAGCAGCTGTATGTCTAGCTTCCGAG 1069
Qy 77 aggatctgggctggaagtgggtcccatgaacctaaagggtactatgccaacttctgctcag 136
Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGCTACGCGCCTACTACTGTGAGG 1129
Qy 137 gcccttgcccat-----acctccgcaagtgcagacacaaacccacagcagcgtgtg 187
Db 1130 GGGAGTGTGCTTCCCTCTGAACCTCTTACATGAACGCCACCAACGCGCCATCTGCAGA 1189
Qy 188 gactgtacaacactctgaacccctgaagcatctgcctgccttctgctgcgtgccccagacc 247
Db 1190 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCTCAAGCCCTGCTGTGCGCCACGCGAGC 1249
Qy 248 tggagccctgaccatccctgactatgttggaggagcccccagaagtggagcagctctcca 307
Db 1250 TCAATGCCATCTCCGTCCTCTACTTCGTGACAGCTCCACAGTCATCCTGAAGAAATACA 1309
Qy 308 acatggtggtg 318
Db 1310 GAAACATGGTG 1320

Search completed: October 30, 2001, 11:50:43
Job time: 4305 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: October 30, 2001, 09:12:22 ; Search time 1009.83 Seconds
 (without alignments)
 3173.324 Million cell updates/sec

Title: TGFB3N
Perfect score: 339
Sequence: 1 gctttgacaccaattactg.....agttctgtaaatgtagctga 339

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	291	85.8	812	174	BG175423	BG175423
4	286.2	84.4	503	150	BF542567	BF542567
5	279	82.3	1820	144	BF101203	BF101203
6	257.4	75.9	477	119	AW670561	AW670561
7	234.8	69.3	560	13	AA915041	AA915041
8	224.6	66.3	966	175	BG244370	BG244370
9	224.2	66.1	509	121	AW23286	AW23286
10	207.6	61.2	530	10	AA657145	AA657145
11	204.6	60.4	505	122	AW58056	AW58056
12	204.6	60.4	598	104	AI951831	AI951831
13	204.6	60.4	600	168	BF726995	BF726995
14	203	59.9	727	16	AI131171	AI131171
15	201.8	59.5	480	16	AI089904	AI089904
16	201.4	59.4	572	111	AW073988	AW073988
17	200.4	59.1	471	150	BE543086	BE543086
18	198.2	58.5	474	138	BE645704	BE645704
19	198.2	58.5	568	136	BE644068	BE644068
20	198.2	58.5	785	16	AI148173	AI148173
21	197.8	58.3	646	117	AW512491	AW512491
22	196.8	58.1	546	24	AI760533	AI760533
23	195.8	57.8	578	103	AI927187	AI927187
24	193.6	57.1	589	104	AI991139	AI991139
25	193.6	57.1	778	24	AI743724	AI743724
26	193.4	57.1	431	174	BG180040	BG180040
27	193.4	57.1	608	173	BG067564	BG067564
28	193.4	57.1	681	18	AI323791	AI323791
29	191.8	56.6	510	122	AW919738	AW919738
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31	191.8	56.6	529	146	BF287476	BF287476
32	190.2	56.1	573	18	AI323392	AI323392
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35	188	55.5	466	118	AW627667	AW627667
36	184.4	54.4	505	20	AI433146	AI433146
37	183.8	54.2	431	1	AA000733	AA000733
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42	178.6	52.7	460	23	AI654506	AI654506
43	176	51.9	339	16	AI157673	AI157673
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55	168.6	49.1	328	19	AI360877	AI360877
56	165.6	48.8	292	18	AI272940	AI272940
57	160.4	47.3	499	18	AI273619	AI273619
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59	155.4	45.8	583	156	C86879	C86879
60	152.8	45.1	576	107	AU016729	AU016729
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62	151.6	44.7	431	191	W98872	W98872
63	151.4	44.7	996	168	BF682484	BF682484
64	146.2	43.1	403	22	AI604914	AI604914
65	145.2	42.8	267	118	AW600938	AW600938
66	144	42.5	558	1	AA021815	AA021815
67	143.6	42.4	889	155	BG540633	BG540633

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c 69	140.2	41.4	348	17	AI192407	AI192407 qc9bc09.x
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c 71	138	40.7	261	118	AW600940	AW600940 RC1-BN001
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c 73	136.4	40.2	456	159	N55274	N55274 YV46005.s1
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c 75	135.2	39.9	878	107	AU050770	AU050770 AU050770
c 76	134.6	39.7	392	103	AI918883	AI918883 tui3b10.x
c 77	134.2	39.6	542	8	AA533093	AA533093 n19a04.s
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c 81	130.4	38.5	465	107	AU016439	AU016439 AU016439
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c 83	127.4	37.6	301	190	W70801	W70801 me44c04.r1
c 84	125.2	36.9	560	159	N36741	N36741 YX90e06.f1
c 85	124.6	36.8	396	20	AI452742	AI452742 tJ45a05.x
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c 87	123	36.3	533	1	AA016946	AA016946 mh35a12.r
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c 89	122.4	36.1	398	187	R36467	R36467 yH88a11.s1
c 90	122	36.0	259	118	AW600942	AW600942 RC1-BN001
c 91	117.6	34.7	288	23	AI689283	AI689283 tx93b05.x
c 92	115.8	34.2	867	145	BF161473	BF161473 601770461
c 93	114.2	33.7	639	168	BF723491	BF723491 mab32f06
c 94	113.6	33.5	684	166	BE377489	BE377489 601228968
c 95	112	33.0	175	164	BE157967	BE157967 MR2-HT037
c 96	112	33.0	255	171	BF901708	BF901708 CM2-MT019
c 97	111	32.7	428	13	AA927529	AA927529 om71a11.s
c 98	110.4	32.6	248	118	AW579188	AW579188 RC1-DT002
c 99	110	32.4	266	118	AW600960	AW600960 RC1-BN001
c 100	109.8	32.4	379	169	BF769366	BF769366 RC3-IT001

ALIGNMENTS

RESULT 1
 AL532438 964 bp mRNA EST 13-FEB-2001
 LOCUS LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODM014YD15 5
 DEFINITION prime, mRNA sequence.

ACCESSION AL532438.1 GI:12795931
 VERSION AL532438.1
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 964)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers
 1. 964

FEATURES
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODM014YD15"
 /clone_lib="LTI_NFL001_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com" 2 others

BASE COUNT 245 a 248 c 269 g 200 t
 ORIGIN

Query Match 100.0%; Score 339; DB 106; Length 964;
 Best Local Similarity 100.0%; Pred. No. 8.1e-86;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtccgcaacttgagagaaactgctgtgccccctc 60
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 Db 311 GCTTTGGACACCAATTACTGCTCCGCAACTTGGAGAGAACTGCTGTGCGCCCTC 370
 |||
 QY 61 tacattgaacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
 |||
 Db 371 TACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 430
 |||
 QY 121 gccaaacttctcagggcccttgccataacctccgcagtgagacacaaacccacagcacg 180
 |||
 Db 431 GCGAACTTCTGCTCAGGCGCTTGCCCATACCTCCGAGTGCAGACACAAACCCACAGCACG 490
 |||
 QY 181 gtgctggagactgtacaacactctgaacctgaacctcgcagtcgagacacacacacagcacg 240
 |||
 Db 491 GTGCTGGGAGCTGTACAACTCTGAACCTCTGAAGCATCTGCCCTGCTGCTCGTCCG 550
 |||
 QY 241 caggacctggagcccttgaccatccctgtactatgttggaggagaccccaaaagtggagcacg 300
 |||
 Db 551 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGTGGAGGAGGCCCAAAAGTGGAGCACG 610
 |||
 QY 301 ctctcaacatggtgtgaagtcttgaatgtactgtga 339
 |||
 Db 611 CTCTCCACATGCTGTGAAGTCTTGTAAATGTAGCTGA 649

RESULT 2

AW412139 645 bp mRNA EST 08-FEB-2000
 LOCUS uq46g03.y1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5'
 DEFINITION similar to gb:M32745 mouse transforming growth factor beta-3 mRNA,
 complete (MOUSE);, mRNA sequence.

ACCESSION AW412139.1 GI:6937994

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 645)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

MGI:1045080

Seq primer: -40RP from Gibco

High quality sequence stop: 446.

FEATURES

source

1. .645

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

↑

↑

↑

↑

↑

↑

/clone="IMAGE:2812468"
 /clone_lib="NCI-CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 159 a 196 c 175 g 115 t
 ORIGIN

Query Match 85.8%; Score 291; DB 115; Length 645;
 Best Local Similarity 91.2%; Pred. No. 3.2e-72;
 Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtccgcaacttgagagaaactgctgtgccccctc 60
 |||
 Db 109 GCCTGGACACCAATTACTGCTCCGCAACCTGGAGGAGAACTGCTGTGTACGCCCTT 168
 |||
 QY 61 tacattgaacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
 |||
 Db 169 TATATTGACTTCCGGCAGGATCTAGGCTGGAATGGTCCACGAACCTAAGGGTTACTAT 228
 |||
 QY 121 gccaaacttctcagggcccttgccataacctccgcagtcgagacacacacacagcacg 180
 |||
 Db 229 GCCAACTTCTGCTCAGGCGCTTGCCCATACCTCCGAGCGGAGACACAAACCCATAGCAG 288
 |||
 QY 181 gtgctggagactgtacaacactctgaacctgaacctggaacctctgctgcctgtgctgctgctc 240
 |||
 Db 289 GTGCTGGACTATACAAACACCTTGAAACCCAGAGGCGCTGCTCGCCATGTGCTGCTCCC 348
 |||
 QY 241 caggacctggagccctgaccatctctactatgttggaggagaccccaaaagtggagcacg 300
 |||
 Db 349 CAGGACCTGGAGCCCTTGACCATCTTGTACTATGTGGCAGACACCCCAAGTGGAGCACG 408
 |||
 QY 301 ctctcaacatggtgtgaagtcttgaatgtactgtga 339
 |||
 Db 409 CTCTCCAAACATGTTGGTGAAGTCTGTGAAGTGCAGCTGA 447

RESULT 3

BG175423 812 bp mRNA EST 06-FEB-2001
 LOCUS 602337778F1 NCI-CGAP_Mam1 Mus musculus cDNA clone IMAGE:4460706 5',
 mRNA sequence.

ACCESSION BG175423

VERSION BG175423.1 GI:12682126

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

REFERENCE 1 (bases 1 to 812)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL0262 row: 1 column: 19

High quality sequence stop: 735.

Location/Qualifiers

1. .812

/organism="Mus musculus"

↑

↑

↑

↑

↑

↑

↑

↑


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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4460706"
/clone_lib="NCI CGAP Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1
, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2p clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column
chromatography, converted to double-stranded circles and
electroporated into DH10B bacteria (Life Technologies) to
generate the UI-R-C3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)."

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```

BASE COUNT      197 a      210 c      245 g      160 t
ORIGIN
Query Match      85.8%; Score 291; DB 174; Length 812;
Best Local Similarity 91.2%; Pred. No. 3 4e-72;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 gcttgacacacattactgctccgcaactggaggagaactgctgtgcccctc 60
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 GCCCTGGACCAATTAAGTCTCCGCAACCTGGAGGAGAACTGCTGTGACGCCCTT 118
QY 61 tacattgacttcgacagagatggtggtggaagtgggtccatgaacctaaaggctactat 120
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 TATATTGACTTCGGCAGGATAGGCTGGAATGGGTCCACGAACCTAAGGGTTACTAT 178
QY 121 gccaaactctcagggccctggccataacctccgagtcagagacacacacagcag 180
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 GCCAACTTCTGCTAGGCCCTTGCCCATACCTCCGCGAGCGACACACCAATAGCAG 238
QY 181 gtgctgggactgtacaactctgaacctgaagcatctgctcgtcgtcgtgccc 240
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Db 239 GTGCTGGACTATACACACCTGACCCAGAGCGCTGCTGCCATGCTGCTGCTCCC 298
QY 241 caggacctggagccctgacctcctctgtactatgttggaggagcccccaagtggagcag 300
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 CAGGACCTGGAGCCCTGACCATCTTGTACTATGTGGCAGAGACCCCAAGGTGGAGCAG 358
QY 301 ctctccaaactggtggaagctctgtaaatgactga 339
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 CTGTCCAACTGGTGGTGAAGTCGTGTAAGTGACAGCTGA 397

```

```

RESULT 4
BF542567 503 bp mRNA EST 11-DEC-2000
LOCUS UI-R-C3-sm-a-12-0-UI.r1 UI-R-C3 Rattus norvegicus cDNA clone
DEFINITION UI-R-C3-sm-a-12-0-UI 5', mRNA sequence.
ACCESSION BF542567
VERSION BF542567.1 GI:11633674
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 503)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at

```

```

LLNL (info@image.llnl.gov). IMAGE ID= 1768868
Seq primer: M13 Forward.
Location/Qualifiers
source
1..503
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1
, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2p clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column
chromatography, converted to double-stranded circles and
electroporated into DH10B bacteria (Life Technologies) to
generate the UI-R-C3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)."

```

```

BASE COUNT      106 a      151 c      133 g      112 t      1 others
ORIGIN

```

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Query Match      84.4%; Score 286.2; DB 150; Length 503;
Best Local Similarity 91.5%; Pred. No. 7.1e-71;
Matches 303; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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```

QY 9 caccattactgctccgcaactggaggagaactgctgtgccccctctacattga 68
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CACCGACTACTGCTTCGCAACTTGGAGAGAACTGCTGTGCGCCCTCTACATTGA 120
QY 69 ctccgacagatctgggctggaagtgggtccatgaacctaaaggctactatgccaaact 128
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CTTCCGGCAGGATCTAGGCTGGAATGGTCCACGAACCTAAGGTTACTATGCCAACT 180
QY 129 ctgctcggcccttgcccatacctcgcagtcagagacacacacacacacagcagctgg 188
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CTGCTCAGGCGCTTGCCCTTACCTCCGAGCTCAGACACACACACAGCAGCGTGTG 240
QY 189 actatacaactcctgaacctgaacctgacctgctcgcctgctgctgctgctgctgct 248
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACTATACAACACCTTGAAACCGGAGGCATCGCCCTCGGCATCTGTGTGCCCCAGACCT 300
QY 249 ggagccctgacctcctgtactatgttggaggagcccccaagtggagcagctctccaa 308
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGACCTCTGACCATCTGTACTATGTTGGCAGAACCCCAAGGTGGAGCAGCTGTCCAA 360
QY 309 catggtggtgaagtctgttaaatgtagtga 339
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CATGGTGGTGAAGTCGTGTAAGTGCAGCTGA 391

```

```

RESULT 5
BF101203
LOCUS BF101203 1820 bp mRNA EST 19-OCT-2000
DEFINITION 601754782F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:398358 5',

```


factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

AA915041
VERSION AA915041.1 GI:3054433
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:684788
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 473.

FEATURES

source
1..560
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314492"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].
TGTTACCACTCTCAAGTGGGAGCGCGCGAATGGTGTGTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 149 a 165 c 142 g 104 t
ORIGIN

Query Match 69.3%; Score 234.8; DB 13; Length 560;
Best Local Similarity 90.4%; Pred. No. 2.9e-56;
Matches 273; Conservative 0; Mismatches 27; Indels 2; Gaps 2;
QY 1 gcttgagacccaattactgtccgcaactgtgagagaaactgtgtgccccctc 60
|||
DB 261 GCCTTGACACCAATTACTGCTCCGCAACCTGGAGGAACTGCTGTGACGCCCTT 320
QY 61 tacattgacttcagacaggatctgggtggaagtgggtccatgaacctaaaggctactat 120
|||
DB 321 TATATTGACTTCGGCAGAGTCTAGGCTGGAATGGGTCCACGAACCTTAAGGGTTACTAT 380
QY 121 gcaactcttgcagagcccttgccatacctccgagtgagagacacacacagacag 180
DB 381 GCCAACTTCTGCTCAGGCCCTTGCCATACCTCCGAGCGAGACACAAACCATAGCAG 440
QY 181 gtcttgagactgtacaacactctgaacccctgaagcatctgccttgctgctgctgcc 240
|||
DB 441 GTGCTTGACTATACAAACCCCTGAACCCAGAGCGGTCTG-CTGCCATGCTGGGT-CCC 498

QY 241 caggacctggagccctgacctctgtactatgttggaggagcccccaagtggagcag 300
|||
DB 499 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGGCAGAACCCCAAGGTGGAGCAG 558
QY 301 ct 302
DB 559 ct 560
RESULT 8
BG244370 966 bp mRNA EST 13-FEB-2001
LOCUS 602356090F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4484686 5',
DEFINITION mRNA sequence.
ACCESSION BG244370
VERSION BG244370.1 GI:12754185
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10325 row: c column: 23
High quality sequence stop: 656.

FEATURES

source
1..966
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4484686"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH108"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 228 a 273 c 251 g 214 t
ORIGIN

Query Match 66.3%; Score 224.6; DB 175; Length 966;
Best Local Similarity 85.8%; Pred. No. 2.5e-53;
Matches 284; Conservative 0; Mismatches 44; Indels 3; Gaps 3;
QY 12 caattactgtctccgcaactgtgagagaaactgtgtgccccctcacattgactt 71
|||
DB 682 CCATTACTGTCTCCGCAACCTGGAGGAACTGCTGTGTGACGCCCTTGATGTGACT 623
QY 72 ccgacagatctggctggaagtgggtccatgaacctaaagggtact-atgccaactct 130
|||
DB 622 TCCGCCAGGATCTAGTGGAAATGGGTCCACGAACCTAAGGGTTACTAATGCCAACTTCT 563
QY 131 gctcagggcccttgccatacctcccgagtgcagacac-aacccacagcaggtgctggga 189
|||
DB 562 GCTCAGGCCCTTGCCCATACCTCCGAGCGGACACAAACCATAGCAGCGTGTGGA 503
QY 190 ctgtacaacactctgaacccctgaagcatctgctc-gccttgctgctgccccagacct 248
|||

Db	288	TATATTGACTTCCGGCAGGATCTAGGCTGCAAAATGGGTCCACGAACCTTAAGGGTTACTAT	347
Qy	121	gccaaacttctgcagcccttgcaccatactccgcagtgagacacaacccacagcacg	180
Db	348	GCCTAGCTTCTGCTCAGGCCCTTGCCCATACCTCGGAGCGCAGACACAACCCATAGCAGC	407
Qy	181	gtctggtgagctgtacaacactctgaacctggaacctggaagcatctgcctcgcttgcctgctgctg	240
Db	408	GGGCTTGAGCTATACACACCCCTGACCCAGAGCGCTGTCCTCGCC-TCCTGCGGCCCN	466
Qy	241	caggacctggagccctgaccatctgtactatgttggaggga	283
Db	467	CANGACCTGGAGCCCTGACCATCTTGTACTATGTGCCAGAA	509

RESULT 10

AA657145

LOCUS

DEFINITION

IMAGE:1121765 5' similar to gb:J03241 TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

AA657145

AA657145.1 GI:2593299

EST

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA657145

530 bp

mRNA

EST

04-NOV-1997

vr26d03.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone

IMAGE:1121765 5' similar to gb:J03241 TRANSFORMING GROWTH FACTOR

BETA 3 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth

factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

AA657145

AA657145.1

GI:2593299

EST

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 530)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Treising,B., Wylie,T., Lehnon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:611101

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 183.

Location/Qualifiers

1. .530

/organism="Mus musculus"

/strain="C3H"

/db_xref="taxon:10090"

/clone="IMAGE:1121765"

/clone_lib="Barstead mouse myotubes MPLRB5"

/cell_line="C2C12"

/lab_host="DH10B"

/notes="Vector: pT7T3D-pac (Pharmacia) with a modified

polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTAGCATCTGAGTGGGAGCGCCGCTTTTGTGTGTGTGTGTGTGTGTGT

3'] ; double-stranded cDNA was ligated to Eco RI adaptor

[AATTGGATCTTG], digested with Not I and cloned into the

Not I and Eco RI sites of the modified pT7T3 vector.

Library constructed by Bob Barstead. The C2C12 cell line

(available from ATCC, catalog # CRL-1772) differentiated

rapidly, forming contractile myotubes and producing

characteristic muscle proteins. "

124 a 147 c 150 g 109 t

BASE COUNT

ORIGIN


```
Db 416 TACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 357
QY 121 gcaactctgtcagcccttgcacatacctccgcagtcgagacacacacacagcag 180
Db 356 GCAAACTTCTGCTGGGCGCTGCCCTACATTGGAGCGTGGACACGAGTACAGCAAG 297
QY 181 gtgctgggactcaacaactctgaacctgaacctgaacctgtcctcgtcgtgctgccc 240
Db 296 GTCCCTGGCCCTGTACAACACAGATACCCGGGCGCTCGCGGCGCGCTGCTGCGTGGCG 237
QY 241 caggacctgagcccttaccactctgtactatgttggaggagaccccccaaaagtggagcag 300
Db 236 CAGGCGCTGGAGCCCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 177
QY 301 ctctcaacatggtggtgaagtctgttaaatgtagctga 339
Db 176 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 138

RESULT 13
LOCUS BF726995 600 bp mRNA EST 05-JAN-2001
DEFINITION by15c03.y1 Human Lens cDNA (Un-normalized, unamplified): BY Homo sapiens cDNA clone by15c03 5', mRNA sequence.
ACCESSION BF726995
VERSION BF726995.1 GI:12042906
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Wislow G.J., Bernstein S., Behal A. and Smith D.
TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 15 row: c column: 03
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
Location/Qualifiers
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="by15c03"
/clone_lib="Human Lens cDNA (Un-normalized, unamplified): BY"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/Note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses from different adults (both approximately 40 years old) together yielded 20ug of total RNA and 150ng mRNA for cDNA library synthesis. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript plasmid system full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5', -pGAGTAGTCTAGATCGGAGCGCGCC(T)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT 91 a 170 c 216 g 122 t
ORIGIN

Query Match , 60.4%; Score 204.6; DB 168; Length 600;
```

```
Best Local Similarity 75.2%; Pred. No. 1.1e-47;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1 gcttggacacaaactactctccgcaacttggagagaaactgctgtgtgccccctc 60
Db 512 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGTGGCGAGCTG 453
QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaacctaaagggtactat 120
Db 452 TACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 393
QY 121 gcaactctgtcagcccttgcacatacctccgcagtcgagacacacacacagcag 180
Db 392 GCAAACTTCTGCTGGGCGCTGCCCTACATTGGAGCGCTGGACACGAGTACAGCAAG 333
QY 181 gtgctgggactcaacaactctgaacctgaacctgaacctgctcgtcgtgctgccc 240
Db 332 GTCTGGCCCTGTACAACACAGATACCCGGGCGCTCGCGGCGCGCTGCTGCGTGGCG 273
QY 241 caggacctgagcccttaccactctgtactatgttggaggagaccccccaaaagtggagcag 300
Db 272 CAGGCGCTGGAGCCCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
QY 301 ctctcaacatggtggtgaagtctgttaaatgtagctga 339
Db 212 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 174

RESULT 14
LOCUS AI131171/c
DEFINITION AI131171 727 bp mRNA EST 27-OCT-1998
q15c11.x1 Soares fetal heart_NBH19W Homo sapiens cDNA clone
IMAGE:1709684 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 TAR1
repetitive element ;, mRNA sequence.
ACCESSION AI131171
VERSION AI131171.1 GI:3601187
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390.
FEATURES
Location/Qualifiers
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1709684"
/clone_lib="Soares_fetal_heart_NBH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DHI0B (ampicillin resistant)"
/Note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site:1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTCAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the
```


found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 396.

FEATURES

Location/Qualifiers
 1..572
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2575474"
 /clone_lib="NCI_CGAP_GUI"
 /tissue_type="2 pooled high-grade transitional cell tumors"
 /lab_host="DH10B"
 /note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
 93 a 159 c 206 g 114 t

BASE COUNT

ORIGIN 93 a 159 c 206 g 114 t

Query Match 59.4%; Score 201.4; DB 111; Length 572;
 Best Local Similarity 74.6%; Pred. No. 8.8e-47;
 Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgaacttggaggagaactgtgtgtgccccctc 60
 Db 488 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAAACTGCTGCTGGCGAGCTG 429
 Qy 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
 Db 428 TACATTGACTTCGCGAAGGACCTCGCGTGGAAAGTGATCCAGAGCCCAAGGGCTACCAT 369
 Qy 121 gccaaacttctcagggccttgccatccctccgcagtcgacagacacacacagcacg 180
 Db 368 GCCAACTTTTGGCTCGGGCCCTGCCCTACATTTGGAGCGTCGACACGCGAGTACAGCAG 309
 Qy 181 gtgtggagactgtacaaactctgaacctgaagcatctgctgccttgcgtgctgccc 240
 Db 308 GTCTCGGCCCTGTACAAACGACGATAACCGGGCGCTCGCGCGCGCTGCTGCGTGGCG 249
 Qy 241 caggacctggagccctgacactctgtactatgttgaggagaccccaaatggagcag 300
 Db 248 CAGGCGCTGGAGCCCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
 Qy 301 ctctccaaatggtggtgaagctcttgaatgtactgtgaaatgtactga 339
 Db 188 CTGTCCAACATGATGCTGGCTCTCTGCAAGTGCACCTGA 150

RESULT 17

BF543086/c
 LOCUS BF543086 471 bp mRNA EST 11-DEC-2000
 DEFINITION UI-R-AFL1-aag-f-07-0-UI.r1 UI-R-AFL1 Rattus norvegicus cDNA clone
 UI-R-AFL1-aag-f-07-0-UI 5', mRNA sequence.
 ACCESSION BF543086
 VERSION BF543086.1 GI:11634193
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 471)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA

FEATURES

Location/Qualifiers
 1..471
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-AFL1-aag-f-07-0-UI"
 /clone_lib="UI-R-AFL1"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AFL1
 library is a normalized library constructed from 15 dpc
 rat atrioventricular (AV) canal. The tag is a string of 5
 nucleotides present between the Not I site and the
 oligo-dT track. The library was constructed as described
 by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
 , 1996. Tissue provided by Jim Lin, Department of Biology,
 University of Iowa."
 118 a 105 c 110 g 137 t 1 others

BASE COUNT

ORIGIN 118 a 105 c 110 g 137 t 1 others

Query Match 59.1%; Score 200.4; DB 150; Length 471;
 Best Local Similarity 74.3%; Pred. No. 1.6e-46;
 Matches 252; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgaacttggaggagaactgtgtgccccctc 60
 Db 464 GCTTTTGGATGCCCTTATTGCTTTAGGAATGTGCAGGATAATTGCTGCTTCCGCTCTT 405
 Qy 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
 Db 404 TACATTGATTTTAAGAGGATCTTGGATGGAATGGATCCATGAACCAAGGATACAAT 345
 Qy 121 gccaaacttctcagggccttgccatccctccgcagtcgacagacacacacacagcacg 180
 Db 344 GCTAACTTCTGCTGGGCGATGCCCTTATCTGCTGGAGTTTACACACACACACACAAA 285
 Qy 181 gtgtgggagactgtacaaactctgaacctgaagcatctgctgccttgcgtgctgccc 240
 Db 284 GTCTCAGCCTGTACAAACACCAATAAACCCCGAAGCTTCTGCTTCCCTTGTGTGCTCC 225
 Qy 241 caggacctggagccctgacactctgtactatgttggaggagaccccccaaatggagcag 300
 Db 224 CAGGATCTGGAGACCACTGACCACTCCCTTACTACATTGGCAATACGCCCAAGATCGAACA 165
 Qy 301 ctctccaaatggtggtgaagctcttgaatgtactgtgaaatgtactga 339
 Db 164 CTTTCCAACATGATGCTCAAGTCTTGTGAATGACAGCTAA 126

RESULT 18

BE645704/c
 LOCUS BE645704 474 bp mRNA EST 05-SEP-2000
 DEFINITION 7e74h10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288259 3'
 similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
 sequence.
 ACCESSION BE645704
 VERSION BE645704.1 GI:9970015
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

REFERENCE 1 (bases 1 to 474)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          DNA Sequencing by: Greg Lennon, Ph.D.
          Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL, send email to:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco.
          Location/Qualifiers
FEATURES   source
            1..474
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3288259"
            /clone_lib="NCI_CGAP_Pr28"
            /sex="male"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
            with a modified polylinker; Plasmid DNA from the
            normalized library NCI_CGAP_Pr22 was prepared, and ss
            circles were made in vitro. Following HAP purification,
            this DNA was used as tracer in a subtractive hybridization
            reaction. The driver was PCR-amplified cDNAs from a pool
            of 5,000 clones made from the same library (clonesIDs
            985608-986759, 1101192-1101959, and 1217928-1220615)."
            Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT 75 a 138 c 176 g 85 t
ORIGIN
Query Match 58.5%; Score 198.2; DB 138; Length 474;
Best Local Similarity 74.9%; Pred. No. 6.9e-46;
Matches 248; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 9 caccattactcttcgcgaacttgaggagaaactgtgtgtgccccctctacattga 68
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 474 CACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTCGTGGCGCAGGTGATGTA 415
QY 69 cttccgacaggaatctggtctgaagtgggtccatgaacctaaagggtctactatgc 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 414 CTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAAC 355
QY 129 ctgctcagggcccttgccatactccgcagtcagacagacacacacacacagcggtg 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 354 TTGCTCGGGCCCTGCCCTACATTGGAGCCTGGACACGCGATGACGAAAGGTCTCTGGC 295
QY 189 actgtacacactctgaacccctgaagcatctgcctgcctctgtcgtgctcccccagac 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 294 CTGTGTACACACAGCATACCCGGGGCCCTCGGGGGCGCGTCTGCTGCGCGCAGCGCT 235
QY 249 ggagcccttgaccatctctgtactatgtgtggaggaccccccaagtggagcagctctccaa 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 GGAGCGCGTCCCATCTGTACTACTGTGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAA 175
QY 309 catgtgtggaagtcttttaaatgtagtga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 CATGATCGTGGCGCTCTCTGCAAGTGCAGCTGA 144

RESULT 19
BE464068/c BE464068 568 bp mRNA EST 27-JUL-2000
LOCUS      hx84h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194547 3'
DEFINITION similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains element TAR1 TARI repetitive element ;,

```

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mRNA sequence.
BE464068 BE464068.1 GI:9509843
VERSION 1
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Sequencing by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL, send email to:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco
          High quality sequence stop: 395.
FEATURES   Location/Qualifiers
            source
            1..568
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3194547"
            /clone_lib="NCI_CGAP_Kid11"
            /lab_host="DH10B"
            /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
            a modified polylinker; Site:1: Not I; Site:2: Eco RI;
            Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
            prepared, and ss circles were made in vitro. Following HAP
            purification, this DNA was used as tracer in a subtractive
            hybridization reaction. The driver was PCR-amplified cDNAs
            from a pool of 5,000 clones made from the same library
            (clonesIDs 1322376-1323911, 1456007-1456775, and
            1500552-1502855). Subtraction by Bento Soares and M.
            Fatima Bonaldo.
BASE COUNT 96 a 159 c 203 g 110 t
ORIGIN
Query Match 58.5%; Score 198.2; DB 136; Length 568;
Best Local Similarity 74.0%; Pred. No. 7.1e-46;
Matches 251; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 1 gctttggaaccaattactgcttcgcgaacttgaggagaaactgctgtgtgccccctc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 GCCTTGACACCAACTATTGCTTCAGCTCCACGGAGAGAAATGCTGCTGGGAAGTGTG 420
QY 61 tacattgaactccgacaggaatctgtggaagtgggtcccatgaacctaaagggtactat 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 419 TACATTGACTTCCGACAGGACCTCGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 360
QY 121 gcaaacctctgtcagggcccttgccatactccgcagtcagacacacacacacagcagc 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 GCCAACTTTTGCCTCGGGCCCTGCCCTACATTGAGCCCTGGACACGACGATACAGCAAG 300
QY 181 gtctgggaactgtacaacactctgaacctctgaacctctgctcgtcgtgtgtgtgtgcc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 GTCTGTGCCCTGTACAACACGACATTAACCGGGCGCTCGGGGGCGCGCTGTGCTGTGCG 240
QY 241 caggacctggagccctgaccatctgtactatgttggagagcccccaagtggagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 CAGCGCTGGAGCGCGCTGCCCTACGTGTACTGTGAGCCCGCCCAAGCCCAAGTGGAGCAG 180
QY 301 ctctcccaactggtggtggaagctctgttaaatgtagtga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 CTGTCCAACATGATCGTGGCTTCTCTGCAAGTGCAGCTGA 141

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RESULT 20
A1148173/c
LOCUS      785 bp      mRNA      EST      26-OCT-1998
DEFINITION q56d01.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3'
            similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains PTR5.b3 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION  A1148173
VERSION     A1148173.1  GI:3675855
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1  (bases 1 to 785)
AUTHORS     NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.lnl.gov/bbrp/image/image.html
            Insert length: 953 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 356.
FEATURES    Location/Qualifiers
             1..785
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:1704097"
                /clone_lib="NCI-CGAP_Brn23"
                /tissue_type="glioblastoma (pooled)"
                /lab_host="DH10B"
                /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
                modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                TGTACCAATCTGAAGTGGAGGCGCGCATATCTTTTCTTTTCTTTTCTTTTCTTTT
                T 3']; double-stranded cDNA was ligated to Eco RI
                adaptors (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of the modified pT7T3 vector.
                Library is normalized, and was constructed by Bento
                Soares and M.Fatima Bonaldo."
BASE COUNT  137 a  217 c  267 g  164 t
ORIGIN

```

```

Query Match      58.5%; Score 198.2; DB 16; Length 785;
Best Local Similarity 74.0%; Pred. No. 7.6e-46;
Matches 251; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 gcttgagacacattactgttcgcaacttgagagagaactgtgtgtgccccctc 60
Db 497 GCCCTGGACACCAATATTGCTTCAGCTCCACGGAGAAGAACTGCTGGCTGGCAGCTG 438

QY 61 tacattactccgacaggaactgtggaagtgggtccatgaacctaaaggtactat 120
Db 437 TACATTGACTTCCGACAGGACTCGGTGGAAATGGATCCACGAGCCCAAGGGGTACCAT 378

QY 121 gccaaactctgctcaggcccttgcatactccgcagtcgagacacacacacagcag 180
Db 377 GCCAACTTTTGGCTCGGGCCCTGCCCCCTACATTTGGAGCCCTGGACACGACGTACAGCAAG 318

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QY 181 gtgctggagactgtacaacactctgaaccctgaagcatctcctcgctgtgctggtgccc 240
Db 317 GTCTTGGCCCTGTACAAACAGCATAACCCGGCGCCCTCGCGCGGTGCTGCTGCTCCG 258

QY 241 caggacctggagccctcgaccatcctgtactatgttgggaggaacccccaaagtggagcag 300
Db 257 CAGGCCCTGGAGGACCATGCCATCGTGTACTAGTGGGCGCAGCAAGCCCAAGGTGGAGCAG 198

QY 301 ctctccaaacatggtggtgaagctctttaaagttagctga 339
Db 197 CTGTCCACATGATCGTGGCGCTCTCGAAGTGCACATTA 159

RESULT 21
A512491/c
LOCUS      646 bp      mRNA      EST      03-MAR-2000
DEFINITION xx75d02.x1 NCI-CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2849475 3'
            similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION  A512491
VERSION     A512491.1  GI:7150569
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1  (bases 1 to 646)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11547-015
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40UP from Gibco
            High quality sequence stop: 396.
FEATURES    Location/Qualifiers
             1..646
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2849475"
                /clone_lib="NCI-CGAP_Lym12"
                /tissue_type="lymphoma, follicular mixed small and large
                cell"
                /lab_host="DH10B"
                /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
                SalI; Site_2: NotI; Cloned unidirectionally. Primer:
                Oligo df. Average insert size 1.25 kb. Life Technologies
                catalog #: 11547-015"
BASE COUNT  115 a  178 c  208 g  144 t  1 others
ORIGIN

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Query Match      58.3%; Score 197.8; DB 117; Length 646;
Best Local Similarity 74.0%; Pred. No. 9.5e-46;
Matches 250; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 2 ctttgagacacattactgttcgcaacttgagagagaactgtgtgccccctct 61
Db 495 CCTTGGACACAAATATTGCTTCAGCTCCACGGAGAAGAACTGCTGGCTGGCAGCTGT 436

QY 62 acattgactccgacaggaactgtgggtggaagtgggtccatgaacctaaaggtactat 121
Db 435 ACATTGACTTCGCAAGGACCTCGCTGGAACTGGATCCACGAGCCCAAGGGGTACCATG 376

QY 122 ccaactctgtcagggcccttgcatactccgcagtcgagacacacacacagcagcag 181
Db 375 CCAACTTTTGGCTCGGGCCCTGCCCCCTACATTTGGAGCCCTGGACACGACGTACAGCAAG 316

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ORIGIN

Query Match 57.8%; Score 195.8; DB 103; Length 578;
 Best Local Similarity 73.2%; Pred. No. 3.4e-45;
 Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgtctccgcaacttgagagaaactgtgtgccccctc 60
 DB 475 GCTTGGATACACTTATGTTAGCTCTATGGAGAAGAAATGCTGTGTGGCAGCTG 416
 QY 61 tacattgacttcgacaggaatctgggctggaagtgggtccatgaacctaaaggctactat 120
 DB 415 TACATTGACTTCGGCAAGGACTTTGNTGGAGTGTATCCACGAGCCCAAGGCTACCAT 356
 QY 121 gcaactttgtctcagggccttgcccaactcctcgcagtcagtcagacacacccacagcag 180
 DB 355 GCGCACTTTTGGCTCGGGCCCTGCCCTACATTTGGAGCGCTGGACACGCGAGTACAGCAAG 296
 QY 181 gtgctgggactgtacaaactcgaacctgaacctgaacctgaacctgctcgtcgtcgtgccc 240
 DB 295 GTCTGGCCCTGTACAAACGAGCAGTAAACCGGGCGCTCGGGCGCGCGCTGNTGCGTGGC 236
 QY 241 caggacctgagccctgacctcctgtactatgttgaggagagaccccccacaaagtggagcag 300
 DB 235 CAGGGCTGGAGCGCGTGCCTCGTGTACTACGTGGGCGCGAAGCCCAAGGTGGAGCAG 176
 QY 301 ctctccaaactggtggtgaagtcttgaatgtagctga 339
 DB 175 CTGTCCAACTGATGCTGGCGCTCCTGCAAGTGCAGCTGA 137

RESULT 24

AI991139/c

LOCUS

AI991139 589 bp mRNA EST 27-OCT-1999
 wu38q03.xl Soares Dieckgraebe.colon.NHCD Homo sapiens cDNA clone
 IMAGE:2522356 3', similar to gb:X02812.cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 TAR1
 repetitive element ;, mRNA sequence.

ACCESSION

AI991139

VERSION

AI991139.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

1 (bases 1 to 589)

TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -400P from Gibco

High quality sequence stop: 459.

FEATURES

Location/Qualifiers

1..589

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2522356"

/tissue_type="colonic mucosa from 3 patients with Crohn's
 disease"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pT7D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGCTCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library

source

1..778

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2368787"

/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/lab_host="DH10B"

went through one round of normalization. Tissue samples
 provided by Dr. Brian Dieckgraebe (Washington University,
 dieck@im.wustl.edu); colonic mucosa represents a range of
 disease involvement from moderate to severe Crohn's
 disease; samples include both perforating (fistulas) and
 non-perforating samples. Library constructed by Bento
 Soares and M. Fatima Bonaldo.

BASE COUNT 93 a 171 c 215 g 105 t 5 others
 ORIGIN

Query Match 57.1%; Score 193.6; DB 104; Length 589;
 Best Local Similarity 75.0%; Pred. No. 1.5e-44;
 Matches 255; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

QY 1 gctttgacacaaattactgtctccgcaacttgagagaaactgtgtgccccctc 60
 DB 476 GCCTGGACACCACTATGCTTCAGGTCACGGAGAGAACTGCTGCTGGCAGCTG 417
 QY 61 tacattgacttcgacaggaatctgggctggaagtgggtccatgaacctaaaggctactat 120
 DB 416 TACATTGACTTCGCAAGGACCTCGGCTGGAGTGTATCCACGAGCCCAAGGCTACCAT 357
 QY 121 gcaactttgtctcagggccttgcccaactcctcgcagtcagtcagacacacccacagcag 180
 DB 356 GCGCACTTTTGGCTCGGGCCCTGCGCTTGTGGAGCGCTGGACACGCGAGTACAGCAAG 297
 QY 181 gtgctgggactgtacaa-cactctgaaacctgaacctgaacctgctcgtcgtcgtgccc 239
 DB 296 GTCTGGCCCTGTACAAACGAGCAGTAAACCGGGCGCTTCGGCGCGCGCTGCTGCGTGGC 237
 QY 240 ccaggacctgagccctgacctcctgtactatgttgaggagagaccccccacaaagtggagca 299
 DB 236 GCAGGCGCTGGAGCGCGTGCCTATCGTGTACTACGTGGGCGCGAAGCCCAAGGTGGAGCA 177
 QY 300 gctctccaaactggtggtgaagtcttgaatgtagctga 339
 DB 176 GCTGTCCAACTGATGCTGGCTCCTGCTGCAAGTGCAGCTGA 137

RESULT 25

AI743724/c

LOCUS

AI743724 778 bp mRNA EST 19-DEC-1999

DEFINITION

wg53b06.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:2368787 3', similar to gb:X02812.cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); contains element MSR1 repetitive
 element ;, mRNA sequence.

ACCESSION

AI743724

VERSION

AI743724.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

1 (bases 1 to 778)

TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 863 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 449.

FEATURES

Location/Qualifiers

1..778

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2368787"

/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/lab_host="DH10B"

visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3055 row: G column: 07
 Seq primer: -21M13 Forward
 High quality sequence stop: 608
 POLYA=Yes.

FEATURES

source
 1..608
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="H3055G07"
 /clone_lib="NIA Mouse 15k cDNA Clone Set"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA libraries"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
 BASE COUNT 151 a 137 c 145 g 174 t 1 others
 ORIGIN

Query Match 57.1%; Score 193.4; DB 173; Length 608;
 Best Local Similarity 73.2%; Pred. No. 1.7e-44;
 Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
 QY 1 gctttgacacaaattactgttcgcaactggaggagaaactgctgtggtgccccctc 60
 Db 452 GCTTTGGATGCTGCTACTGCTTTAGAAATGTCAGGATAATTGCTGCTTGCCTCTT 393
 QY 61 tacattgacttcgacaggaatctggctgggaagtgggtccatgaacctaaaggctactat 120
 Db 392 TACATTGATTTTAAGAGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGGTACAA 333
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgagtcgagacacacccacagcag 180
 Db 332 GCTAACTTCTGTGTGGGGCATGCCATATCTATGGAGTTTACAGACATCAACACACAAA 273
 QY 181 gtgctggagactgtacaacactctgaacctgaagcatctgcctgccttgcgtgctgcc 240
 Db 272 GTCTCAGCTGTACACACACCAATAATCCCGAAGCTTCGGCTTCCCTTGTGTGTGCC 213
 QY 241 cagacactggagccctgacacctctgtactatgttgggagagacccccaaagtggagag 300
 Db 212 CAGGATCTGGAAACCACTGACCATTTCTATTACATTTGGAATACGCCCAAGATCGAAC 153
 QY 301 ctctcccaactgggtggaagtctgttaaatgtagctga 339
 Db 152 CTTTCCCAATATGATGTCAACTCTGTAAATGCAGCTAA 114

RESULT 28
 AI323791/c 681 bp mRNA EST 23-DEC-1998
 LOCUS mm47e08.x1 Stratagene mouse melanoma (#937312) Mus musculus cDNA
 DEFINITION clone IMAGE:524678 3' similar to gb:x57413 Mouse mRNA for

ACCESSION

AI323791 GI:4058220
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM

REFERENCE

AUTHORS
 1 (bases 1 to 681)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

TITLE

JOURNAL
 COMMENT
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:318526
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 High quality sequence stop: 366.
 Location/Qualifiers
 1..681
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:524678"
 /clone_lib="Stratagene mouse melanoma (#937312)"
 /tissue_type="melanoma"
 /dev_stage="M2 cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally, Primer: Oligo dT. From M2 cells, a highly metastatic derivative of the K-1735 (mouse) melanoma. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCAGTGTGTTTTTTTTTTT 3' "

FEATURES

source
 164 a 151 c 163 g 200 t 3 others
 ORIGIN

Query Match 57.1%; Score 193.4; DB 18; Length 681;
 Best Local Similarity 73.2%; Pred. No. 1.7e-44;
 Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
 QY 1 gctttgacacaaattactgttcgcaactggaggagaaactgctgtggtgccccctc 60
 Db 461 GCTTTGGATGCTGCTTACTGCTTTAGAAATGTCAGGATAATTGCTGCTTGCCTCTT 402
 QY 61 tacattgacttcgacaggaatctggctgggaagtgggtccatgaacctaaaggctactat 120
 Db 401 TACATTGATTTAAGAGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGTACAAT 342
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgagtcgagacacacccacagcag 180
 Db 341 GCTAACTTCTGTGTGGGGCATGCCCATATCTATGGAGTTTACAGACTCAACACACAAA 282
 QY 181 gtgctggagactgtacaacactctgaacctgaagcatctgcctgccttgcgtgctgcc 240
 Db 281 GTCCCTCAGCCTGTACACACACCAATAATCCGAAGCTTCGGCTTCCCTTGTGTGTGCC 222
 QY 241 caggaacctggagccctgacacctctgtactatgttgggagagacccccaaagtggagcag 300
 Db 221 CAGGATCTGGAAACCACTGACCATTTCTATTACATTTGGAATACGCCCAAGATCGAACAG 162
 QY 301 ctctcccaactgggtggaagtctgttaaatgtagctga 339

transforming growth factor-beta2 (MOUSE);, mRNA sequence.
 AI323791 GI:4058220
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 681)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:318526
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 High quality sequence stop: 366.
 Location/Qualifiers
 1..681
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:524678"
 /clone_lib="Stratagene mouse melanoma (#937312)"
 /tissue_type="melanoma"
 /dev_stage="M2 cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally, Primer: Oligo dT. From M2 cells, a highly metastatic derivative of the K-1735 (mouse) melanoma. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCAGTGTGTTTTTTTTTTT 3' "

BASE COUNT 164 a 151 c 163 g 200 t 3 others
 ORIGIN

Query Match 57.1%; Score 193.4; DB 18; Length 681;
 Best Local Similarity 73.2%; Pred. No. 1.7e-44;
 Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
 QY 1 gctttgacacaaattactgttcgcaactggaggagaaactgctgtggtgccccctc 60
 Db 461 GCTTTGGATGCTGCTTACTGCTTTAGAAATGTCAGGATAATTGCTGCTTGCCTCTT 402
 QY 61 tacattgacttcgacaggaatctggctgggaagtgggtccatgaacctaaaggctactat 120
 Db 401 TACATTGATTTAAGAGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGTACAAT 342
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgagtcgagacacacccacagcag 180
 Db 341 GCTAACTTCTGTGTGGGGCATGCCCATATCTATGGAGTTTACAGACTCAACACACAAA 282
 QY 181 gtgctggagactgtacaacactctgaacctgaagcatctgcctgccttgcgtgctgcc 240
 Db 281 GTCCCTCAGCCTGTACACACACCAATAATCCGAAGCTTCGGCTTCCCTTGTGTGTGCC 222
 QY 241 caggaacctggagccctgacacctctgtactatgttgggagagacccccaaagtggagcag 300
 Db 221 CAGGATCTGGAAACCACTGACCATTTCTATTACATTTGGAATACGCCCAAGATCGAACAG 162
 QY 301 ctctcccaactgggtggaagtctgttaaatgtagctga 339

LOCUS	BF287476	529 bp	mrna	EST	28-NOV-2000			
DEFINITION	EST452067 Rat Gene Index, normalized rat, Rattus norvegicus cdNA							
ACCESSION	Rattus norvegicus cdNA clone RGIG52 3' sequence, mRNA sequence.							
VERSION	BF287476							
KEYWORDS	BF287476.1	GI:11218546						
SOURCE	EST.							
ORGANISM	Norway rat.							
REFERENCE	Rattus norvegicus							
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.							
TITLE	1 (bases 1 to 529)							
JOURNAL	Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G., Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.							
COMMENT	Generation of ESTs from Normalized Rat Embryo, Bento Soares Unpublished (2000) Other_ESTs: EST351042 Contact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information. Location/Qualifiers 1. 529 /organism="Rattus norvegicus" /db_xref="taxon:10116" /clone="RGIG52" /clone_lib="Rat Gene Index, normalized rat, Rattus norvegicus cdNA" /tissue_type="mixed tissue" /lab_host="DH5-alpha" /note="Vector: pR37Pac; Site_1: EcoRI; Site_2: NotI; Combination of ROV, RBR, RKI, RLI, RPL, REM, RMD, RSP, RHE, RPC, RPN" 91 a 141 c 190 g 107 t							
BASE COUNT	91 a	141 c	190 g	107 t				
ORIGIN								
Query Match	56.6%; Score 191.8; DB 146; Length 529;							
Best Local Similarity	72.9%; Pred. No. 4.6e-44;							
Matches 247:	Conservative	0;	Mismatches 92;	Indels 0;	Gaps 0;			
QY	1	gctttgacaccaattactgcttcgcgaacttgagagagaactctgtgtgccccctc	60					
Db	477	GCCTTGATACCAATTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTACGCGACGTG	418					
QY	61	tacattgactccgacaggacttggttggaagtgggtccatgaacctaaagggtactat	120					
Db	417	TACATTGACTTTAGAGAGGACCTGGTGTGAAGTGGATTCACAGAGCCCAAGGGGTACCAT	358					
QY	121	gcaactctgtcaggcccttggccctacatctccgcagtcgagacacacccacagcacg	180					
Db	357	GCCAACTCTGTCTGGGGCCCTGCCCCCTACATTGTGAGCCTGGACACACAGTACAGCAAG	298					
QY	181	gtgctggagctgtacaacactctgaacctgaacctgaagcatctgctcgcttgctggtgcc	240					
Db	297	GTCCTTGCCCTTTACAAACCAACACAAACCGGGTGCTTCCCGCATCCGCTGATGCGTGC	238					
QY	241	caggacctgagcccttgacctctgtactctatctgttgaggaccctcccaagtggacag	300					
Db	237	CAGCCTTTGGAGGCACATGCCCATCGTTTACTTACGTGGGTGCGAAGCCCAAGGTGGAGCAG	178					
QY	301	ctctcccaactggtggtggaagctctgttaaatgtagctga	339					
Db	177	TTGTCCAACATGATCGTGGCGCTCTCTGCAAGTGTCAGCTGA	139					
RESULT 32								
A1323392/c								
LOCUS	A1323392	573 bp	mrna	EST	23-DEC-1998			


```

FEATURES
source
Location/Qualifiers
1. 505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2132156"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH108"
/notes="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt:
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT      76 a   147 c   187 g   95 t
ORIGIN
Query Match      54.4%; Score 184.4; DB 20; Length 505;
Best Local Similarity 72.4%; Pred. No. 5.8e-42;
Matches 239; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 10 accaattactgttcgcgaacttggaggagaactgtgtgccccctctacattgac 69
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 ACACACTAATGCTTACGCTCCAGGAGAAGAAGTGTGCGTGGCGAGCTGACATTGAC 412
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 ttccgacagatctgggtggaagtgggtccatgaacctaaagggtactatgccaaattc 129
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 TTCCGCAAGACCTCGGCTGGAAGTGGATCCAGAGCCCAAGGGCTACCATGCCAACTTC 352
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 130 tgcacagcccttgccatccctccgcagtcgagacacaaacacagcagcgggtgctggga 189
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 TGCTCGGGCCCTGCCCTACATTTGGAGCTGGACACGCGAGTACAGCAAGGTCTCGGCC 292
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 ctgtacaacactctgaacctgaagcatctgcctgcctgtctgtcgtgccccaggaactg 249
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 CTGTACAACCAAGCATACCCCGGGCGCTCGCGGCGCGCTGCTGCGTGGCGAGCGCGCTG 232
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 250 gagccctgacctctgtactatgttggaggagaccacaaagtggagcagctctccaac 309
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 GAGCGCTGCCATCGTGTACTACGTGGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAAC 172
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 310 atggtggtgaagtcttgtaaatgactga 339
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 ATGATGCTGGCTCCTGCAAGTGCAGCTGA 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 37
AA000733
LOCUS
DEFINITION
mg33b06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:425747 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
AA000733
VERSION
AA000733.1 GI:1436599
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
REFERENCE
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geiseli,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
JOURNAL
Contact: Marra M/Mouse EST Project
COMMENT
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

```

```

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:260299
Putative full length read
vector to vector length is 661
Seq primer: ETPrimer
High quality sequence stop: 321.
Location/Qualifiers
1. 431
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:425747"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCCGCGGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ); double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaído."

BASE COUNT      94 a   140 c   113 g   84 t
ORIGIN
Query Match      54.2%; Score 183.8; DB 1; Length 431;
Best Local Similarity 71.4%; Pred. No. 8.3e-42;
Matches 242; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 gcttggacacacaaacttactgtctccgcaacttggaggagaactgtgtgtgcgccctc 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93 GCCCTGGATACCAACTATTGCTTCAGTCCACAGAGAAGAACTGCTGTGTGCGCAGTGA 152
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 tacattgacttcgacagatctgggtggaagtgggtccatgaacctaaagggtactat 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 TACATTGACTTTAGGAAGGACCTGGGTGGAGTGGATCCAGAGCCCAAGGGCTACCAT 212
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 gccaaactctgtcagcccttgcctacacacctccgcagtcgacagacacacccacgacg 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 GCCAACTTCTGTCTGGGACCCCTGCCCTATATTTGGAGGCTGGACACACAGTACAGCAAG 272
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 gtctggagactgtacaacactctgaacctgaagcatctgcctcgcttgcgtgcgtgcc 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 GTCTTGTGCCCTCTACAACCAACACACACCCGGCGCTTCGGCGTCCACCGTCTCGTGGCGG 332
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 caggacctggagccctgacctcctgtactatgttgggagaccccccaagtggagcag 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 CGCGTTATGGAGCCCACTGCCCTACTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 392
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 ctctccacatggtgtgaagtcttgaatgtactga 339
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 TTGTCCAACATGATGTGGCTGCTCTCTGCAAGTGCAGCTGA 431
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 38
AI434956/c
LOCUS
DEFINITION
ti46f04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2133535 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
sequence.
AI434956
ACCESSION
AI434956

```

```

VERSION      AT134956.1  GI:4299804
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 567)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL
COMMENT      Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapsb-r@mail.nih.gov
              Life Technologies catalog #: 11547-015
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Insert length: 873 Std Error: 0.00
              Seq primer: -400p from Gibco
              High quality sequence stop: 380.
FEATURES
    source    1..567
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:2133535"
               /clone_lib="NCI_CGAP_Lym12"
               /tissue_type="lymphoma, follicular mixed small and large
               cell"
               /lab_host="DH10B"
               /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
               SalI; Site_2: NotI; Cloned unidirectionally. Primer:
               Oligo dT. Average insert size 1.25 kb. Life Technologies
               catalog #: 11547-015"
BASE COUNT   87 a 163 c 209 g 107 t 1 others
ORIGIN
Query Match      54.0%; Score 183; DB 20; Length 567;
Best Local Similarity 72.3%; Pred. No. 1.5e-41;
Matches 237; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 12 caattactgttcgcgaacttgaggaggaaactgtgtgctgcgccctctacattgact 71
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 CAACTATTGCTTACGTCACGAGAGAGACTGCTGCCGTGGCGCAGCTGTACATTGACTT 412

Qy 72 ccgacagatctggctggagtggtgcctatgaacctaaaggtctactatgccaaactctg 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 CGCAAGGACCTCGGCTGNAAGTGGATCCAGAGCCCAAGGGCTACCATGCCAACTTCTG 352

Qy 132 ctccaggcccttgccatctacctccgacgtgcagacacacccacagacggtgtctgggact 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 CCTCGGCGCTTCGCCCTTACATTTGAGCCCTGGACACGACGATCAGCAAGGTCTCTGGCCCT 292

Qy 192 gtacaaacctctgaacctgaagcatctgcctgccttgcgtgcgtgccagacacctgga 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 GTACAACAGCATAAACCGGGCGGCTCGCGCGGCGCGCTGTGCTGCCGACGGCGCTGGA 232

Qy 252 gccctgaccatctgtactatgttggaggaaccccccaagtgagcagctctctccaaacat 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 GCCGTCGCCATCTGTGTACTGTACGTGGGCGCAAGGCCCAAGGTGGAGCAGCTGTCCAACAT 172

Qy 312 ggtggtgaagtcttgaatgtagctga 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 GATCGTGGCTCTCTGCAAGTGCAGCTGA 144

RESULT 39
BF042894/c
LOCUS      BF042894      515 bp      mRNA
DEFINITION BP250019B10B3 Soares normalized bovine placenta Bos taurus cDNA
clone BP250019B10B3 5', mRNA sequence.
ACCESSION BF042894

```



```
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. "
BASE COUNT 106 a 155 c 126 g 90 t 1 others
ORIGIN

Query Match 52.7%; Score 178.8; DB 190; Length 478;
Best Local Similarity 72.3%; Pred. No. 2.2e-40;
Matches 245; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 1 gcttggaccacaaattactgctccqcaacttggagagaaactgctgtgtgcccctc 60
  || || || || || || || || || || || || || || || || || || || ||
Db 141 GCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGCGGCA-CTG 199

QY 61 tacattgactccgacaggaatggtggtggaagtgggtccatgaacctaaagggtactat 120
  || || || || || || || || || || || || || || || || || || || ||
Db 200 TACATTGACTTTAGGAAGACCTGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 259

QY 121 gcaacttctgcaggcccttgcccatcctccgcagtcgagacacacccacacagcag 180
  || || || || || || || || || || || || || || || || || || || ||
Db 260 GCCAACTTGTGCTGGGACCCTGCCCTTATATTGGAGGCTGGSACACACAGTACAGCAAG 319

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgcctcgcttgcctgctgccc 240
  || || || || || || || || || || || || || || || || || || || ||
Db 320 GTCTTGGCCTCTACNACCAACACACACCGGGGCTTCGGCGTCAACCGTGCCTGCGG 379

QY 241 caggacctggagcccttgaccatctctgtactatgttggaggagaccccccagaagtggagcag 300
  || || || || || || || || || || || || || || || || || || || ||
Db 380 CAGTTNATGGAGCCACTGCCCTACTGCTACTACGTGGTTCGCAAGCCCAAGTGGAGCAG 439

QY 301 ctctcacaactggtggtgaagtcttgttaaatgtagtga 339
  || || || || || || || || || || || || || || || || || || || ||
Db 440 TTGTCCACATGATTGTGGGCTCCTGCAAGTGCAGCTGA 478

RESULT 42
AI654506/c
LOCUS AI654506 460 bp mRNA EST 17-DEC-1999
DEFINITION wb63d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2310343 3',
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains PTR5.t3 PTR5 MSRI repetitive element ;,
mRNA sequence.
ACCESSION AI654506
VERSION AI654506.1 GI:4738485
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 519 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 206.
Location/Qualifiers
FEATURES
source
1..460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2310343"
```

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/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 68 a 131 c 166 g 93 t 2 others
ORIGIN

Query Match 52.7%; Score 178.6; DB 23; Length 460;
Best Local Similarity 73.8%; Pred. No. 2.5e-40;
Matches 226; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 33 ggaggagaactgctgtgtgcgccccctctacattgacttcgcacagatctgggctgaa 92
  || || || || || || || || || || || || || || || || || || || ||
Db 459 GGAAGAAGAACTGCTGCTGGCGGAGCTGTACATTGACTTCGCGAAGGACCTCGGCTGAA 400

QY 93 gtgggtccatgaacctaaagggtactatgccaaacttctgtcagggcccttgcccatacct 152
  || || || || || || || || || || || || || || || || || || || ||
Db 399 GTGGATCCCGAGAGCCCAAGGGCTACCATGCCAACTTNTGCTCGGGCCCTGCCCCCTACAT 340

QY 153 ccgcagtcgacagacacacccacagcagtgctggtgggactgtataaacactctgaacctga 212
  || || || || || || || || || || || || || || || || || || || ||
Db 339 TTGGAGCCTGGACACCGCAGTACAGCAAGGTCCTGGCCCTGTACACACGACGATAACCCGGG 280

QY 213 agcatctgcctgccttgcctgcccagacactgagccctgacccctctgttacta 272
  || || || || || || || || || || || || || || || || || || || ||
Db 279 CGCTCGGGCGCGCGTGTGTCGGTCCGCGAGGCGCTGGAACCGCTGCGCATGTGTGCTACTA 220

QY 273 tgttggaggagcccccaaaagtggagcagctctccaaatggtggtgaagtcttttaagt 332
  || || || || || || || || || || || || || || || || || || || ||
Db 219 CGTGGCGCGCAAGCCCAAGTGGAGCAGCTGTCCAACATGATCGTGGCTCTCTCAAGTG 160

QY 333 tagctga 339
  || || || || || || || || || || || || || || || || || || || ||
Db 159 CAGCTGA 153

RESULT 43
AI157673
LOCUS AI157673 339 bp mRNA EST 30-SEP-1998
DEFINITION ue48g10.r2 Soares.mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1494402 5' similar to gb:M32745 mouse transforming growth
factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION AI157673
VERSION AI157673.1 GI:3686142
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
```

This clone is available royalty-free through L1NL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:932006
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 267.

FEATURES

Location/Qualifiers
 1..339
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1494402"
 /clone_lib="Soares_mammary_gland_NMLMG"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 87 a 110 c 81 g 60 t 1 others
 ORIGIN

Query Match 51.9%; Score 176; DB 16; Length 339;

Best Local Similarity 90.0%; Pred. No. 1.3e-39;
 Matches 199; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 1 gcttggacacaaattactgtctccgaacttggagagaaactgtgtgtgccccctc 60

Db 109 GCCCTGGACACCAATTACTGCTCCGCAACTGGAGGAGAACTGCTGTACGCCCTT 168

QY 61 tacattgacttcgacagagatggctggaagtgggtccatgaacctaaagggctactat 120

Db 169 TATATTGACTTCCGGCA-GATCTAGGCTGGAAATGGTCCACCACTAAGGGTTACTAT 227

QY 121 gcaactctgtcagggcccttgccatactccgagtcagagacacacacacagcacg 180

Db 228 GCCAACTTCTGCTCAGGCCCTTNGCCATACCTCCGAGCGCAGACACACCATAGCAG 287

QY 181 gtctgggagctgacacacacttgaacctgaagcatctgc 221

Db 288 GTGCTGGAGTATACACACCTGTAACCCAGAGCGGCTGCG 328

RESULT 44

AI824845/c

LOCUS

DEFINITION wb02f01.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2304505 3' similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TARI MER22 repetitive element ; mRNA sequence.

ACCESSION AI824845

VERSION AI824845.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 441)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Insert length: 497 Std Error: 0.00
 Seq primer: -40UP from Gibco

High quality sequence stop: 347.
 Location/Qualifiers

FEATURES

source
 1..441
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2304505"
 /clone_lib="NCI-CGAP-GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP-GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 129 c 165 g 81 t

ORIGIN

Query Match 51.9%; Score 176; DB 102; Length 441;

Best Local Similarity 74.7%; Pred. No. 1.4e-39;

Matches 221; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 44 gctgtgtgcgccccctctacattgacttccgacagatctgggctggaagtgggtccatg 103

Db 441 GCTGCTGCGGCGAGCTGTACATTGACTTCCCGAAGACCTCGGCTGGAAGTGATCCACG 382

QY 104 accttaagggctactatgccaaactctgtcagggcccttggccatacctccagtcgag 163

Db 381 AGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGG 322

QY 164 acacaacccacagacggtgtgtggaactgtacaacactctgaacctgaagctatgcct 223

Db 321 ACACGCAGTACAGCAAGGTCTCTGGCCCTGTACAACAGCATACCCGGCGCTCGCGCG 262

QY 224 cgcttctgtcgtgccacagacctggagcccttgaacctctgtactactgttggaggga 283

Db 261 CGCCGTGCTGCTGCGCGAGGCGCTGGAGCCGCTGCCCATCTGTGTACTACGTGGCGCGCA 202

QY 284 ccccaaaagtggagcagctctccaaacatggtgtgaagtcttgaatgtagctga 339

Db 201 AGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 146

RESULT 45

BE074350

LOCUS

DEFINITION QV3-BT0571-030200-078-d08 BT0571 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE074350

VERSION BE074350.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 517)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-QV3-BT0571-030
200-078-d08st3-2000-02-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 516.
Location/Qualifiers
1. .517
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/db_xref="taxon:9606"
/clone_lib="BT0571"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 130 a 131 c 150 g 106 t
ORIGIN

Query Match 51.9%; Score 176; DB 163; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.4e-39;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 acacaaccacagcagcgtgctggagctgtacaaactctgaacctgaagcatctgcct 223
|||||
Db 9 ACACACCCACACAGCAGCGTGGGACTGTACAACTCTGAACCCCTGAAGCACTGCGCT 68
QY 224 cgcttgcgtgcgtgccccaggacctggagccctgacctcctgtactatgttggaggga 283
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Db 69 CGCCTTGTGCGTGGCCGCCAGGACCTGGAGCCCTGACCTCCTGTACTATGTTGGGAGGA 128
QY 284 ccccaaaagtggagcagctctccaaacatggtggtgaagtctgttaaagttagctga 339
|||||
Db 129 CCCCCAAAGTGGAGCAGCTCTCCACATGGTGGTGAAGTCTTTGTAATGTAGCTGA 184

RESULT 46
AW600944 336 bp mRNA EST 23-MAR-2000
LOCUS RC1-BN0014-210100-012-e01 BN0014 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW600944
VERSION AW600944.1 GI:7305683
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
REFERENCE HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-QV3-BT0571-030
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High quality sequence stop: 336.
Location/Qualifiers
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/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 101 a 77 c 67 g 91 t
ORIGIN

Query Match 51.8%; Score 175.6; DB 118; Length 336;
Best Local Similarity 71.3%; Pred. No. 1.7e-39;
Matches 232; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 14 attactgttcgcgaacttgaggaggaactgtgtgccccctctacattgacttcc 73
|||||
Db 7 ACTATTGCTTTGAAATGTGCAGGATAATTGCTGCTACGTCCACTTTACATTGATTCA 66
QY 74 gacagatctgggctgggaagtgggtccatgaacctgaaggctactatgccaacttctgct 133
|||||
Db 67 AGAGGGACCTAGGTGGAAATGGATACACGAAACCCAAAGGTTACAAATGCCAACTTCTGTG 126
QY 134 caggcccttggccatcctccgagtcagtcagacacacacccacagcagcgtgctggagactgt 193
|||||
Db 127 CTGGAGCATGCCCGTATTATTGAGAGTTCAGACACTCAGCAGCAGGAGGCTCTGAGCTTAT 186
QY 194 acaacactctgaacctgaagcattcctgcctgcctgctgcgtgccccagacactggagc 253
|||||
Db 187 ATAATACCATAAACCCAGAGCATCTCTCTCTCTGCTGCGTGTCCCAAGATTAGAAC 246
QY 254 ccttgaccatcctgtactatgttggggagcccccccccaagtggagcagctctccaaatgg 313
|||||
Db 247 CTCTAACCATCTCTACTACATTGGCAAAACACCCAAAGATTGAACAGCTTTCTAATATGA 306
QY 314 tggtagactctgtataatgtagtga 339
|||||
Db 307 TTGTAAAGTCTTGCAATGCAGCTAA 332

RESULT 47
BG058796/c 403 bp mRNA EST 25-JAN-2001
LOCUS naf10f12.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4140814 3'
DEFINITION similar to SW:TFGL_CERAE P09533 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR ; contains element PTR5 repetitive element ;, mRNA
sequence.
ACCESSION BG058796
VERSION BG058796.1 GI:12525613
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

Qy	275	ttgggagagcccccgaagtggagcagctctccaacatggtggtgaagtcttggtaaattga	334
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Qy	335	gctga	339
Db	301	gctga	305
RESULT	49		
AI421250/c			
LOCUS	AI421250	540 bp	mrna
DEFINITION	tfi14g02.xl	NCI_CGAP_Brn23	Homo sapiens
	EST	cdna	clone IMAGE:2096163
	3' similar to gb: X02812	cds1	TRANSFORMING GROWTH FACTOR BETA 1
	PRECURSOR (HUMAN);	contains element TAR1	repetitive element ;, mrna
	sequence.		
ACCESSION	AI421250		
VERSION	AI421250.1	GI:4267181	
KEYWORDS	EST		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 540)		
	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
	National Cancer Institute / National Institute of Neurological		
	Disorders and Stroke, Brain Tumor Genome Anatomy Project		
	(CGAP/BTGNP), Tumor Gene Index		
JOURNAL	Unpublished (1998)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,		
	Ph.D.		
	cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima		
	Bonaldo, Ph.D.		
	cdna Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	www.bio.llnl.gov/bbrp/image/image.html		
	Insert Length: 874	Std Error: 0.00	
	Seq primer: -400P from Gibco		
	High quality sequence stop: 373.		
FEATURES	Location/Qualifiers		
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	/clone_lib="NCI_CGAP_Brn23"		
	/tissue_type="glioblastoma (pooled)"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a		
	modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st		
	strand cdna was primed with a Not I - oligo(dT) primer [5'		
	TGTTACCAATCTGAAGTGGGCGCGCATATCTTTTTTTTTTTTTTTTTTTTTTTTTTTT		
	T 3']; double-stranded cdna was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pT7T3 vector.		
	Library is normalized, and was constructed by Bento		
	Soares and M.Fatima Bonaldo."		
BASE COUNT	85 a	156 c	201 g
ORIGIN	98 t		
Query Match	51.2%;	Score 173.6;	DB 20; Length 540;
Best Local Similarity	72.6%;	Pred. No. 6.8e-39;	
Matches	238;	Conservative	0; Mismatches 89; Indels 1; Gaps 1;
Qy	12	caataactgtcttcgcaacttggagagagaactctgtgtgctgcgccctctacattgaatt	71
Db	464	CAACTAATGGCTAGCTCCACGAGAAAGAACTCTCCCGTGGCGAGCTGTACATTGACTT	405


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BASE COUNT      Soares (University of Iowa). "
97 a      148 c      206 g      108 t

Query Match      50.4%; Score 171; DB 173; Length 559;
Best Local Similarity 71.1%; Pred. No. 3.8e-38;
Matches 241; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 gcttggacacaaattactgctccgcaacttggagagaactgctgtgccccctc 60
  || || || || || || || || || || || || || || || || || || ||
Db 481 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGAACTTCTGCGTACGGAAC 422

QY 61 tacattgactccgacagagatctgggctggaagtgggtccatgaacctaaaggtactat 120
  || || || || || || || || || || || || || || || || || || ||
Db 421 TACATTGACTTCA---AGGACCTCGGCTGTAAGTGGATCCTAGCCCAAGGGCTTCCAT 365

QY 121 gcaactctctcagcccttgccatactccgcagtcgacagacaacccacagcag 180
  || || || || || || || || || || || || || || || || || || ||
Db 364 GCAACTTTTGCTCGGGCCCTGCCCCCTACATTTGGAGCGCTGGACAGTACAGCAAG 305

QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgtgctgctgcccc 240
  || || || || || || || || || || || || || || || || || || ||
Db 304 GTCTGGCCCTGTACACACAGCATACCCGGCGGCTCGCGGCCCTGCTGCTGCTCG 245

QY 241 caggacctggagccctgacctctgtactatgtttgggagagacccccaaagtggagcag 300
  || || || || || || || || || || || || || || || || || || ||
Db 244 CAGGCGCTGGAACCGCTGCCATCGGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 185

QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
  || || || || || || || || || || || || || || || || || || ||
Db 184 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGTTTA 146

RESULT 53
AL530080/c      AL530080      798 bp      mRNA      EST      13-FEB-2001
LOCUS      AL530080 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YM06 3
DEFINITION      prime, mRNA sequence.
ACCESSION      AL530080
VERSION      AL530080.1 GI:12793573
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT      142 a      228 c      274 g      145 t      9 others
ORIGIN

Query Match      50.4%; Score 170.8; DB 106; Length 798;
Best Local Similarity 72.8%; Pred. No. 4.6e-38;
Matches 246; Conservative 1; Mismatches 88; Indels 3; Gaps 2;

QY 1 gcttggacacaaattactgctccgcaacttggagagaactgctgtgccccctc 60
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Db 402 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGAACTGCTGCTGCGCAGCTG 343

QY 61 tacattgactccgacagagatctgggctggaagtgggtccatgaacctaaaggtactat 120
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Db 342 TACATTAACTTCGCAAGAGACCTCGGCTGGAGTGGATCCACGAGCCCAAGGGCTWCCAT 283

QY 121 gcaactctctcagcccttgccatactccgcagtcgacagacaacccacagcag 180
  || || || || || || || || || || || || || || || || || || ||
Db 282 GCAACTTTTGCTCGGGCCCTGCCCCCTACATTTGGAGCGCTGGACAGGAGCAAG 223

QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgtgctgctgcccc 240
  || || || || || || || || || || || || || || || || || || ||
Db 222 GTCTGGCCCTGTACACACAGCATACCCGG--GCCTCGGGCGCGCTGCGTGGCG 166

QY 241 caggacctggagccctgacctctgtactatgtttgggagagacccccaaagtggagcag 300
  || || || || || || || || || || || || || || || || || || ||
Db 165 CAGGCGCTGGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 106

QY 301 ctctcaacatggtggtgaagtcttgaatgtagctg 338
  || || || || || || || || || || || || || || || || || || ||
Db 105 CTGTCCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 68

RESULT 54
AL304490/c      AL304490      449 bp      mRNA      EST      01-FEB-1999
LOCUS      q054e06.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1912354 3'
DEFINITION      similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR (HUMAN); contains PTRS.t3 TARI repetitive element ;, mRNA
sequence.
ACCESSION      AL304490
VERSION      AL304490.1 GI:3988179
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@rmail.nih.gov
Tissue Procurement: Christopher Moskaiuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 933 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 385.
Location/Qualifiers
1..449
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/db_xref="taxon:9606"
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/tissue_type="adenocarcinoma"
/lab_host="DH10B"
FEATURES
source

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/notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
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oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      66 a 128 c 163 g  92 t
ORIGIN

Query Match      49.7%; Score 168.6; DB 18; Length 449;
Best Local Similarity 74.2%; Pred. No. 1.7e-37;
Matches 213; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 53 gccccctcacattgctccagagatctggctggaagtggtccatgaacccaag 112
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Db 449 GGCAGCTGTACATTGACTTCGCGAAGGACCTCGCTGGAAGTGGATCCACGAGCCCAAGG 390

QY 113 gtactatgcacaacttctgctcaggcccttggcccatatccctccgagtcgacacacccc 172
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QY 173 acaagcaggtgtggagactgtacaacactctgaacctgaagcatctgctcgtctgct 232
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QY 233 qcgtgccagagacctggagccctgacctctgtactatgttgtaggagacccccaaag 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GCGTGGCGGAGGCGCTGGAGCGCTGCCCATGTGTACTACGTGGGCGCGCAAGCCCAAGG 210

QY 293 tggagcagctctccacatggtgtgaagtctgtgtaaatgtagtga 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TGGAGCAGCTGCCACATGATCGTGGCTCTCTGCACAGTCGACGTGA 163

RESULT 55
AI360877/c
LOCUS      AI360877      328 bp      mRNA      EST      15-FEB-1999
DEFINITION qy01c06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2010730 3'
            similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  AI360877
VERSION     AI360877.1 GI:4112498
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1. (bases 1 to 328)
AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
JOURNAL    Unpublished (1998)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabps-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            CDNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

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Location/Qualifiers

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            /lab_host="DH10B"
            /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5',
            TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT  69 a  96 c 104 g  59 t
ORIGIN

Query Match      49.1%; Score 166.4; DB 19; Length 328;
Best Local Similarity 69.2%; Pred. No. 6.9e-37;
Matches 227; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 10 accaattactcttcgcgaacttgagagaaactgctgtgtgcgccccctctacattgac 69
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Db 328 ACCAGCTATTGGCTCAGCTCCGCTAGGAAGATCTGCTGGTGGCGAGCTGTACATTGAC 269

QY 70 ttccgacaggtatcggtggaagtgggtccatgaacctaaaggtactactatgccaaattc 129
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Db 268 TTCCGCAAGTACCTCGGCTGGAAAGTGGATTCTCGAGACACAAGGGCTACCATGTCAAGTTTC 209

QY 130 tgcctcagcccttgcctacatctccgcagtgagacacacccacagcagcgtgtcgtggga 189
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Db 208 TGCCTCGGGCCCTGCCCTACATTGGAGCCTGGACTCCGACAGCAAGGTTCCTGGGCC 149

QY 190 ctgtacaacactctgaacctgaacatctgcctgccttgcgtgcgtgcgccccaggacctg 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 CTGTACATCCAGCATACCCGGGCGCTCGGCGGTGCGGTGCTACCGCAGGCGCTG 89

QY 250 gagcccttgaccatctctactatgttggaggagacccccaaagtggagcagctctctccaa 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 GATCGCTGCCCATCGTGTACTACTTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTTTCAAC 29

QY 310 atggtggtgaagtcttgtaaaatgtagct 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 ATGATCGTGGCTCTCTGCAAGTGCAGCT 1

RESULT 56
AI272940/c
LOCUS      AI272940      292 bp      mRNA      EST      18-NOV-1998
DEFINITION q156g01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876368
            3', similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
            sequence.
ACCESSION  AI272940
VERSION     AI272940.1 GI:3895208
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1. (bases 1 to 292)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabps-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality

```

FEATURES

227

/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"

/note="Torgan; mixed (see below). Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI. Equal amounts of plasmid DNA from three normalized libraries (metanocyte 2NDH9, pregnant uterus NBHPu, and fetal heart NDH919W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

a	131 c	170 q	113 t	1 others
---	-------	-------	-------	----------

Query Match 47.3%; Score 160.4; DB 18; Length 499;
Best Local Similarity 70.8%; Pred. No. 3.8e-35;

Best Local Similarity	70.8%;	Pred: No. 3.8e-35;	Indole	1.	
Matches	226.	Conservative	0.	Mismatches	92.

Matches 220; conservative 0; mismatches 52; indels 1; gaps

22 ttccgcaacttggaggagaaactgctgtgtgcgcc-cctctacattgacttccgacagga 80

b 482 TTCCGCTCCCGGAAAAAATTGTTGGGTGGGCCCAAGTTGACTTGACATGTGTACATTGACTTCGCCAAGGA 42

87 tctgggctggaaattgggtccatgaacctaaaggctactatgccaaacttctactcagggcc 14

Y cccyyycyccyyaccyccacccccc
| | | | | | | | | |
vz cccyyycyccyyaccyccacccccc
| | | | | | | | | |

b 422 CCTCGGCTGGAAGTGGATCCACGAGCCCCAAGGGCTACCATGCCAACTTTGGCCTCGGGCC 36

141 ttgccataacctccgcagtgccagacacacccacagcacggtgctgggactgtacaacac 20

362 CTGCCCTACATTGGAGCCTGGACACGCAGTACAGCAAGTCTTGGCCCTGTACACCA 30

0
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Z

201 tctgaacctgaagcatctgcctcgcccttgctgcgtgccccaggacctggagccctgac 26

b 302 GCATAACCCGGGCGCCTCGGGCGGCCGTTNTGCGTGCCGCGCAGCGCTGGAACCCCTGCC 24

261 catcctgtactatgttggaggagaccccccaaaagtggagcagctctccaaacatggtggtgaa 32

RESULT	57				
AI273619/c					
LOCUS		AI273619	499 bp	mRNA	EST
DEFINITION		q156c01.xl Soares_NHHPu_Sl Homo sapiens cDNA clone IMAGE:1876320 3' similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.t3 PTR5 repetitive element ; mRNA			29-JAN-1999

LOCUS	AT273619	459 bp	mRNA	EST	29-JAN-1999
DEFINITION	<p>q356c01.x1 Soares_NHMPu_11 Homo sapiens cDNA clone IMAGE:1876320 3. similar to gp:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.t3 PTR5 repetitive element ; mRNA sequence.</p>				

VERSION AI273619.1 GI:3895887

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Ch

Mammalia; Eutheria; Pr

REFERENCE 1 (bases 1 to 499)

AUTHORS NCI-CGAP <http://www.nci.nih.gov>

TITLE National Cancer Institute

Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Straus

Email: cgapbs-remail.n

This clone is available


```

TITLE      The WashU-HMMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
           WashU-HMMI Mouse EST Project
           Washington University School of Medicinep
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:256016

Trace considered overall poor quality
Seq primer: Exprimer
High quality sequence stop: 1.
          Location/Qualifiers
source    1..431
          /organism="Mus musculus"
          /strain="C57BL/6J"
          /db_xref="taxon:10090"
          /clone_name="IMAGE:421464"
          /clone_lib="Soares mouse embryo NBME13.5 14.5"
          /sex="unknown"
          /tissue_type="embryo"
          /dev_stage="13.5-14.5dpc total fetus"
          /lab_host="DH10B"
          /notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Site 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTTTT]
T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT   91 a 138 c 117 g      85 t
ORIGIN

Query Match       44.7%; Score 151.6; DB 191; Length 431;
Best Local Similarity 71.4%; Pred.No.1.2e-32;
Matches 227; Conservative 0; Mismatches 89; Indels 2; Gaps 2;

Qy  1  gcttgaccaccaattactgcttcgcgaacttgaggagaaactcgtgtgcgccctc 60
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  98  GCCCTGGATACCAACTATTGTTCAGTCCACAGAGAAGAACTGCTGTGTGCGGCATG 157

Qy  61  tacattgactccgcacaggatctggctggaagtgggtccatgaacctaaaggctactat 120
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  158 TACATTGACTTTAGGAGGACCCTGGGTGGAGTGGATCCACGAGGCCAAGGGGTACCAT 217

Qy  121 gccaaactctgctcaggcccttgcccatactccgcagtcgagcacacaacccaagcacg 180
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  218 GCCAACTCTCTCTGGGACCCTGCCCCCTATATTGGAGCCTGGACACACAGTACAGCAAG 277

Qy  181 gtgctggagctgtacacacactctgaacctgaagcatctgctcgctgtgctgctgcccc 240
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  278 GTCTTGGCCCTCTACAACCAACACAAACCGGGCGCTTCGGGCTCACCGTGTGCGTGC 337

Qy  241 caggacctgaagccctgacacatctctactatgtttggaggaccccccaagtggagcag 300
     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  338 CA-GTTTGGGAGCCACTGGTTCATCGTCTACTACGTGGGAGCAAGCCC-AGGTTGTGCAG 395

Qy  301 ctctccaacatggtggtg 318
     ||| ||| ||| ||| |||
Db  396 TTGTCCACACATGGATGTG 413

RESULT 63
BF682484/c

```


Best Local Similarity 71.0%; Pred. No. 1.8e-30;									
Matches 218; Conservative 0; Mismatches 86; Indels 3; Gaps 2;									
Qy	1	gcttggacacaaattactgtcttcgcgaacttgagagaaactgtgtgctgcgcctc	60						
Db	222	GCCTGGATACCAACTATTCCTCAGCTCCACAGAGAAGAACTCTGTGTGGCAGTNG	281						
Qy	61	tacattgactccgcacaggatctggctgggaagtgggtccatgaacctaaaggctactat	120						
Db	282	TACATTGACTTTAGGAAGGACCTGGTTTGGAGTGGATCCACGAGCCCAAGGCTACCAT	341						
Qy	121	gccaaactctgtcaggcccttgcccatatccctgcagtcgcagacacaaaccacagcacy	180						
Db	342	GCCAACTTCTCTCGGGACCCCTGCCCTATATTTGGAGCCCTGGACACACAGTACAGAAG	401						
Qy	181	gtcgtggagctgtacaacactctgaacctgaacctgaacctcctgcctgcctgtgtcgctgcc	240						
Db	402	GTCTTCGCCCTCTACAACCAACACAACCCGGCGCTTCGGCGTCCACGCTGCTGGTGGCG	461						
Qy	241	caggacctggagcccttgacctcctgtactatgttgggagagacccccaaagtggagcag	300						
Db	462	ACG--TTTGGAGCCACTGCCCATCGTCTACTACG-TGGGTCCGAACCCAAAGTGGAGCAG	518						
Qy	301	ctctccca 307							
Db	519	TTGTCCA 525							
RESULT	67								
BG540633		889 bp	EST	03-APR-2001					
LOCUS	602570520F1	NIH_MGC_77	Human sapiens cDNA clone	IMAGE:4694836	5',				
DEFINITION	BG540633		mRNA						
ACCESSION	BG540633								
VERSION	BG540633.1	GI:13532879							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	1 (bases 1 to 889)								
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .								
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)								
	Contact: Robert Strausberg, Ph.D.								
	Email: cgapb-r@email.nih.gov								
	Tissue Procurement: CLONTECH Laboratories, Inc.								
	cDNA Library Preparation: CLONTECH Laboratories, Inc.								
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)								
	DNA Sequencing by: Incyte Genomics, Inc.								
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov								
	Plate: LCM1519 row: h column: 05								
	High quality sequence stop: 562.								
FEATURES	Location/Qualifiers								
source	1. .889								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
	/clone="IMAGE:4694836"								
	/clone_lib="NIH_MGC_77"								
	/lab_host="DH10B (T1 phage-resistant)"								
	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1: Sfil (ggcgccctgcgc); Site:2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGGCACATG-dt(30)BN-3' (where B = A, C, G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."								
BASE COUNT	260 a 230 c 190 g 209 t								

BASE COUNT	260 a	230 c	190 g	209 t
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ORIGIN
Query Match      42.4%;   Score 143.6; DB 155; Length 889;
Best Local Similarity 68.2%; Pred. No. 2.5e-30;
Matches 214; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

QY    1 gctttggacaccattactgcttccgcgaacttgagaggagaactgtgtgccccctc 60
Db    274 GCTTTGGATCGGGCCTATTGCTTTAGAATAATGCAGGATAATTGTGCTACGTCCACTT 333

QY    61 tacattgactccc-gacaggatctgggctggaagtgggtccataaacctaagggcacta 119
Db    334 TACATTGATTTCAAGAGGGCATCTAGGGTGGAATGGATACAGNACCACCAAGGGTACAA 393

QY    120 tgcacaattctgtctcaggcccttggccataacctccgcagtcgagacacacccacgac 179
Db    394 TGCCAACATTCTGTCTGGAGCATGCCCGTAATTTATGGAGTTTCAGACACTCAGCACAGCAG 453

QY    180 ggctgtgggactgTcacaaactctgaaacctgaaagcatctgccctcgcttctgcgtgcc 239
Db    454 GGTCCTGAGCTTATATAATACCATAAATCCAGANGCATCTGCTTCTCCTGCTGGCTGTC 513

QY    240 ccaggacctggagccctgaccatctgtactatgttggggagcccccaagtggagca 299
Db    514 CCAAGATTGAACCCCCCTAAACATTTCTACTACATTGGAAAACACCCCAAGATGSAACAG 573

QY    300 gctctccaacatgg 313
Db    574 CTTTTCTAATATTG 587

```

RESULT	68
AW295761/c	
LOCUS	
DEFINITION	AW295761 409 bp mRNA EST 16-JAN-2000 UT-H-BIL-afh-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721675 3', mRNA sequence.
ACCESSION	AW295761
VERSION	AW295761.1 GI:6702397
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 409)
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CCAP clone distribution information can be found through the I. M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 102-157,

```
>GC_rich#low_complexity
Seq primer: M13 Forward
POLYA=Yes.
```

```

FEATURES
source
Location/Qualifiers
1. .409
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2721675"

```

```

/clone_lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library

```



```
source
1: 1430
/organism="Homo sapiens"
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1. .456
/organism="Homo sapiens"

Db	352	AATGCTGAAACAAATATCTCAGATTTTGGCCCTTGACAAAGCATCACAAACCCAGGAGCC	411
Qy	217	tctgctcgccttgctgctgcccaggacctggagccctgaccactcctgtactatgtt	276
Db	412	TTGGCCACCCCTGCTGTGTTCCCAAGGACTGGACCCACTGCCAATCCTCTACTAGTG	471
Qy	277	ggagagcccccacaaagtggagcagctctccacatagtgtgtaagtcttgtaaatagc	336
Db	472	GCAGCAACACAAGGTGGAGCAGCTGTCCAATATGATCGTGAAGTCTTGCAAGTAGC	531
Qy	337	tga 339	
Db	532	TAA 534	
RESULT	76		
LOCUS	AI918883	392 bp mRNA EST	28-JUL-1999
DEFINITION	tu13b10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250907 3' similar to gb:X02812 cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 MER22 repetitive element ;, mRNA sequence.		
ACCESSION	AI918883		
VERSION	AI918883.1	GI:5638738	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 335.		
FEATURES	Location/Qualifiers		
source	1..392		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2250907"		
	/clone_lib="NCI_CGAP_Pr28"		
	/sex="male"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIds 985608-986759, 1101192-1101959, and 1217528-122615). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	57 a	117 c	150 g
ORIGIN	67 t 1 others		
Query Match	39.7%;	Score 134.6;	DB 103; Length 392;
Best Local Similarity	73.6%;	Pred. No. 7.7e-28;	
Matches 184;	Conservative 0;	Mismatches 65;	Indels 1; Gaps 1;

Qy	90	gaagtgggtccatgaacctaaagggtactactatgccaactctctgctcagggcccttgcccata	149
Db	388	GAAGTGGATCCAGAGCC-AAGGGCTACCATGGCCNACTTCTGCGGCGCTCGCCCTA	330
Qy	150	ctcccgagtcgagacacacacacagcagcggtgctgggactgtacacactctgaaccc	209
Db	329	CAITTTGGAGCCTGGACACGAGTACACAGAGTCTTGCCCTGTACAAACGACATACCC	270
Qy	210	tgaagcatctgccttcgcttgcctgctgctgccccaggacctggagcccttgaccctctgta	269
Db	269	GGCGCGCTCGCGCGCGCGTCTGCTGCGCGCAGCGCTGGAGCGCTGCGCCATCGTGTA	210
Qy	270	ctatgttgaggagaccccccaaaagtggagcagctctcaacatggtggtgaagtctttaa	329
Db	209	CTAGTGGCGCCGAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCCTCTCGAA	150
Qy	330	atgtagctga 339	
Db	149	GTGACGCTGA 140	
RESULT	77		
LOCUS	AA533093/c	542 bp mRNA EST	21-AUG-1997
DEFINITION	nj19g04.s1 NCI_CGAP_AAL Homo sapiens cDNA clone IMAGE:992982 3' similar to gb:X02812 cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA sequence.		
ACCESSION	AA533093		
VERSION	AA533093.1	GI:2277189	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 542)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert length: 1687 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 142.		
FEATURES	Location/Qualifiers		
Source	1..542		
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	/clone="IMAGE:992982"		
	/clone_lib="NCI_CGAP_AAL"		
	/tissue_type="adrenal adenoma"		
	/lab_host="SOLR (kanamycin resistant)"		
	/note="Organ: adrenal gland; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Two pooled bulk adrenal adenomas. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.6 kb."		
BASE COUNT	92 a	152 c	196 g
ORIGIN	102 t		
Query Match	39.6%;	Score 134.2;	DB 8; Length 542;

T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Patima Bonaldo."

```

BASE COUNT      129 a   168 c   150 g   106 t
ORIGIN

Query Match      39.4%;   Score 133.4;   DB 1;   Length 553;
Best Local Similarity 72.4%;   Pred. No. 1.8e-27;
Matches 173;   Conservative 0;   Mismatches 66;   Indels 0;   Gaps 0;

QY 1 gcttggacaccaatactgctccgaaactggaggagaactgtgtgtgcgccccctc 60
    || || || || || || || || || || || || || || || || || || || ||
DB 222 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAAGTGTGTGCGGCACG 281

QY 61 tacattgactccgacagatctggctgggaagtgggtccatgaacctaaaggtactat 120
    || || || || || || || || || || || || || || || || || || || ||
DB 282 TACATTGACTTTAGGAAGGACCTGGGTGGGAAGTGGATCCACGAGCCCAAGGCTACCAT 341

QY 121 gcaactctctcagcccttgcccatcctcccgagtcgacagacacacccacagcacg 180
    || || || || || || || || || || || || || || || || || || || ||
DB 342 GCCAATTCTGCTGGGACCCCTGCCCTATATTGGAGCCTGCACACAGTACAGCAAG 401

QY 181 gtgtgggactgtacacactctgaacctgaagcatctgcctgcctgtgtgtgcgtgcc 239
    || || || || || || || || || || || || || || || || || || || ||
DB 402 GTCCTTGCCCTCTACACCAACACACACCGGGCGCTTCGGCGCTCACCGTGCTCGTGCC 460

RESULT 80
C86748/c
LOCUS      C86748      589 bp      mRNA      EST      11-MAR-1998
DEFINITION C86748 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA
ACCESSION C86748
VERSION    C86748.1 GI:2918705
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 589)
AUTHORS    Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
            DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., and Doi,H.
            Systematic analyses of genes expressed in fertilized mouse eggs(The
            ERATO/Doi Project at Wayne State University)
JOURNAL    Unpublished (1998)
COMMENT    Contact: Hirofumi Doi
            Doi Biosymmetry Project, ERATO
            Japan Science and Technology Corporation (JST)
            WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
            Email: hdebioa.jst.go.jp.
            Location/Qualifiers
FEATURES    source
            1..589
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="J0232C11"
            /clone_lib="Mouse fertilized one-cell-embryo cDNA"
            /dev_stage="fertilized one-cell-embryo"

BASE COUNT      145 a   123 c   141 g   171 t   9 others
ORIGIN

Query Match      39.2%;   Score 133;   DB 156;   Length 589;
Best Local Similarity 67.4%;   Pred. No. 2.4e-27;
Matches 230;   Conservative 0;   Mismatches 107;   Indels 4;   Gaps 3;

QY 3 ttggacaccaatactgctccgaaactggaggagaactgtgtgtgcgcccc-ctct 61
    || || || || || || || || || || || || || || || || || || || ||
DB 454 TTGGAATGCTCCCTACTGCTTTGAAATGTGAGGATAATGCTGCCTTTTCGCCNCTTT 395

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QY 62 acattgactccgacaggaatctgggtggaatgg--gtccatgaacctaaagggctacta 119
    || || || || || || || || || || || || || || || || || || || ||
DB 394 ACATGAATTTTAAAGAGGATCTTTGGATGGAATGGAATCATGAANCCCAAGGGTACAA 335

QY 120 tgccaactctctcagggcccttg-cccatacctccgagtcagacacacacccacagca 178
    || || || || || || || || || || || || || || || || || || || ||
DB 334 TGCTAACTTTCTGTGCTGGGGCATGCCCATATCTATCTATGTAGTTCAGACACTCAACACACCA 275

QY 179 cggctgtggagactgtacaacactctgaacctctgaacctctgcctgcctctgcgtgc 238
    || || || || || || || || || || || || || || || || || || || ||
DB 274 AAGTCCTCAGCCCTGTACAACACCATAAATCCGAAGCTTCGCCCTTCCTGCTGTGTGTGT 215

QY 239 ccagagactctggagcccttgacctctgttactatgttgggagagaccccccaaaagtgcg 298
    || || || || || || || || || || || || || || || || || || || ||
DB 214 CCAGAGACTGTGGAACCACTGACCATTCTCTATTACATTGGAAATACGCCCAAGATCGAAC 155

QY 299 agctctccacaatcgtgtgtggaagtcttgtaaatgtagtctga 339
    || || || || || || || || || || || || || || || || || || || ||
DB 154 AGCTTTCCAATATGATTGTCAAGTCTTGTAAATGCAGCTAA 114

RESULT 81
A0016439/c
LOCUS      A0016439      465 bp      mRNA      EST      15-OCT-1998
DEFINITION A0016439 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone
ACCESSION A0016439
VERSION    A0016439.1 GI:3371443
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 465)
AUTHORS    Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., DePalma,G.E.,
            Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
            Systematic analyses of genes expressed in 2-cell stage mouse
            embryos (The ERATO/Doi Project at Wayne State University) (Ko
            ,M.S.H. et al.)
JOURNAL    Unpublished (1998)
COMMENT    Contact: Hirofumi Doi
            Doi Biosymmetry Project, ERATO
            Japan Science and Technology Corporation (JST)
            WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
            Email: hdebioa.jst.go.jp.
            Location/Qualifiers
FEATURES    source
            1..465
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="J0725B08"
            /clone_lib="Mouse two-cell stage embryo cDNA"
            /dev_stage="two-cell stage embryo"

BASE COUNT      123 a   97 c   112 g   127 t   6 others
ORIGIN

Query Match      38.5%;   Score 130.4;   DB 107;   Length 465;
Best Local Similarity 70.7%;   Pred. No. 1.2e-26;
Matches 212;   Conservative 0;   Mismatches 85;   Indels 3;   Gaps 3;

QY 42 ctgctgtgtgcgccccctctacattgacttccgacaggaatctgtggctggagtggtgcc 101
    || || || || || || || || || || || || || || || || || || || ||
DB 412 CTGNCCTTCGCCCTCTCTTTTACATTGATTTTANGNGGGATCTGGNATGGAATGGATCCC 353

QY 102 tgaacctaaaggctactatcccaac-ttctgctcaggcccttgcctacactccgcagtg 160
    || || || || || || || || || || || || || || || || || || || ||
DB 352 ATGACCCAAAGGGTACAATGCTAATCTTCTGCTGGGGCATGCCCATATCTATGGAGTT 293

QY 161 cagacacacac-ccacagcagcgtgtgtgggactgtacaacactctgaacctctgaacctct 219
    || || || || || || || || || || || || || || || || || || || ||
DB 292 CAGACACTTCAACACACCAACCAAGCTCTCAGCCTGTGTACAAACACCATATAAATCCCGAA-CTTCC 234

```

Qy	220	gcttcgcgttgctgctggccccaggagacctggagcccccgtaccatcctgttactattgtttggg	279
Db	233	GCTTCCCTTGCTGCTGTGTGCCAGGATCTGGAAACCACTGCACCATTCTCTATTACATTGA	174
Qy	280	aggacccccaaagtggacgagctctccaacatggtgtagtgaagcttgtataatgtagctga	339
Db	173	AATACGCCCAAGATCGAACAGCTTTCCAATATGATTGTCAAAGTCTTGTAATAACGACTAA	114
RESULT 82			
BE737006			
LOCUS	BE737006	915 bp mRNA EST	15-SEP-2000
DEFINITION	601306767F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641081 5', mRNA sequence.		
ACCESSION	BE737006		
VERSION	BE737006.1 GI:10150998		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 915)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ARCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LCM346 row: e column: 18 High quality sequence stop: 424.		
FEATURES	Location/Qualifiers		
source	1..915		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3641081"		
	/clone_lib="NIH_MGC_39"		
	/tissue_type="adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: pancreas; Vector: pOTB7; Site1: XhoI; Site2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(C). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	229 a	279 c	276 g 131 t
ORIGIN			
Query Match	38.1%;	Score 129.2;	DB 139; Length 915;
Best Local Similarity	73.4%;	Pred.No. 3.1e-26;	
Matches 179;	Conservative	0;	Mismatches 63; Indels 2; Gaps
Qy	1	gccttgacaccaattactgtctccgcaacttggaggagaactgctgtgcgcccccctc	60
Db	189	GCCTTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGACTGCTGCGTGGCAGAGCTG	248
Qy	61	tacattgacttcgcagagcatgtggctcggaagtgggtccatgaaacctaaagggtcactat	120
Db	249	TACATTGACTTCGCAAGGACCTCGCTGGAGTGGATCCACGAGCCCAAGGCGTACCAT	308
Qy	121	gccaaacttctgcaggcccttgccccataacctccgcagtcgacagacaaccccacagcacg	180
Db	309	GCCAACTTCTGCTCGGGCCCTGCCCTCATATTGGAGCTTGACACGACGAGTACAGCAAG	368

<p>double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."</p>										
BASE COUNT	195 a	102 c	107 g	154 t	2 others					
ORIGIN										
Query Match	36.9%;	Score 125.2;	DB 159;	Length 560;						
Best Local Similarity	71.88;	Pred.No. 3.8e-25;								
Matches 163;	Conservative	0;	Mismatches 64;	Indels	0;	Gaps	0;			
Qy	113	gctactatgcaaacctctgtcgagcccttgcccataccctccgagtcgagcacacaccc	172							
Db	6	GGTAACTGCCAACTTCTGCTGAGCATGCCCGTATTATGGAGTTGAGACACTCAGC	65							
Qy	173	acagcagcgtgctgggactgtacacactctgaacctgaacctgcctgcctgccttgc	232							
Db	66	ACACAGCGGTCTGAGCTTATATAATACCAATAATCAGGAAGCATCTGCTTCCNTGCT	125							
Qy	233	gcctgccccaggaacctgagccctgacacactcctgtactatgctgggagagaccccaag	292							
Db	126	CGGTGTCCTCCAGAGATTAGAACCTCTAACCACTTCTACTATGGCAAAACACCCAA	185							
Qy	293	tggagcagctctccaacatggtggtgaagctcttgtaaatgtagctga	339							
Db	186	TTGAACAGCTTCTAATATGATGTAAAGCTCTTGCAATACGACTAA	232							
RESULT 85										
AI452742/c										
LOCUS	AI452742	396 bp	mrna	EST	13-APR-1999					
DEFINITION	tj45a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone									
	IMAGE:2144432 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH									
	FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.t3 MSRI repetitive									
	element ;, mRNA sequence.									
ACCESSION	AI452742									
VERSION	AI452742.1	GI:4287481								
KEYWORDS	EST.									
SOURCE	human.									
ORGANISM	Homo sapiens									
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 396)									
AUTHORS	NCI-CCAP									
TITLE	http://www.ncbi.nlm.nih.gov/ncicgap.									
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),									
	Tumor Gene Index									
JOURNAL	Unpublished (1997)									
COMMENT	Contact: Robert Strausberg, Ph.D.									
	Email: cgapbs-r@mail.nih.gov									
	This clone is available royalty-free through LML; contact the									
	IMAGE Consortium (info@image.llnl.gov) for further information.									
	Insert Length: 529 Std Error: 0.00									
	Seq primer: -40UP from Gibco.									
FEATURES	Location/Qualifiers									
source	1..396									
	/organism="Homo sapiens"									
	/db_xref="taxon:9606"									
	/clone="IMAGE:2144432"									
	/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"									
	/lab_host="DH10B"									
	/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with									
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;									
	Equal amounts of plasmid DNA from five normalized									
	libraries were mixed, and ss circles were made in vitro.									
	Following HAP purification, this DNA was used as tracer in									
	a subtractive hybridization reaction. The driver was									
	PCR-amplified cDNAs from pools of 5,000 clones made from									
	the same 5 libraries. The pools consisted of the following									
	libraries and clones: Soares NBHSF pool 1:									
	309384-310919, 323208-325895 Soares NB2HP pool 1:									

145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 57 a 106 c 144 g 88 t 1 others
ORIGIN

Query Match 36.8%; Score 124.6; DB 20; Length 396;
Best Local Similarity 71.5%; Pred. No. 5.3e-25;
Matches 163; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 112 ggtactatgccaactctgtcagcccttgccctacccctgcagtcagacacac 171
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 396 GGCTACCATGCCAATCTGCTCGGCGCTGCCCTACATTTGGAGCCTGGACACG 337
QY 172 cacagcacaggtgtggagctgtacacactctgaacccctgaacccctgtgc 231
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 336 TACAGCAAGGTCTGCTGCCCTGTACACACGATACCCGGCGCTCGGCGCGCTT 277
QY 232 tgcgtgccacaggaacctgaagccctgaccatctgtactatgttgaggagaccccaaa 291
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 TCGCTTCCGAGCGCTGGAACCGCTGCCCATCGTACTACGTGGGCCCAAGCCCAAG 217
QY 292 gtggagcagctctccaacatgggtggaagtcttgaatgtagctga 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 GTGGACGAGCTGTCCAAACATGATCGTGGCGCTCTGCAAGTGCAGTGA 169

RESULT 86
BF682938
LOCUS 748 bp mRNA EST 21-DEC-2000
DEFINITION 602117568F1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 5', mRNA sequence.
ACCESSION BF682938
VERSION BF682938.1 GI:11956937
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 748)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM8476 row: h column: 18
High quality sequence start: 26
High quality sequence stop: 746.
Location/Qualifiers
1. .748
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3468737"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not

FEATURES
source
1. .748
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3468737"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the
modified pTT3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 189 a 220 c 189 g 150 t
ORIGIN

Query Match 36.5%; Score 123.6; DB 168; Length 748;
Best Local Similarity 72.7%; Pred. No. 1.2e-24;
Matches 173; Conservative 0; Mismatches 64; Indels 1; Gaps 1;
QY 1 gcttggacacccaattactgtcttcgaacttggaggagaactgtgtgtgccccctc 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 GCCTGGATACCACTATTGCTTCAGTCCACAGAGAGAACTGCTGTGGCGGACGTG 571
QY 61 tacattgattccacaggaatctggctgggaagtgcctgaacctgaagggctactat 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 TACATTGACTTTAGGAGGACCTGGGTGGAGTGGATCCAGGCCCAAGGCTACCAT 631
QY 121 gccaaacttctcagggcccttgcctacatctccgcagtcagacacacacacagcagc 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 GCCAACTTCTGCTGGGACCTGCCCCCTATATTGGAGCTGGACACACAGTACAGCAAG 691
QY 181 gtgctggagctgtacacactctgaacccctgaagcatctgcctcgtctgctgtgc 238
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 GTCCTTGCCCTCTAACAA-ACACAACCCGGCGCTTCGGCGTCCACCGTCTGCGTGC 748

RESULT 87
AA016946
LOCUS 533 bp mRNA EST 21-JAN-1997
DEFINITION AA016946.1 GI:1478533
ACCESSION AA016946
VERSION AA016946.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 533)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:269814
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 133.
Location/Qualifiers
1. .533
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:44478"
/clone_lib="Soares mouse placenta 4NBMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"

FEATURES
source
1. .533
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:44478"
/clone_lib="Soares mouse placenta 4NBMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"

found through the I.M.A.G.E. Consortium/LLNL at:

source

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1. .639
/organism="Mus musculus"
/db xref="taxon.10090"
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/clone="IMAGE:3972226"
/clone_lib="Soares_NMEBA_branchial_arch"
/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAAGTGGAGCGCCGATCATTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT      159 a 192 c 160 g 123 t      5 others
ORIGIN

Query Match      33.7%; Score 114.2; DB 168; Length 639;
Best Local Similarity 70.6%; Pred. No. 5.3e-22;
Matches 149; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgaactggagagaactgctgtgagccccc 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 427 GCCTGGATACCAATTATTGCTTCACCTCCACAGAGAAGAACTGCTGTGCGG 486
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 tacattgaactccgacagatctggctggagagtggtggtccatgaacctaaaggctactat 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 487 TACATTGACTNTANGAAGGACCTGNGTTGGAAGTGTGATCCAGGCCCAAGGCTACCAT 546
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 gccaaacttctgcagccctggccatccctccgcagtcgacgacacaaacacagca 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 GCCAACTTCTGTGGAGCCCTGCCCTATATNTGGAGCTGGACACACAGTACAGCAAG 606
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 gtgctggagactgtacaaactctgaacctgt 211
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 607 GTCCTTGCCCTCTACAAACCAACACACCCCG 637
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 94
BE377489
LOCUS      BE377489      684 bp      mRNA      EST      21-JUL-2000
DEFINITION 601228968F1 NC1_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3592768 5',
mRNA sequence.
ACCESSION  BE377489
VERSION    BE377489
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 684)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.lnl.gov
          Plate: LAM8764 row: h column: 17
          High quality sequence stop: 575.
          Location/Qualifiers
            1..684
              /organism="Mus musculus"
              /strain="FVB/N"
              /db_xref="taxon:10090"
              /clone="IMAGE:3592768"
              /clone_lib="NC1_CGAP_Mam1"

FEATURES             source
  source
    1..684
      /organism="Mus musculus"
      /db_xref="taxon:10090"
      /clone="IMAGE:3592768"
      /clone_lib="NC1_CGAP_Mam1"

```

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/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT      152 a 170 c 212 g 150 t
ORIGIN

Query Match      33.5%; Score 113.6; DB 166; Length 684;
Best Local Similarity 89.7%; Pred. No. 7.9e-22;
Matches 122; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 204 gaaccctgaagcatctgctcgcttgcgtgccccagagctggagccctgacct 263
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAACCCAGAGCGCTGCTGCTCGCCATGCTGCTGCCCCAGGACCTGGAGCCCTGACCAT 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 264 cctgtactatgttggaggagcccccaagtgagcagctctccaaacatggtgtagtc 323
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CTTCTACTATGTGGCAGAACCCCAAGGTGGAGCAGCTGTCCAACATGTTGGTGAAGTC 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 324 ttgtaaatgtagctga 339
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GTGTAAGTGCAGCTGA 136
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RESULT 95
BE157967/c
LOCUS      BE157967      175 bp      mRNA      EST      21-JUN-2000
DEFINITION MR2-HT0377-150200-202-d09 HT0377 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE157967
VERSION    BE157967.1 GI:8620688
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 175)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE  20202663
COMMENT   Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-MR2-HT0377-150
          200-202-d09et3-2000-02-15et4-1)
          Seq primer: puc 18 forward
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              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_lib="HT0377"
              /dev_stage="Adult"
              /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
              Site_2: SmaI; A mini-library was made by cloning products

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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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BASE COUNT      36 a   53 c   45 g   41 t
ORIGIN

Query Match      33.0%; Score 112; DB 164; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgaacttggaggaactgtgtgtgccccctc 60
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Db 136 GCTTTGGACACCAATTACTTCTCCCACTTGGAGGAGAACTGCTGTGCGCCCTC 77
|||||

QY 61 tacattgactccgacagatctggctggaagtggctccatgaacctaaag 112
|||||
Db 76 TACATTGACTCCGACAGGATCGGGTGGAGTGGTCCATGACCTAAGG 25
|||||

RESULT 96
BF901708/c      255 bp      mRNA      EST      18-JAN-2001
LOCUS
DEFINITION      CM2-MT0190-091200-595-a10 MT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BF901708
VERSION
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM2&t2=CM2-MT0190-
091200-595-a10&t3=2000-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 234.
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Location/Qualifiers
1..255
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0190"
/dev_stage="Adult"
/Note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      47 a   72 c   85 g   51 t
ORIGIN

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ORIGIN

Query Match 33.0%; Score 112; DB 171; Length 255;
Best Local Similarity 72.1%; Pred. No. 1.8e-21;
Matches 173; Conservative 0; Mismatches 65; Indels 2; Gaps 2;

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QY 1 gctttggacacaaattactgtctccgaacttggaggaactgtgtgtgccccctc 60
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Db 239 GCATTGGACACCAACTATTCTTCAGTTCCACGGAGAAAGAACTGCTGCTGCGCAGCTG 180
|||||

QY 61 tacattgactccgacagatctggctggaagtggctccatgaacctaaagggctactat 120
|||||
Db 179 TACATTGACTTCCGCAAGGACCCCGCTGGAGTGGATCCACGAGCCCAAGGGCTACCAT 120
|||||

QY 121 gccaaactcttg-ctcaggcccttgcctacatccctccgagtcagacacacacacagcac 179
|||||
Db 119 GCCAACTTCTGCTCGGGCCCTGCCCATACATTTTGAGCCCTGTACACGAGTACAG-AA 61
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QY 180 ggtgtgggactgtacacacactctgaacctgtgcctcgaagcatctgcctctgtgctgtgcc 239
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Db 60 GGTCTTGGGCTGTACAACCAACGCAACCCGGCGCTACGGCGCGCGTCTCGCGGCC 1
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RESULT 97

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AA927529      428 bp      mRNA      EST      17-JUN-1998
om71a11.s1 NCI-CGAP.GC4 Homo sapiens cDNA clone IMAGE:1552604 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR (HUMAN);, mRNA sequence.
AA927529
AA927529.1 GI:3076426
EST.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 501 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 141.
FEATURES
Location/Qualifiers
1..428
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1552604"
/clone_lib="NCI-CGAP.GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pT7D3-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      74 a   118 c   154 g   82 t
ORIGIN

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Query Match          32.7%; Score 111; DB 13; Length 428;
Best Local Similarity 66.8%; Pred. No. 3.9e-21;
Matches 189; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY 58 ctctacattgacttcgcacagatctggctggaagtgg-gtccatgaacctaaaggcta 116
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DB 424 CTGTACATTGACTTCGCGAAGGACCTCGCGCTGGAAGTGGATTCCAGCTAGCCAAAGGGGTA 365

QY 117 ctatgcacacttctcctcaggccctggccatccctccagtcgacacacacccacag 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 CCATGCCCACTTCTGTCCCTCGCGCTGCCCTTACATTTGGAGCCTGGACGAGTACAT 305

QY 177 cagcgtgctgggactgtacacactctgaacctgaagcatctgctcgtcgttgcgtg 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 CAAGGTCTTGCCTGTACAAACAGCATATTACCCGCGCTCGCGCGCGGTGTGCGTG- 244

QY 237 gcccagggacctggagccctgacctctgtactatgttgggagaccccccaagtggg 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 --CGAGGCGCTGGAGCGCTGCCATCGTGTACTACGTGTGCGCGAAGCCCAAGGTGGA 188

QY 297 qcagctctccaacatggtgtgaagtctgtgaaatgactga 339
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DB 187 GCAGCTGTCCACATGATCGTGGCTCTGCAAGTGCAGCTGA 145

RESULT 98
AW579188/c
LOCUS          AW579188      248 bp      mRNA      EST      16-MAR-2000
DEFINITION    RC1-DT0028-130100-011-h01_1 DT0028 Homo sapiens cDNA, mRNA
sequence.
ACCESSION    AW579188
VERSION      AW579188.1 GI:7254237
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 248)
AUTHORS      HCGP http://www.ludwig.org.br/ORESTES.
TITLE        The FAPESP/LICR Human Cancer Genome Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-DT0028-130100-011-h01.1&t3=2000-01-13&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 206.

FEATURES
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               /db_xref="taxon:9606"
               /clone_lib="DT0028"
               /dev_stage="Adult"
               /note="Organ: denis_drash; Vector: puc18; Site_1: SmaI;
               Site_2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
BASE COUNT    65 a 49 c 58 g 76 t
ORIGIN

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Query Match          32.6%; Score 110.4; DB 118; Length 248;
Best Local Similarity 69.4%; Pred. No. 5.2e-21;
Matches 150; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 124 aacttctgctcagcccttggccatccctcgcagtcgacacacacccacacgcggtg 183
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DB 220 AACATCAGAGCTGGAGCATGCCGTATTATTATGGAGTTCAGACACTCAGCACAGGGTTC 161

QY 184 ctgggactgtacaacactctgaacctgaacatctgctcgccttgcgtgcgcacag 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 CTGAGCTTATTATTATACCATTAAGTCTCTGAAGCATCTGCTTCTCTCTGTCGGGGTCCCAA 101

QY 244 gacctggagcccttgaccatctgtactatgttgggagaccccccaagtggagcagctc 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 GATTTAGAACCTCTAACCATTTCTACTTACATTGGCATTAACCCCAAGATTGAACAGCTT 41

QY 304 tccaacatggtggtgaagctctgttaaatgtagctga 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 40 TCTTATATGATTGTAAAGTCTTGTCAAATGCAGCTAA 5

RESULT 99
AW600960/c
LOCUS          AW600960      266 bp      mRNA      EST      23-MAR-2000
DEFINITION    RC1-BN0014-210100-012-h01_1 BN0014 Homo sapiens cDNA, mRNA
sequence.
ACCESSION    AW600960
VERSION      AW600960.1 GI:7305699
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 266)
AUTHORS      HCGP http://www.ludwig.org.br/ORESTES.
TITLE        The FAPESP/LICR Human Cancer Genome Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-210100-012-h01.1&t3=2000-01-21&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 218.

FEATURES
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               /clone_lib="BN0014"
               /dev_stage="Adult"
               /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
               Site_2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
BASE COUNT    72 a 51 c 59 g 84 t
ORIGIN

```

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Query Match          32.4%; Score 110; DB 118; Length 266;
Best Local Similarity 72.2%; Pred. No. 6.9e-21;
Matches 143; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 30, 2001, 08:48:51 ; Search time 17.46 Seconds
(without alignments)
392.355 Million cell updates/sec

Title: TGFB3P

Perfect score: 634

Sequence: 1 ALDNYCFRNLNCCVRPL.....RTPKVEQLSNVMVKCKCSX 113

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	633	99.8	112 12 AAR12404	Transforming Growth
2	633	99.8	112 14 AAR39640	Mature human Trans
3	633	99.8	112 17 AAR92772	Human TGF-beta 3.
4	633	99.8	112 17 AAR91958	Human transforming
5	633	99.8	112 18 AAW26173	Mature transformin
6	633	99.8	112 18 AAW08175	TGF active fragmen
7	633	99.8	112 20 AAY08301	Human growth facto
8	633	99.8	112 20 AAW97093	The mature form of
9	633	99.8	112 20 AAW84209	Transforming growth
10	633	99.8	112 21 AAY92012	Human transforming
11	633	99.8	112 22 AAB35939	TGF-beta 3 amino a

12	633	99.8	115	22	AAB73206	TGF-beta3 C-termin
13	633	99.8	202	11	AAR06548	Protein with tumou
14	633	99.8	412	13	AAR20621	Transforming Growt
15	633	99.8	412	16	AAR73598	Human TGF-beta 3 p
16	633	99.8	412	19	AAW80417	Amino acid sequenc
17	630	99.4	112	19	AAW78782	Human transforming
18	630	99.4	204	15	AAR46229	Human TGF-beta-3.
19	630	99.4	204	19	AAW78787	Human transforming
20	630	99.4	457	11	AAR04080	Polypeptide sequen
21	627	98.9	413	13	AAR22038	Mutant transformin
22	621	97.9	112	11	AAR04078	Sequence of porcin
23	621	97.9	112	19	AAW78783	Pig transforming g
24	621	97.9	456	15	AAR46228	Pig TGF-beta-3. S
25	621	97.9	456	19	AAW78786	Pig transforming g
26	620	97.8	112	17	AAR86770	Tissue-derived tum
27	620	97.8	165	17	AAR86771	Tissue-derived tum
28	617	97.3	412	11	AAR08264	Tumour growth inhi
29	612	96.5	112	11	AAR04077	Sequence of human
30	595	93.8	112	14	AAR39642	Transforming Growt
31	595	93.8	112	17	AAR92775	Hybrid TGF-beta 1-
32	595	93.8	112	17	AAR91959	Human TGF-beta-lik
33	591	93.2	112	14	AAR39644	Transforming Growt
34	591	93.2	112	17	AAR91960	Human TGF-beta-lik
35	591	93.2	112	17	AAR92776	Transforming Growt
36	577	91.0	112	14	AAR39646	Transforming Growt
37	577	91.0	112	17	AAR91961	Human TGF-beta-lik
38	577	91.0	112	17	AAR92777	Hybrid TGF-beta 3-
39	555	87.5	98	12	AAR11944	Truncated TGF-beta
40	555	87.5	98	20	AAY16699	WO9914235 Seq ID N
41	555	87.5	98	21	AAB09521	Human TGF-beta 3,
42	555	87.5	98	21	AAB02787	Human TGF-beta3 am
43	555	87.5	98	21	AAY92556	TGF-beta 3 finger-
44	539	85.0	112	14	AAR39641	Transforming Growt
45	538	84.9	112	14	AAR39645	Transforming Growt
46	535	84.4	112	9	AAP80462	Sequence from whic
47	535	84.4	112	12	AAR12403	Transforming Growt
48	535	84.4	112	14	AAR39639	Mature human Trans
49	535	84.4	112	17	AAR92774	Human TGF-beta 2.
50	535	84.4	112	17	AAR91957	Human transforming
51	535	84.4	112	18	AAW08174	TGF active fragmen
52	535	84.4	112	20	AAY08300	Human growth facto
53	535	84.4	112	20	AAW97092	The mature form of
54	535	84.4	112	20	AAW84208	Transforming growt
55	535	84.4	112	21	AAY92011	Human transforming
56	535	84.4	112	22	AAB35938	TGF-beta 2 amino a
57	535	84.4	115	22	AAB73205	TGF-beta2 C-termin
58	535	84.4	390	13	AAR20126	Sequence of hybrid
59	535	84.4	414	16	AAR83055	Transforming growt
60	535	84.4	414	16	AAR73597	Human TGF-beta 2 p
61	535	84.4	442	10	AAP91899	Sequence encoded b
62	535	84.4	442	11	AAR05748	Human TGF-Beta2-44
63	535	84.4	442	13	AAR20125	Sequence of human
64	535	84.4	442	16	AAR99922	Human transforming
65	533	84.1	391	10	AAP91900	Sequence encoded b
66	532	83.9	390	11	AAR05665	Human Transforming
67	532	83.9	390	11	AAR05666	Hybrid transformin
68	532	83.9	390	11	AAR05749	Human TGF-Beta2 ex
69	513	80.9	390	13	AAR27522	TGF-beta 1/beta 2
70	507	80.0	389	16	AAR79921	Simian-human hybri
71	503	79.3	390	11	AAR05492	Chimeric simian TG
72	500	78.9	112	11	AAR04076	Sequence of mature
73	500	78.9	112	11	AAR08142	Platelet-derived h
74	500	78.9	112	13	AAR22134	PDGF subunit a. H
75	500	78.9	112	14	AAR43263	TGF-beta. Homo sa
76	500	78.9	112	14	AAR42311	Recombinant human
77	500	78.9	112	17	AAR92773	Human TGF-beta 1.
78	500	78.9	112	17	AAR91956	Human transforming
79	500	78.9	112	18	AAW08173	TGF-beta1 active f
80	500	78.9	112	19	AAW78781	Human transforming
81	500	78.9	112	20	AAY08299	Human growth facto
82	500	78.9	112	20	AAW97091	The mature form of
83	500	78.9	112	20	AAW84207	Transforming growt
84	500	78.9	112	21	AAY92010	Human transforming

85 500 78.9 112 21 AAY67950 Human transforming
 86 500 78.9 112 22 AAB35937 TGF-beta 1 amino a
 87 500 78.9 115 22 AAB73204 TGF-beta1 C-termin
 88 500 78.9 118 18 AAW08176 TGF-beta fusion pr
 89 500 78.9 122 18 AAW08181 TGF-beta fusion pr
 90 500 78.9 124 18 AAW08177 TGF-beta fusion pr
 91 500 78.9 128 18 AAW08188 TGF-beta fusion pr
 92 500 78.9 130 18 AAW08185 TGF-beta fusion pr
 93 500 78.9 131 18 AAW08182 TGF-beta fusion pr
 94 500 78.9 132 18 AAW08189 TGF-beta fusion pr
 95 500 78.9 133 18 AAW08178 TGF-beta fusion pr
 96 500 78.9 134 18 AAW08187 TGF-beta fusion pr
 97 500 78.9 134 18 AAW08190 TGF-beta fusion pr
 98 500 78.9 135 18 AAW08183 TGF-beta fusion pr
 99 500 78.9 136 18 AAW08186 TGF-beta fusion pr
 100 500 78.9 137 18 AAW08180 TGF-beta fusion pr

ALIGNMENTS

RESULT 1

AAR12404
 ID AAR12404 standard; Protein; 112 AA.

XX
 AC AAR12404;

DT 29-AUG-1991 (first entry)

XX Transforming Growth Factor beta 3.

XX TGF-beta3; biologically active protein production.

XX Homo sapiens.

XX EP433225-A.

XX 19-JUN-1991.

XX 27-NOV-1990; 90EP-0810922.

XX 06-DEC-1989; 89GB-0027546.

XX (CIBA) CIBA GEIGY AG.

XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

XX WPI; 1991-180005/25.

XX N-PSDB; AAQ11995.

XX Prodn. of Transforming Growth Factor type-beta-like proteins - by
 PT subjecting denatured monomeric form to refolding conditions

XX Example; Page 27; 35pp; English.

XX The TGF-beta3 coding sequence was isolated from the CI-215 human
 CC glioma cell line. It was incorporated into an appropriate vector to
 CC transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1
 CC was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M
 CC NaCl, 5mM EDTA, 2mM reduced glutathione, 1mM oxidised glutathione
 CC and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and
 CC the mixture was conc. 10 times. The conc. soln was diluted to the
 CC original vol. with 10mM HCl and conc to a final vol of 10 ml. The
 CC supernatant from centrifugation at 5000g for 30 min contained
 CC disulphide-linked dimeric TGF-beta3.

XX Sequence 112 AA;

Query Match 99.8%; Score 633; DB 12; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWWHEPKGYGVANFCSGPCPYLRSADTTHTST 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 aldtncyfnleencvvrplyidfrqdlgkwkwhpkgygvancsgpcpylrsadtthst 60
 QY 61 VLGLYNTLNPEASASPCCVPODLEPLTILYVVGRTPKVEQLSNMVKSCKCS 112
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 vlglyntlnpeasaspcvvpqdlepltillyvvgtrtpkveqlsnmvksckcs 112

RESULT 2

AAR39640
 ID AAR39640 standard; Protein; 112 AA.

XX
 AC AAR39640;

DT 26-AUG-1993 (first entry)

XX Mature human Transforming Growth Factor-beta3.

XX hTGF-beta3; hybrid protein; wound healing; cancer treatment;
 KW bone repair; growth regulation.

XX Homo sapiens.

XX EP542679-A.

XX 19-MAY-1993.

XX 03-NOV-1992; 92EP-0810845.

XX 11-NOV-1991; 91EP-0810870.

XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;

XX WPI; 1993-161126/20.

XX N-PSDB; AAQ41601.

XX New hybrid transforming growth factor-beta molecules - comprise
 PT portions of mature TGF-beta isoforms; useful as wound healants,
 PT cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX Claim 4; Page 24; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
 CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
 CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
 CC derived from different parent isoforms are pref. between amino acids
 CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
 CC molecules promote cell migration, inhibit the growth of A375
 CC melanoma cells, accelerate the healing of partial-thickness burn
 CC wounds and full-thickness incisional wounds and increase formation
 CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.

XX Sequence 112 AA;

Query Match 99.8%; Score 633; DB 14; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWWHEPKGYGVANFCSGPCPYLRSADTTHTST 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 aldtncyfnleencvvrplyidfrqdlgkwkwhpkgygvancsgpcpylrsadtthst 60

QY 61 VLGLYNTLNPEASASPCCVPODLEPLTILYVVGRTPKVEQLSNMVKSCKCS 112
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 vlglyntlnpeasaspcvvpqdlepltillyvvgtrtpkveqlsnmvksckcs 112

RESULT 3
 AAR92772

```

ID  AAR92772 standard; Protein; 112 AA.
XX
AC  AAR92772;
XX
DT  17-JUL-1996 (first entry)
XX
DE  Human TGF-beta 3.
XX
KW  Transforming growth factor type beta; TGF-beta 3;
KW  protein renaturation; protein folding.
XX
OS  Homo sapiens.
XX
PN  WO9603433-A1.
XX
PD  08-FEB-1996.
XX
PF  12-JUL-1995; 95WO-EP02719.
XX
PR  25-JUL-1994; 94EP-0810439.
XX
PA  (CIBA ) CIBA GEIGY AG.
XX
PI  Cerletti N;
XX
DR  N-PSDB; AAT17234.
XX
PT  Prodn. of dimeric biologically active transforming growth factor
PT  by refolding denatured monomer in detergent-free folding buffer
PT  contg. specific organic solvent to improve yield
XX
PS  Example 1B; Page 34; 54pp; English.
XX
CC  Non-soluble, monomeric transforming growth factor TGF-beta 3
CC  (AAR92772) was recovered from E. coli LC 137 (DSM 5658) transformants
CC  carrying plasmid pPLMu.TGF-beta 3, which includes the coding
CC  sequence (AAT17234) for TGF-beta 3. A biologically active, dimeric
CC  form of TGF-beta 3 was obtd. by refolding this monomer in detergent-
CC  free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773)
CC  and TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77),
CC  were also produced.
XX
SQ  Sequence 112 AA;

Query Match 99.8%; Score 633; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYVAFNFCGPGPYLRSADTTHT 60
DB 1 aldtncfrnleencvrrplyidfrqdlgkwvhepkgyvafncsgpcpylrsadtthst 60
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
DB 61 vlglntlnpeaspcvcpqdleptilivvgrtpkveqlsnmvksckes 112

RESULT 4
AAR91958
ID AAR91958 standard; Protein; 112 AA.
XX
AC AAR91958;
XX
DT 10-JUN-1996 (first entry)
XX
DE Human transforming growth factor beta 3.
XX
KW Transforming growth factor beta; TGF; regulator; method;
KW proliferation; differentiation; wound healing; solvent.
XX
OS Homo sapiens.

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XX WO9603432-A1.
XX
PD 08-FEB-1996.
XX
PF 12-JUL-1995; 95WO-EP02718.
XX
PR 25-JUL-1994; 94EP-0810438.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Cerletti N;
XX
DR WPI; 1996-116999/12.
DR N-PSDB; AAT15464.
XX
PT Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
PS Claim 17; Page 38; 59pp; English.
XX
CC AAR91956-B91958 are the amino acid sequences of human transforming
CC growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to
CC produce TGF beta-like proteins in dimeric form. The TGF beta-like
CC proteins produced are hybrids of 2 different types of TGF beta e.g.
CC TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g.
CC BMP-2. The TGF beta hybrids were made using a new process of producing
CC dimeric, biologically active TGF beta-like proteins. The new process
CC involves treating denatured TGF beta monomers with folding buffer contg.
CC a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF
CC (dimethyl formamide). The detergent allows folding of the monomer such
CC that, after dimerisation, the TGF beta-like protein retains biological
CC activity and remains in soluble form. The method allows relatively high
CC yields of biologically active TGF beta-like proteins in their native
CC dimeric form. TGF-beta like proteins are multifunctional regulators of
CC cellular activity and a typical use is to stimulate wound healing.
XX
SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYVAFNFCGPGPYLRSADTTHT 60
DB 1 aldtncfrnleencvrrplyidfrqdlgkwvhepkgyvafncsgpcpylrsadtthst 60
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
DB 61 vlglntlnpeaspcvcpqdleptilivvgrtpkveqlsnmvksckes 112

RESULT 5
AAW26173
ID AAW26173 standard; Protein; 112 AA.
XX
AC AAW26173;
XX
DT 28-NOV-1997 (first entry)
XX
DE Mature transforming growth factor beta3.
XX
KW Transforming growth factor beta3; TGF-beta3; human; mature protein;
KW acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation;
KW cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis;
KW bone disease; bone repair; therapy.
XX
OS Homo sapiens.
XX
PN WO9705166-A1.

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XX PD 13-FEB-1997.
XX PF 17-JUL-1996; 96WO-EF03140.
XX PR 25-JUL-1995; 95EP-0810484.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Arvinte T, Grutter M, Mittl P;
XX PR WPI: 1997-145621/13.
XX DR N-PSDB; AAT80110.
XX PT Crystalline form of transforming growth factor beta-3 - useful in
XX compns. as slow release form of TGF, e.g. for wound healing, and
XX for structure determ. in rational drug design
XX PS Example 1; Page 26; 34pp; English.
XX CC This sequence represents the mature human transforming growth factor
XX beta3 (TGF-beta3). TGF-beta3 is one of five distinct homodimeric
XX TGFbeta's. TGF-beta3 is an acid-stable and heat-stable disulphide linked
XX homodimer. All the TGF-beta's are produced as 390-412 amino acid
XX precursors, which undergo proteolytic cleavage to produce mature forms
XX which consist of the C-terminal 112 amino acids. Depending upon cell and
XX tissue type, and the presence of other growth factors, TGF-beta may
XX either stimulate mitogenesis, cell proliferation and growth, or inhibit
XX these processes. Many of the actions of TGF-beta are related to the
XX response of cells or tissues to stress or injury, and to the repair of
XX resultant damage. A crystalline form of TGF-beta3 can be produced by a
XX method of the invention. Crystalline TGF-beta3 is useful in slow release
XX compositions for treatment of conditions such as wounds, oral or
XX intestinal mucositis, osteoarthritis, bone disease and repair, generally
XX wherever TGF-beta3 is normally used. The crystalline form is also used
XX for structure determination in rational drug design. Crystalline
XX TGF-beta3 shows lower tendency than the dissolved protein to adsorb on
XX the walls of vials and is more stable against oxidation. Variation of the
XX properties, e.g. size, of the crystals allows control over the rate at
XX which active TGF is released in vivo.
XX SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 18; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 60
Db 1 aldtncfrnleencvrrplyidfrqdlgkwkwhpkgyanfcsgpcpylrsadtthst 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
Db 61 vlglyntlnpeasaspcvcpqdlepltilyyvgrtpkveqlsnmrvksckcs 112

RESULT 6
AAW08175
ID AAW08175 standard; Peptide; 112 AA.
XX AC AAW08175;
XX DT 26-AUG-1997 (first entry)
XX DE TGF active fragment of a TGF-beta fusion protein.
XX KW Transforming growth factor-beta fusion protein; wound healing;
XX artificial skin; surgery recovery time.
XX OS Homo sapiens.
XX PN WO9639430-A1.

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XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US08973.
XX PR 06-JUN-1995; 95US-0470837.
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMV/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX DR WPI: 1997-043065/04.
XX DR N-PSDB; AAT42773.
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX reduce surgery recovery time and to prepare artificial skin
XX PS Claim 12; Page 49; 59pp; English.
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX comprises a purification tag and a TGF active fragment. The present
XX sequence represents a specifically claimed TGF active fragment.
XX Additionally, the fusion protein may comprise proteinase-sensitive
XX linker sites and binding domain so the protein sequence may contain
XX some or all of the following elements: purification tag;proteinase
XX site;ECM binding site;proteinase site:TGF-beta. TGF-beta promotes
XX wound healing, and in the preparation of artificial skin. The inclusion
XX of a purification tag facilitates purification of the fusion protein.
XX The proteinase site is included to permit cleavage and release of the
XX purification tag after purification if desired. The extracellular
XX matrix binding site facilitates delivery of the fusion protein to the
XX desired site of action. Delivery of the TGF-beta to the site to be
XX treated reduces the amount of TGF-beta required to be administered to
XX be effective and reduces the concentration of circulating TGF-beta
XX which may result in undesirable effects.
XX SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 18; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 60
Db 1 aldtncfrnleencvrrplyidfrqdlgkwkwhpkgyanfcsgpcpylrsadtthst 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
Db 61 vlglyntlnpeasaspcvcpqdlepltilyyvgrtpkveqlsnmrvksckcs 112

RESULT 7
AAY08301
ID AAY08301 standard; Protein; 112 AA.
XX AC AAY08301;
XX DT 14-JUL-1999 (first entry)
XX DE Human growth factor protein fragment TGF-Beta3.
XX KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
XX pharmaceutical.
XX OS Homo sapiens.
XX PN DE19748734-A1.

```


PT tag and a bone morphogenetic active fragment, used for enhancing
 XX wound healing or bone growth
 PS Disclosure: Page 43-44; 64pp; English.
 XX
 CC The present sequence represents a transforming growth factor beta active
 CC fragment. The protein can be used in place of a bone morphogenetic
 CC active fragment to create the fusion proteins of the invention. When a
 CC bone morphogenetic active fragment is used, the fusion proteins are
 CC designated bone morphogenetic fusion proteins. The bone morphogenetic
 CC fusion protein may contain some or all of the following elements: a
 CC purification tag, a proteinase site, an ECM/bone binding site, a second
 CC proteinase site, and a bone morphogenetic protein active fragment.
 CC The bone morphogenetic fusion proteins can be used for enhancing wound
 CC healing or bone growth.
 XX
 SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 20; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSDTTHTST 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 aldtncfrnleencvrrplyidfrqdlgkwkwhpkgyanfcsgpcpylrsadtthst 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 vlglyntlnpeasapccvpqdleptililyyvgtrpkveqlsnmrvksckcs 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
 AAY92012
 ID AAY92012 standard; Protein; 112 AA.
 AC AAY92012;
 XX
 XX 19-JUL-2000 (first entry)
 DT
 XX Human transforming growth factor beta 3 monomer.
 DE
 XX human transforming growth factor beta 3 monomer; CKGF; mutant;
 KW cystine knot growth factor; hairpin loop; infertility.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..20
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 FT Domain 21..40
 FT /label= beta_hairpin_loop_1
 FT /note= "mutant optionally comprises one or more
 FT substitutions in these residues"
 FT
 FT Misc-difference 41..81
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 FT Domain 82..102
 FT /label= beta_hairpin_loop_3
 FT /note= "mutant optionally comprises one or more
 FT substitutions in these residues"
 FT
 FT Misc-difference 103..112
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 XX WO200017360-A1.
 PN
 XX 30-MAR-2000.
 PD
 XX

PF 19-MAR-1999; 99WO-US05908.
 XX
 PR 22-SEP-1998; 98WO-US19772.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 PI Weintraub BD, Szkudlinski MW;
 XX
 DR WPI; 2000-283585/24.
 XX
 CC New mutant cystine knot growth factor proteins comprising one or more
 CC mutant subunits, useful for treating or preventing diseases e.g.
 CC hypothyroidism and thyroid cancer
 PT
 PT Claim 223; Page 301; 320pp; English.
 XX
 XX This is the wild type human transforming growth factor beta 3 monomer.
 CC Mutants comprise at least one electrostatic charge altering mutation in a
 CC beta hairpin loop, resulting in increased bioactivity.
 CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more
 CC mutant subunits and having novel properties or improved pharmacological
 CC properties, compared to wild type CKGFs, are claimed. The CKGF
 CC superfamily comprises at least four families of growth factors: the
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
 CC the neurotrophins and the transforming growth factor-beta family; the
 CC families are known to be structurally similar (especially comprising the
 CC cystine knot topology) and it was shown that mutations at certain
 CC positions in the CKGF hairpin loops of family members and other members
 CC of the CKGF superfamily could significantly alter the biological
 CC activities of the CKGF.
 CC Mutant transforming growth factor family proteins or analogues are useful
 CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
 CC infertility, time-limited conception and in assisted reproduction.
 XX
 SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSDTTHTST 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 aldtncfrnleencvrrplyidfrqdlgkwkwhpkgyanfcsgpcpylrsadtthst 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 vlglyntlnpeasapccvpqdleptililyyvgtrpkveqlsnmrvksckcs 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11
 AAB35939
 ID AAB35939 standard; protein; 112 AA.
 XX
 AC AAB35939;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 XX TGF-beta 3 amino acid sequence.
 DE
 XX Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
 KW wound healing; dermal wound; wound healing; TGF-beta 3.
 KW
 XX Unidentified.
 OS
 XX WO200064481-A1.
 PN
 XX 02-NOV-2000.
 PD
 XX 22-APR-1999; 99WO-IB00800.
 PF
 XX 22-APR-1999; 99WO-IB00800.
 PR
 XX

CC bone-inducing cofactor. This method can be used with any of the 5 human
XX TGF-beta's or with TGF-beta from other species.
SQ Sequence 412 AA;

Query Match 99.8%; Score 633; DB 16; Length 412;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
DB 301 aldtncfrrnleencvrrplyidfrqdlgkwvhepkgyanfcsgpcpylrsadtthst 360
|||||

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 361 vlglntlnpeasaspccvpqdleptlilyvgrtpkveqlsnmvksckcs 412
|||||

RESULT 16
AAW80417
ID AAW80417 standard; Protein; 412 AA.
AC AAW80417;
XX
DT 14-JAN-1999 (first entry)
XX
DE Amino acid sequence of human transforming growth factor-beta 3.
XX
KW Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
XX preeclampsia; pregnancy; choriocarcinoma.
OS Homo sapiens.
XX
XX WO9840747-A1.
XX
XX 17-SEP-1998.
XX
XX 05-MAR-1998; 98WO-CA00180.
XX
XX 07-MAR-1997; 97US-0039919.
XX
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
XX Caniggia I, Lye S, Post M;
XX
XX WPI; 1998-520837/44.
XX N-PSDB; AAV63209.
XX
XX Regulation of trophoblast invasion - by, e.g. transforming growth
XX factor-beta3 inhibitor, useful for detecting or treating
XX preeclampsia in pregnant women
XX
XX Disclosure; Fig 1; 59pp; English.
XX
XX The present sequence encodes human transforming growth factor-beta 3
XX (TGF-beta3). The specification describes a composition for regulating
XX trophoblast invasion which comprises an inhibitor of TGF-beta3,
XX TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
XX (HIF-1 alpha) or oxygen tension. The composition is used in methods of
XX diagnosing, monitoring, preventing or treating conditions requiring
XX regulation of trophoblast invasion, especially preeclampsia in pregnant
XX women or choriocarcinomas.
XX
XX Sequence 412 AA;

Query Match 99.8%; Score 633; DB 19; Length 412;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
DB 301 aldtncfrrnleencvrrplyidfrqdlgkwvhepkgyanfcsgpcpylrsadtthst 360
|||||

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 361 vlglntlnpeasaspccvpqdleptlilyvgrtpkveqlsnmvksckcs 412
|||||

RESULT 17
AAW78782
ID AAW78782 standard; Protein; 112 AA.
XX
AC AAW78782;
XX
DT 21-DEC-1998 (first entry)
XX
DE Human transforming growth factor-beta 3 N-terminal sequence.
XX
KW Transforming growth factor-beta 3; TGF-beta 3; human.
XX
OS Homo sapiens.
XX
XX US5801231-A.
XX
XX 01-SEP-1998.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX 30-MAY-1995; 95US-0454468.
XX (GETH) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1998-494840/42.
XX
XX DNA encoding transforming growth factor-beta precursor sequence.
XX useful for analysis to perform manipulations to increase yield of
XX recombinant production of the protein
XX
XX Disclosure; Fig 3; 26pp; English.
XX
XX This is the amino acid sequence of human transforming growth factor
XX beta-3 (TGF-beta 3, see also AAW78787). The sequence shows homology
XX to human TGF-beta 1 (see AAW78781), porcine TGF-beta 3 (see AAW78783)
XX and bovine TGF-beta 2 (see AAW78784) N-terminal sequences. The
XX invention relates to the recombinant production of TGF-beta. DNA
XX encoding TGF-beta has been isolated and cloned into vectors which
XX are replicated in bacteria and expressed in eukaryotic cells.
XX TGF-beta recovered from transformed cells can be used in known
XX therapeutic applications.
XX
XX Sequence 112 AA;

Query Match 99.4%; Score 630; DB 19; Length 112;
Best Local Similarity 99.1%; Pred. No. 3.2e-56;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
DB 1 aldtncfrrnleencvrrplyidfrqdlgkwvhepkgyanfcsgpcpylrsadtthst 60
|||||

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 61 vlglntlnpeasaspccvpqdleptlilyvgrtpkveqlsnmvksckcs 112
|||||

↑
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RESULT 18
AAR46229
ID AAR46229 standard; Protein; 204 AA.

XX AC AAR46229;
XX DT 09-JUL-1994 (first entry)
XX DE Human TGF-beta-3.

XX FT TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
XX KW transforming growth factor beta-3; recombinant; wound healing;
XX KW vulnerable.

XX OS Homo sapiens.
XX PN US284763-A.
XX PD 08-FEB-1994.
XX PF 22-MAR-1985; 85US-0715142.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.

XX PA (GETH) GENENTECH INC.

XX PI Derynk RMA, Goeddel DV;
XX DR WPI; 1994-056343/07.
XX DR N-PSDB; AAR46229.

XX PT Nucleic acid sequences encoding transforming growth factor-beta -
XX PT diagnostic probes, and for use in therapeutics

XX PS Disclosure; Fig 5; 25pp; English.

XX CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
XX CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
XX CC corresponding amino acid sequences were determined (AAR46227-29,
XX CC respectively). A genomic fragment corresponding to a human TGF-
XX CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
XX CC determined (AAR46230). The sequences have been used in the
XX CC construction of vectors for the expression of recombinant TGF-
XX CC beta.

XX Sequence 204 AA;

Query Match 99.4%; Score 630; DB 15; Length 204;
Best Local Similarity 99.1%; Pred. No. 6.3e-56;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCGCPVLRSDTTHST 60
DB 93 aldtncfrrnleencvrrplyidfrqdlgkwkvhpkgyanfcsgpcpvlrsadtthst 152
QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
DB 153 vlglyntlnpeasapccvqddlepltillyvgrtpkveqlsnmvmvksckcs 204

RESULT 19
AAW78787
ID AAW78787 standard; Protein; 204 AA.
XX AC AAW78787;
XX DT 21-DEC-1998 (first entry)

XX DT 31-MAY-1989 (first entry)

XX DE Human transforming growth factor-beta 3.
XX KW Transforming growth factor-beta 3; TGF-beta 3; pig.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Protein 93..204
XX FT /label= Mat_protein
XX FT Misc-difference 17
XX FT /note= "encoded by ATT"

XX PN US5801231-A.
XX PD 01-SEP-1998.
XX PF 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PR 05-NOV-1993; 93US-0147364.
XX PR 30-MAY-1995; 95US-0454468.

XX PA (GETH) GENENTECH INC.

XX PI Derynk RMA, Goeddel DV;
XX DR WPI; 1998-494840/42.
XX DR N-PSDB; AAV52935.

XX PT DNA encoding transforming growth factor-beta precursor sequence -
XX PT useful for analysis to perform manipulations to increase yield of
XX PT recombinant production of the protein

XX PS Example 6; Fig 5; 26pp; English.

XX CC This is a partial amino acid sequence of the human transforming
XX CC growth factor-beta 3 precursor (preTGF-beta 3), deduced from an
XX CC isolated cDNA clone (see AAV52935). The invention relates to the
XX CC recombinant production of TGF-beta. Biologically active TGF-beta
XX CC is defined as being capable of inducing EGF-potentiated anchorage
XX CC independent growth of target cell lines and/or growth inhibition of
XX CC neoplastic cell lines. Nucleic acids encoding TGF-beta have been
XX CC isolated and cloned into vectors which are replicated in bacteria
XX CC and expressed in eukaryotic cells. TGF-beta recovered from
XX CC transformed cells is used in known therapeutic applications.

XX Sequence 204 AA;

Query Match 99.4%; Score 630; DB 19; Length 204;
Best Local Similarity 99.1%; Pred. No. 6.3e-56;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCGCPVLRSDTTHST 60
DB 93 aldtncfrrnleencvrrplyidfrqdlgkwkvhpkgyanfcsgpcpvlrsadtthst 152
QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
DB 153 vlglyntlnpeasapccvqddlepltillyvgrtpkveqlsnmvmvksckcs 204

RESULT 20
AAR04080
ID AAR04080 standard; protein; 457 AA.
XX AC AAR04080;
XX DT 31-MAY-1989 (first entry)

```

XX DE Polypeptide sequence of porcine TGF-beta 3.
XX KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX KW inhibition.
XX PN WO8912101-A.
XX PN 14-DEC-1989.
XX PD 08-JUN-1988; 88WO-US01945.
XX PF 08-JUN-1988; 88WO-UO01945.
XX PR (GETH ) GENENTECH INC.
XX PA Derynck RM, Goeddel DV;
XX PI WPI; 1990-007474/01.
XX DR N-PSDB; AAQ02819.
XX DR
XX PT Nucleotide sequence encoding transforming growth factor beta-3 used as a
XX PT probe, or to produce TGF beta 3, for inhibiting growth of certain normal
XX PT and neoplastic cells, eg A549.
XX PS Disclosure; Fig. 5; 61pp; English.
XX XX
XX CC This sequence represents porcine transforming growth factor-beta 3 (TGF-
XX CC beta 3) polypeptide. The corresponding nucleic acid sequence of this
XX CC subtype is useful as a probe or to produce this protein for normal and
XX CC neoplastic cell growth inhibition. It differs from human TGF-beta 3 at
XX CC several AA positions.
XX SQ Sequence 457 AA;

Query Match 99.4%; Score 630; DB 11; Length 457;
Best Local Similarity 99.1%; Pred. No. 1.6e-55;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSDTTHT 60
Db 346 aldtncyfrnleencvrrplyidfrdglgkwvhepkgyanfcsgpcpylrsadtthst 405
|||||
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 406 vlglntlnpeaspcvcpqdlepltillyvgrtpkveqlsnmrvksckcs 457
|||||

RESULT 21
AAR22038
ID AAR22038 standard; Protein; 413 AA.
XX AC AAR22038;
XX XX
XX DT 05-MAY-1992 (first entry)
XX DE Mutant Transforming Growth Factor beta-3 coding sequence.
XX XX
XX KW TGF-beta 3; homodimer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1..296
XX FT /note= "amino acids 1-296 of TGF-beta3 precursor"
XX FT Modified-site 74..76
XX FT /label= glycosylation
XX FT Modified-site 135..137
XX FT /label= glycosylation
XX FT Modified-site 142..144
XX FT /label= glycosylation
XX FT Modified-site 158..160

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FT Cleavage-site /label= glycosylation
FT 297..300 /label= Factor_Xa_site
FT Region 302..404
FT /note= "amino acids 301-403 of TGF-beta3 precursor"
FT Misc-difference 405
FT /note= "wild-type = Met; may be substituted by
FT any other amino acid"
FT Region 406..413
FT /note= "amino acids 405-412 of TGF-beta3 precursor"
XX WO9200318-A.
XX 09-JAN-1992.
XX 25-JUN-1991; 91WO-US04541.
XX 25-JUN-1990; 90US-0543348.
XX (ONCO-) ONCOGENE SCI INC.
XX Iwata KK, Foulkes JG, Tendijke P, Haley JD;
XX WPI; 1992-041510/05.
XX DR N-PSDB; AAQ22229.
XX XX
XX PT Transforming growth factor beta 3 proteins, precursors and
XX PT mutants - obd. from polypeptide and antibodies, with optimal
XX PT therapeutic use due to genetic manipulation of coding sequence
XX XX
XX Claim 12; Page 66; 107pp; English.
XX XX
XX CC This sequence has been compiled from the description of a mutant TGF-
XX CC beta3 contained in the claims. The Factor Xa cleavage site may be
XX CC replaced by a similar protease recognition site, e.g. for collagenase.
XX CC The mutant protein may also include a hydrophobic transmembrane amino
XX CC acid sequence, e.g. from c-erbB2 and a "stop transfer"
XX CC sequence. The protease recognition site is located between the
XX CC C-terminal of the transmembrane region (when present) and the
XX CC N-terminal of the TGF-beta 3 precursor. Mature TGF-beta 3 can then be
XX CC efficiently cleaved from the membrane. See also AAQ20576 and AAR20622.
XX SQ Sequence 413 AA;

Query Match 98.9%; Score 627; DB 13; Length 413;
Best Local Similarity 99.1%; Pred. No. 2.8e-55;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSDTTHT 60
Db 302 aldtncyfrnleencvrrplyidfrdglgkwvhepkgyanfcsgpcpylrsadtthst 361
|||||
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 362 vlglntlnpeaspcvcpqdlepltillyvgrtpkveqlsnrvksckcs 413
|||||

RESULT 22
AAR04078
ID AAR04078 standard; protein; 112 AA.
XX AC AAR04078;
XX XX
XX DT 31-MAY-1989 (first entry)
XX DE Sequence of porcine TGF-beta 3.
XX KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX KW inhibition.
XX PN WO8912101-A.

```


CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
 CC corresponding amino acid sequences were determined (AAR46227-29,
 CC respectively). A genomic fragment corresponding to a human TGF-
 CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
 CC determined (AAR46230). The sequences have been used in the
 CC construction of vectors for the expression of recombinant TGF-
 CC beta.

XX Sequence 456 AA;

Query Match 97.9%; Score 621; DB 15; Length 456;
 Best Local Similarity 98.2%; Pred. No. 1.3e-54;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVRLPYIDFRDGLGWKWHPEKGYGYANFCSPCYLRSADTTHST 60
 Db 345 aldtncfrrleencvrrplyidfrdglgwkwhepkgygyanfcsgpcylrsadthss 404
 QY 61 VLGLYNTLNPEASASPCCPVQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112
 Db 405 vlglntlnpeasaspcvcpqdleptilyyvgvrtakveqlsnmrvksckcs 456

RESULT 25

AAW78786
 ID AAW78786 standard; Protein; 456 AA.

XX AC AAW78786;

XX DT 21-DEC-1998 (first entry)

XX DE Pig transforming growth factor-beta 3.

XX KW Transforming growth factor-beta 3; TGF-beta 3; pig.

XX OS Sus scrofa.

XX FH Key Location/Qualifiers

XX FT Protein 345..456

XX FT /label= Mat_protein

XX FT Misc-difference 46

XX FT /note= "alternative N-terminal Met residue"

XX FT Misc-difference 48

XX FT /note= "alternative N-terminal Met residue"

XX FT Misc-difference 119

XX FT /note= "encoded by AAC"

XX US5801231-A.

XX PN 01-SEP-1998.

XX PF 22-MAR-1985; 85US-0715142.

XX PR 13-MAR-1987; 87US-0025423.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PR 05-NOV-1993; 93US-0147364.

XX PR 30-MAY-1995; 95US-0454468.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX DR WPI: 1998-494840/42.

XX DR N-PSDB; AAV52934.

XX DNA encoding transforming growth factor-beta precursor sequence -
 PT useful for analysis to perform manipulations to increase yield of
 PT recombinant production of the protein

XX Example 6; Fig 5; 26pp; English.

PS

XX This is the amino acid sequence of the porcine transforming growth
 CC factor-beta 3 precursor (preTGF-beta 3), deduced from isolated
 CC cDNA sequences (see AAV52934). The invention relates to the
 CC recombinant production of TGF-beta. Biologically active TGF-beta
 CC is defined as being capable of inducing EGF-potentiated anchorage
 CC independent growth of target cell lines and/or growth inhibition of
 CC neoplastic cell lines. Nucleic acids encoding TGF-beta have been
 CC isolated and cloned into vectors which are replicated in bacteria
 CC and expressed in eukaryotic cells. TGF-beta recovered from
 CC transformed cells is used in known therapeutic applications.

XX Sequence 456 AA;

Query Match 97.9%; Score 621; DB 19; Length 456;
 Best Local Similarity 98.2%; Pred. No. 1.3e-54;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVRLPYIDFRDGLGWKWHPEKGYGYANFCSPCYLRSADTTHST 60
 Db 345 aldtncfrrleencvrrplyidfrdglgwkwhepkgygyanfcsgpcylrsadthss 404

QY 61 VLGLYNTLNPEASASPCCPVQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112

Db 405 vlglntlnpeasaspcvcpqdleptilyyvgvrtakveqlsnmrvksckcs 456

RESULT 26

AAR86770
 ID AAR86770 standard; Protein; 112 AA.

XX AC AAR86770;

XX DT 12-JUN-1996 (first entry)

XX DE Tissue-derived tumour growth inhibitor-1.

XX KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
 KW arteriosclerosis; inflammation; psoriasis; therapy; vulnery;
 KW immunomodulator.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 9..28

XX FT /note= "peptide CM-1"

XX PN EP684260-A2.

XX PD 29-NOV-1995.

XX PF 20-OCT-1987; 87EP-0109866.

XX PR 20-OCT-1986; 86US-0922121.

XX PA (ONCO-) ONCOGENE SCI INC.

XX PI Gold LI, Iwata KK, Stephenson JR;

XX DR WPI: 1996-000991/01.

XX DR N-PSDB; AAT06496.

XX Tissue-derived growth inhibitor and corresponding genes - useful for
 PT detection of tumours, inhibition of tumour growth, treatment of
 PT proliferative disorders and healing of burns and wounds.

XX Claim 1; Fig 29; 83pp; English.

XX The sequence represents mature tumor growth inhibitor (TGI), which
 CC is produced by recombinant DNA methods. TGI can be used to
 CC inhibit the growth of human tumour cells, e.g. carcinoma, melanoma
 CC or leukaemia cells, in the treatment of proliferative disorders

CC e.g. arteriosclerosis, inflammation and psoriasis, or for the
CC treatment of burns to facilitate wound healing. TGI can also be
CC used as an immunomodulator. Although the protein has tumour
CC growth inhibitory activity, it is not transforming growth
CC factor-beta-1 or -beta-2. The peptide CM-1 (as featured) inhibits
CC the growth of human tumour cells but not of a mink lung cell line.
XX
SQ Sequence 112 AA;

Query Match 97.8%; Score 620; DB 17; Length 112;
Best Local Similarity 98.2%; Pred. No. 3.3e-55;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCSPCYLRSADTTHT 60
Db 1 aldtncfrnleencvrrplyidfrqdlgkwkvhpkgyanfcspcyllrsadtthst 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 61 vlglyntlnpeasawpcvpqdleptilyyvgtrpkveqlsnmvvksckcs 112

RESULT 27
AAR86771
ID AAR86771 standard; Protein; 165 AA.
XX
AC AAR86771;
XX
DT 12-JUN-1996 (first entry)
XX
DE Tissue-derived tumour growth inhibitor-1 precursor.
XX
KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
KW arteriosclerosis; inflammation; psoriasis; therapy; vulnery;
KW immunomodulator.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..165
FT /note= "tumour growth inhibitor precursor"
FT Misc-difference 53..54 /note= "residues 54-93 of the precursor protein are
FT not specified "
FT Protein 54..165
FT /note= "tumour growth inhibitor (see AAR86770)"
FT Peptide 62..81 /note= "peptide CM-1"
XX
EP684260-A2.
XX
PD 29-NOV-1995.
XX
EF 20-OCT-1987; 87EP-0109866.
XX
PR 20-OCT-1986; 86US-0922121.
XX
PA (ONCO-) ONCOGENE SCI INC.
XX
PI Gold LI, Iwata KK, Stephenson JR;
XX
DR WPI; 1996-000991/01.
DR N-PSDB; AAT06496.
XX
PT Tissue-derived growth inhibitor and corresponding genes - useful for
PT detection of tumours, inhibition of tumour growth, treatment of
PT proliferative disorders and healing of burns and wounds.
XX
PS Claim 4; Fig 29; 83pp; English.
XX
CC The sequence represents the precursor of tumor growth inhibitor
CC (TGI) (see AAR86770), which is produced by recombinant DNA methods.

CC However, amino acids 54-93 of the TGI precursor are not provided in
CC the specification. TGI, or its 205 amino acid precursor, can be
CC used to inhibit the growth of human tumour cells, e.g.
CC carcinoma, melanoma or leukaemia cells, in the treatment of
CC proliferative disorders e.g. arteriosclerosis, inflammation and
CC psoriasis, or for the treatment of burns to facilitate wound
CC healing. The proteins can also be used as immunomodulators.
CC Although the proteins have tumour growth inhibitory activity, they
CC are not transforming growth factor-beta-1 or -beta-2. The 20-amino
CC acid peptide CM-1 (as featured) inhibits the growth of human tumour
CC cells but not of a mink lung cell line.
XX
SQ Sequence 165 AA;

Query Match 97.8%; Score 620; DB 17; Length 165;
Best Local Similarity 98.2%; Pred. No. 5.1e-55;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCSPCYLRSADTTHT 60
Db 54 aldtncfrnleencvrrplyidfrqdlgkwkvhpkgyanfcspcyllrsadtthst 113
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 114 vlglyntlnpeasawpcvpqdleptilyyvgtrpkveqlsnmvvksckcs 165

RESULT 28
AAR08264
ID AAR08264 standard; protein; 412 AA.
XX
AC AAR08264;
XX
DT 05-MAR-1991 (first entry)
XX
DE Tumour growth inhibitor.
XX
KW TGI; Carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
KW psoriasis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 74..76 /label= N-glycosylation site
FT Modified-site 0..137 /label= N-glycosylation site
FT Modified-site 142..144 /label= N-glycosylation site
FT Modified-site 158..160 /label= N-glycosylation site
XX
WO9014360-A.
XX
PD 29-NOV-1990.
XX
EF 17-MAY-1990; 90WO-US02753.
XX
PR 17-MAY-1989; 89US-0353410.
PR 19-APR-1985; 85US-0725003.
PR 07-APR-1986; 86US-0847931.
PR 20-OCT-1986; 86US-0992121.
PR 20-OCT-1987; 87US-0111022.
PR 20-APR-1988; 88US-0183224.
XX
PA (ONCO-) ONCOGENE SCI INC.
XX
PI Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX
DR WPI; 1990-375949/50.
DR N-PSDB; AAQ06845.
XX

QY	1	ALDNTYCFRNLEENCVRPLXIDYDFQDLGKWKVHPEKGYANFCGPGCPYLRSADTTHTST	60
		:	
Db	1	alntnycsfstekncvqlyidfrkldgkwihpkayhanfscgpcpylrsadtthst	60
QY	61	VLGLYNTLNPEASASCCVPQDLEPLTILYVYGRTPKVEQLSNMVVKSKCS	112
Db	61	vlglyntlnpeasasccvpqdlepltilyvygrtpkveqlsnmvvskcs	112
RESULT	32		
AAAR91959			
ID	AAAR91959	standard; Protein; 112 AA.	
XX	AAAR91959;		
XX	10-JUN-1996	(first entry)	
XX	Human TGF-beta-like protein, TGF-beta-1-3.		
XX	Transforming growth factor beta; TGF; regulator; method;		
KW	proliferation; differentiation; wound healing; solvent.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Peptide	1..44	/note= "N-terminal 44 amino acids of
FT			TGF-beta-1"
FT	Peptide	45..112	/note= "C-terminal 68 amino acids of
FT			TGF-beta-3"
XX	W09603432-A1.		
XX	08-FEB-1996.		
XX	12-JUL-1995;	95WO-EP02718.	
XX	25-JUL-1994;	94EP-0810438.	
XX	(CIBA) CIBA GEIGY AG.		
XX	Cerletti N;		
XX	WPI; 1996-116999/12.		
DR	N-PSDB; AAT15465.		
XX	Prodn. of dimeric, biologically active transforming growth factor		
FT	beta - by refolding denatured monomer in buffer contg. mild		
FT	detergent and specific organic solvents to improve yields		
XX	Claim 17; Page 40-41; 59pp; English.		
XX	AAAR91959 is transforming growth factor (TGF) beta-like protein,		
CC	TGF-beta-1-3. TGF-beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta		
CC	hybrids were made using a new process of producing dimeric,		
CC	biologically active TGF beta-like proteins. The new process involves		
CC	treating denatured TGF beta monomers with folding buffer contg. a		
CC	mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the		
CC	solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and		
CC	DMF (dimethyl formamide). The detergent allows folding of the monomer		
CC	such that, after dimerisation, the TGF beta-like protein retains		
CC	biological activity and remains in soluble form. The method allows		
CC	relatively high yields of biologically active TGF beta-like proteins		
CC	in their native dimeric form. TGF-beta like proteins are multifunctional		
CC	regulators of cellular activity and a typical use is to stimulate wound		
CC	healing.		
XX	Sequence	112 AA;	
SQ			

Db 61 vlslyntinpeasaspcvcsqdlptlilyigktpkieqlsnmvksckcs 112

RESULT 39
AAR11944
ID AAR11944 standard; Protein; 98 AA.
AC AAR11944;
XX
XX 23-JUL-1991 (first entry)
XX
XX Truncated TGF-beta #3.
XX
XX Transforming Growth Factor beta; AIDS.
KW
XX Synthetic.
XX
XX WO9105565-A.
PN
XX
XX 02-MAY-1991.
PD
XX
XX 18-OCT-1990; 90WO-US06006.
PF
XX
XX 18-OCT-1989; 89US-0422962.
PR
XX
XX (CREA-) CREATIVE BIOMOLECUL.
PA
XX
XX Cohen CM;
PI
XX
XX WPI; 1991-148530/20.
DR
XX
XX Recombinant truncated transforming growth factor-beta analogues -
PT capable of inducing an anti-proliferative effect in mammalian
PT epithelial cells in vitro
XX
XX
XX Claim 12; Page 27; 42pp; English.
XX
XX This sequence is an example of a highly generic protein (see
CC AAR11954). It can be used to control proliferation of tumour cell lines
CC or for enhancing growth rate of T- and B-lymphocytes in
CC immunosuppressed patients. The first 5 N-terminal residues can be
CC absent.
CC See also AAQ11774-5, AAR11942-RL1947 and AAR11954.
XX
XX Sequence 98 AA;
SQ

Query Match 87.5%; Score 555; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHSTVGLYNTLNPEASA 74
Db 1 ccvrplyidfrqdlgkwwhepkgyanfcsgpgpylrsadtthstvglyntlnpeasa 60
QY 75 SPCCVPDLEPTILYVGRTPKVEQLSNMVKSCKCS 112
Db 61 spccvpqdleptilyyvgtrtpkveqlsnmvksckcs 98

RESULT 40
AAV16699
ID AAV16699 standard; Peptide; 98 AA.
XX
XX AAV16699;
XX
XX 17-AUG-1999 (first entry)
DT
XX
XX WO9914235 Seq ID No: 152.
DE
XX
XX Growth factor; GF; persephin; neuron growth; cellular degeneration;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
XX

KW brain injury; spinal cord injury; nervous system tumour; infection;
KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;
KW metabolic disease; diabetes; renal dysfunction; neuriturin.
XX
XX Unidentified.
XX
XX WO9914235-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 15-SEP-1998; 98WO-US19163.
PF
XX
XX 16-SEP-1997; 97US-0931858.
PR
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX
XX Desauvage F, Johnson EM, Klein R, Kotzbauer PT;
PI Lampe PA, Milbrandt JD;
PI
XX
XX WPI; 1999-244023/20.
DR
XX
XX New isolated persephin growth factor nucleic acids used to, e.g.
PT promote neuronal growth
PT
XX
XX Disclosure; Page 176-177; 222pp; English.
XX
XX The invention relates to a novel isolated and purified growth factor (GF)
CC that comprises persephin or a fragment or a conservatively substituted
CC variant. The persephin GF polypeptides can promote the survival and
CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
CC or polynucleotides can be used for preventing or treating cellular
CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
CC acute brain injury, acute spinal cord injury, nervous system tumours,
CC multiple sclerosis, or infection, hematopoietic cell degeneration or
CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
CC resulting from cardiomyopathy or congestive heart failure. They can also
CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
CC and damage caused by infectious agents. The GF can also be used for
CC promoting the growth and/or differentiation of a cell in a culture
CC medium. The antisense polynucleotides can be used for treating a disease
CC condition mediated by expression of persephin by a population of cells.
CC The products can also be used for detection and diagnosis.
XX
XX Sequence 98 AA;
SQ

Query Match 87.5%; Score 555; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTTHSTVGLYNTLNPEASA 74
Db 1 ccvrplyidfrqdlgkwwhepkgyanfcsgpgpylrsadtthstvglyntlnpeasa 60
QY 75 SPCCVPDLEPTILYVGRTPKVEQLSNMVKSCKCS 112
Db 61 spccvpqdleptilyyvgtrtpkveqlsnmvksckcs 98

RESULT 41
AAB09521
ID AAB09521 standard; Protein; 98 AA.
XX
XX AAB09521;
AC
XX
XX 11-SEP-2000 (first entry)
DT
XX
XX Human TGF-beta 3, SEQ ID NO:42.
DE
XX

RESULT 43
AA92556
ID AA92556 standard; peptide; 98 AA.
XX AC AA92556;
XX
DT 10-AUG-2000 (first entry)
XX
DE TGB-beta 3 finger-1-heel-finger-2 sequence.
XX
KW finger domain; heel region; BMP; TGF-beta family; protein refolding;
KW fusion protein; osteopathic; antibacterial; cyostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 2..29
FT /label= finger_1
FT Region 35..62
FT /label= heel
FT Domain 65..94
FT /label= finger_2
XX
PN W020020449-A2.
XX
PD 13-APR-2000.
XX
XX 07-OCT-1999; 99WO-US23372.
XX
XX 07-OCT-1998; 98US-0103418.
XX
XX 16-AUG-1999; 99US-0375333.
XX
XX (STYC) STRYKER CORP.
XX
XX Oppermann H, Tai M, McCartney J;
XX
XX WPI; 2000-303743/26.
XX
XX A biologically active TGF-beta family member fusion protein competent
XX to refold, comprising a C-terminal linked TGF-beta family protein
XX
XX Disclosure; Page 138-139; 160pp; English.
XX
XX AA92554-82 show the finger 1, heel and finger 2 domains of TGF-beta
XX superfamily members. These sequences can be used to form novel fusion
XX proteins. Novel proteins comprise biologically active TGF-beta family
XX member fusion proteins competent to refold under suitable refolding
XX conditions. The fusion proteins comprise: (1) a TGF-beta family protein
XX C-terminal seven cysteine domain, comprising finger 1, finger 2 and heel
XX subdomains; and (2) a heterologous leader sequence domain operatively
XX linked to the C-terminal domain. Truncations, heterodimers and mutants
XX of these fusion proteins and methods of purifying the heterodimers are
XX also claimed. The TGF-beta family proteins can be used to induce the
XX full cascade of morphogenic events which culminate in skeletal tissue
XX formation, including cartilage and endochondral bone formation. They are
XX useful in the binding of fibrin and fibronectin to the implanted matrix,
XX chemotaxis of cells, proliferation of fibroblasts, differentiation into
XX chondroblasts, cartilage formation, vascular invasion, bone formation,
XX remodeling, and bone marrow differentiation. The proteins have improved
XX physical properties such as solubility and stability, improved
XX biological activity, including altered receptor binding and improved
XX targeting capabilities.
XX
XX Sequence 98 AA;

Query Match 87.5%; Score 555; DB 21; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRDGLGWKWHPEKGYANFCGPGCPYLRSDTHTSTVGLYNTLNPEASA 74

Db 1 CCVRPLYIDFRDGLGWKWHPEKGYANFCGPGCPYLRSDTHTSTVGLYNTLNPEASA 60
QY 75 SPCCVPDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
XX AC SPCCVPDLEPLTILYVGRTPKVEQLSNMVKSKCS 98
Db 61 SPCCVPDLEPLTILYVGRTPKVEQLSNMVKSKCS 98
RESULT 44
AAR39641
ID AAR39641 standard; Protein; 112 AA.
XX AC AAR39641;
XX
DT 26-AUG-1993 (first entry)
XX
DE Transforming Growth Factor-beta1(44/45)beta2 hybrid.
XX
KW hTGF-beta1; hTGF-beta2; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..44
FT /note= "amino acids 1-44 of hTGF-beta1"
FT Region 45..112
FT /note= "amino acids 45-112 of hTGF-beta2"
XX
PN EP542679-A.
XX
XX 19-MAY-1993.
XX
XX 03-NOV-1992; 92EP-0810845.
XX
XX 11-NOV-1991; 91EP-0810870.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
XX
XX N-PSDB; AAQ41602.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
XX portions of mature TGF-beta isoforms; useful as wound healants,
XX cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 8; Page 25-26; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
XX of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX derived from different parent isoforms are pref.between amino acids
XX 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
XX possible hybrids formed using these hinge points and one part each
XX from two of the isoforms, 6 are preferred including the hybrid
XX TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration,
XX inhibit the growth of A375 melanoma cells, accelerate the healing of
XX partial-thickness burn wounds and full-thickness incisional wounds and
XX increase formation of fibrous granular tissue.
XX See also AAQ41603-Q41607 for the other pref. hybrids.
XX
XX Sequence 112 AA;

Query Match 85.0%; Score 539; DB 14; Length 112;
Best Local Similarity 81.2%; Pred. No. 4.6e-47;
Matches 91; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFNLENCVVRPLYIDFRDGLGWKWHPEKGYANFCGPGCPYLRSDTHTST 60
XX AC ALDNTNCFNLENCVVRPLYIDFRDGLGWKWHPEKGYANFCGPGCPYLRSDTHTST 60
Db 1 ALDNTNCFNLENCVVRPLYIDFRDGLGWKWHPEKGYANFCGPGCPYLRSDTHTST 60


```
OS Homo sapiens.
XX EP433225-A.
XX PN
XX 19-JUN-1991.
XX PD
XX 27-NOV-1990; 90EP-0810922.
XX PF
XX 06-DEC-1989; 89GB-0027546.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;
XX PI WPI; 1991-180005/25.
XX PN N-PSDB; AAQ11994.
XX DR
XX Prodn. of Transforming Growth Factor type-beta-like proteins - by
XX PT subjecting denatured monomeric form to refolding conditions
XX PS Example; Page 27; 35pp; English.
XX PS
XX The TGF-beta2 coding sequence was isolated from the C1-215 human
XX CC glioma cell line. It was incorporated into an appropriate vector to
XX CC transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1
XX CC was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M
XX CC NaCl, 5mM EDTA, 2mM reduced glutathione, 1mM oxidised glutathione
XX CC and 3mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and
XX CC the mixture was conc. 10 times. The conc. soln was diluted to the
XX CC original vol. with 10mM HCl and conc to a final vol of 10 ml. The
XX CC supernatant from centrifugation at 5000g for 30 min contained
XX CC disulphide-linked dimeric TGF-beta2.
XX CC
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 12; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYVYANFCSGPCPYLRSADTTHST 60
Db ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 aldaaycfrnvqncclrpdyidfrdlgwkwihpkgydnanfcagacpylwsdsdqhsr 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 vlslyntinpeasapccvsqdlleptilyigktpkieqlsnmivksckcs 112

Sequence 112 AA;

Query Match 84.4%; Score 535; DB 12; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYVYANFCSGPCPYLRSADTTHST 60
Db ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 aldaaycfrnvqncclrpdyidfrdlgwkwihpkgydnanfcagacpylwsdsdqhsr 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 vlslyntinpeasapccvsqdlleptilyigktpkieqlsnmivksckcs 112

RESULT 48
AAR39639
ID AAR39639 standard; Protein; 112 AA.
XX
XX AC AAR39639;
XX
XX 26-AUG-1993 (first entry)
XX
XX DE Mature human Transforming Growth Factor-beta2.
XX
XX hTGF-beta2; hybrid protein; wound healing; cancer treatment;
XX KW bone repair; growth regulation.
XX
XX OS Homo sapiens.
XX
XX EP542679-A.
XX PN
XX 19-MAY-1993.
XX PD
XX 03-NOV-1992; 92EP-0810845.
XX PF
XX 11-NOV-1991; 91EP-0810870.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
```

```
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX PI WPI; 1993-161126/20.
XX DR N-PSDB; AAQ41600.
XX DR
XX New hybrid transforming growth factor-beta molecules - comprise
XX PT portions of mature TGF-beta isoforms; useful as wound healants,
XX PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 4; Page 22-23; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
XX CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX CC derived from different parent isoforms are pref. between amino acids
XX CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
XX CC molecules promote cell migration, inhibit the growth of A375
XX CC melanoma cells, accelerate the healing of partial-thickness burn
XX CC wounds and full-thickness incisional wounds and increase formation
XX CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
XX
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 14; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYVYANFCSGPCPYLRSADTTHST 60
Db ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 aldaaycfrnvqncclrpdyidfrdlgwkwihpkgydnanfcagacpylwsdsdqhsr 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 vlslyntinpeasapccvsqdlleptilyigktpkieqlsnmivksckcs 112

RESULT 49
AAR92774
ID AAR92774 standard; Protein; 112 AA.
XX
XX AC AAR92774;
XX
XX 17-JUL-1996 (first entry)
XX
XX DE Human TGF-beta 2.
XX
XX Transforming growth factor type beta; TGF-beta 2;
XX KW protein renaturation; protein folding.
XX
XX OS Homo sapiens.
XX
XX WO9603433-A1.
XX PN
XX 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02719.
XX PF
XX 25-JUL-1994; 94EP-0810439.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
XX Cerletti N;
XX PI
XX WPI; 1996-117000/12.
XX DR N-PSDB; AAT17236.
XX
XX Prodn. of dimeric biologically active transforming growth factor
XX PT by refolding denatured monomer in detergent-free folding buffer
XX PT contg. specific organic solvent to improve yield
XX
XX Example 1B; Page 31-32; 54pp; English.
XX PS
```

XX Non-soluble, monomeric transforming growth factor TGF-beta 2
 CC (AAR92774) was recovered from E. coli LC 137 (DSM 5658) transformants
 CC carrying plasmid pLMu.TGF-beta 2, which includes the coding
 CC sequence (AAT17236) for TGF-beta 2. A biologically active, dimeric
 CC form of TGF-beta 2 was obtd. by refolding this monomer in detergent-
 CC free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773)
 CC and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-77),
 CC were also produced.
 XX Sequence 112 AA;
 SQ

Query Match 84.4%; Score 535; DB 17; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYIANFCSGPCPYLRSADTHTST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 aldaaycfrrvqncclrpdyldfkdrlgkwihhepkgyanfcagacpylwsdtdqshr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 vislyntinpeasaspcvsgdpleltilyyigktpkieqlsnmivksckcs 112
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 50
 AAR91957
 ID AAR91957 standard; Protein; 112 AA.
 XX
 AC AAR91957;
 XX
 DT 10-JUN-1996 (first entry)
 XX
 DE Human transforming growth factor beta 2.
 XX
 KW Transforming growth factor beta; TGF; regulator; method;
 KW proliferation; differentiation; wound healing; solvent.
 XX
 OS Homo sapiens.
 XX
 PN WO9603432-A1.
 XX
 PD 08-FEB-1996.
 XX
 PE 12-JUL-1995; 95WO-EP02718.
 XX
 PR 25-JUL-1994; 94EP-0810438.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Cerletti N;
 XX
 DR WPI; 1996-116999/12.
 DR N-PSDB; AAT15463.
 XX
 PT Prodn. of dimeric, biologically active transforming growth factor
 PT beta - by refolding denatured monomer in buffer contg. mild
 PT detergent and specific organic solvents to improve yields
 XX
 PS Claim 17; Page 35-36; 59pp; English.
 XX
 CC AAR91956-R91958 are the amino acid sequences of human transforming
 CC growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to
 CC produce TGF beta-like proteins in dimeric form. The TGF beta-like
 CC proteins produced are hybrids of 2 different types of TGF beta e.g.
 CC TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g.
 CC BMP-2. The TGF beta hybrids were made using a new process of producing
 CC dimeric, biologically active TGF beta-like proteins. The new process
 CC involves treating denatured TGF beta monomers with folding buffer contg.
 CC a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
 CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF
 CC (dimethyl formamide). The detergent allows folding of the monomer such

CC that, after dimerisation, the TGF beta-like protein retains biological
 CC activity and remains in soluble form. The method allows relatively high
 CC yields of biologically active TGF beta-like proteins in their native
 CC dimeric form. TGF-beta like proteins are multifunctional regulators of
 CC cellular activity and a typical use is to stimulate wound healing.
 XX Sequence 112 AA;
 SQ

Query Match 84.4%; Score 535; DB 17; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYIANFCSGPCPYLRSADTHTST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 aldaaycfrrvqncclrpdyldfkdrlgkwihhepkgyanfcagacpylwsdtdqshr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 vislyntinpeasaspcvsgdpleltilyyigktpkieqlsnmivksckcs 112
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 51
 AAW08174
 ID AAW08174 standard; Peptide; 112 AA.
 XX
 AC AAW08174;
 XX
 DT 26-AUG-1997 (first entry)
 XX
 DE TGF active fragment of a TGF-beta fusion protein.
 XX
 KW Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX
 OS Homo sapiens.
 XX
 PN WO9639430-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US08973.
 XX
 PR 06-JUN-1995; 95US-0470837.
 XX
 PA (CHEU/) CHEUNG D T.
 PA (HALL/) HALL F L.
 PA (NIMN/) NIMNI M E.
 PA (TUAN/) TUAN T.
 PA (WULL/) WU L.
 XX
 PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 XX
 DR WPI; 1997-043065/04.
 DR N-PSDB; AAT42772.
 XX
 PT Prepn. of transforming growth factor-beta fusion protein - useful to
 PT reduce surgery recovery time and to prepare artificial skin
 XX
 PS Claim 12; Page 47-48; 59pp; English.
 XX
 CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. The present
 CC sequence represents a specifically claimed TGF active fragment.
 CC Additionally, the fusion protein may comprise proteinase-sensitive
 CC linker sites and binding domain so the protein sequence may contain
 CC some or all of the following elements: purification tag:proteinase
 CC site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes
 CC wound healing, and the fusion protein can be used to reduce surgery
 CC recovery time and in the preparation of artificial skin. The inclusion
 CC of a purification tag facilitates purification of the fusion protein.
 CC The proteinase site is included to permit cleavage and release of the
 CC purification tag after purification if desired. The extracellular

CC matrix binding site facilitates delivery of the fusion protein to the
 CC desired site of action. Delivery of the TGF-beta to the site to be
 CC treated reduces the amount of TGF-beta required to be administered to
 CC be effective and reduces the concentration of circulating TGF-beta
 CC which may result in undesirable effects.

XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 18; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCGPPCYLRSADTTHTST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncncrlplyidfkrdlgkwkwihepkgnanfcagacpylwsdtqhsr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 52

AA08300
 ID AAY08300 standard; Protein; 112 AA.

XX AC AAY08300;

XX DT 14-JUL-1999 (first entry)

XX DE Human growth factor protein fragment TGF-Beta2.

XX KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
 XX pharmaceutical.

XX OS Homo sapiens.

XX PN DE19748734-A1.

XX PD 06-MAY-1999.

XX PF 05-NOV-1997; 97DE-1048734.

XX PR 05-NOV-1997; 97DE-1048734.

XX PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX PI Erdmann H, Kaerst U, Mueller C, Rinas U, Weich H;

XX DR WPI; 1999-278785/24.

XX PT Preparing active growth factor dimers from inclusion bodies in high
 XX yield

XX PS Claim 14; Page 12; 14pp; German.

XX CC This invention describes the novel preparation of biologically active
 CC dimers of recombinant human growth factors of the cysteine knot family
 CC starting from cellular inclusion bodies. Such dimers are are useful in
 CC pharmaceutical compositions and the method provides yields of 31-39.7%,
 CC in examples, compared with about 10% for the conventional method (see
 CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
 CC protein fragments used in the method of the invention.

XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCGPPCYLRSADTTHTST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncncrlplyidfkrdlgkwkwihepkgnanfcagacpylwsdtqhsr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 53

AAW97092

ID AAW97092 standard; Protein; 112 AA.

XX AC AAW97092;

XX DT 28-APR-1999 (first entry)

XX DE The mature form of transforming growth factor-beta-2.

XX KW Transforming growth factor-beta-2; TGF-beta-like protein;
 XX S-sulphonated TGF-beta-like protein; wound treatment; cancer;
 XX bone repair; tissue repair; bone marrow protective agent;
 XX cardioprotection; anti-inflammatory; immunosuppressive;
 XX ulcer; bed sore.

XX OS Homo sapiens.

XX PN EP891985-A1.

XX PD 20-JAN-1999.

XX PF 27-NOV-1990; 90EP-0810922.

XX PR 06-DEC-1989; 89GB-0027546.

XX PA (NOVS) NOVARTIS AG.

XX PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;

XX PN WPI; 1999-083520/08.

XX DR N-PSDB; AAX15246.

XX PT Producing biologically active dimeric Transforming Growth
 XX Factor-beta - by refolding new monomeric Transforming Growth
 XX Factor-beta, useful for treatment of wounds and cancer

XX PS Example 1; Page 29; 32pp; English.

XX CC The present sequence represents the mature form of transforming growth
 XX factor-beta-2. Dimeric, biologically active TGF-beta-like protein
 XX can be produced by subjecting the denatured monomeric form to refolding
 XX conditions. The new monomeric S-sulphonated TGF-beta-like protein is
 XX useful for the production of the dimeric, biologically active
 XX TGF-beta-like protein, which is useful for the treatment of wounds
 XX (surface or internal) and cancer in a mammal, in bone and tissue
 XX repair, as a bone marrow protective agent, a mediator of
 XX cardioprotection, for the production of an anti-inflammatory or
 XX immunosuppressive preparation. Treatment is useful for animals,
 XX especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
 XX particularly useful for the elderly.

XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYANFCGPPCYLRSADTTHTST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncncrlplyidfkrdlgkwkwihepkgnanfcagacpylwsdtqhsr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 54
AAW84208
ID AAW84208 standard; Protein; 112 AA.
XX
XX AC AAW84208;
XX
XX DT 25-MAR-1999 (first entry)
XX
XX DE Transforming growth factor beta active fragment.
XX
XX KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
XX KW bone morphogenetic protein; transforming growth factor beta;
XX KW active fragment; wound healing; bone growth; purification tag.
XX
XX OS Homo sapiens.
XX
XX PN WO9855137-A1.
XX
XX PD 10-DEC-1998.
XX
XX PF 02-JUN-1998; 98WO-US11189.
XX
XX PR 03-JUN-1997; 97US-0868452.
XX
XX PA (HALL/) HALL F L.
XX PA (HANS/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX
XX WPI: 1999-059875/05.
XX
XX DR N-PSDB; AAV99376.
XX
XX
XX PT New bone morphogenetic fusion proteins - comprising a purification
XX tag and a bone morphogenetic active fragment, used for enhancing
XX wound healing or bone growth
XX
XX PS Disclosure; Page 42-43; 64pp; English.
XX
XX
XX CC The present sequence represents a transforming growth factor beta active
XX fragment. The protein can be used in place of a bone morphogenetic
XX active fragment to create the fusion proteins of the invention. When a
XX bone morphogenetic active fragment is used, the fusion proteins are
XX designated bone morphogenetic fusion proteins. The bone morphogenetic
XX fusion protein may contain some or all of the following elements: a
XX purification tag, a proteinase site, an ECM/bone binding site, a second
XX proteinase site, and a bone morphogenetic protein active fragment.
XX The bone morphogenetic fusion proteins can be used for enhancing wound
XX healing or bone growth.
XX
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFNLSENCVRPLYIDFRDLGKWKVWHEPKGYANFCSPCYLRSADTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 aldaaycfnvqdnccrlplydfkrdlgkwkwihepkgyanfcagacpylwsdtqshr 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVSQLSNMVVKSCKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 vlslyntlnpeasapccvqsqdepltillylgktpkieqlsmivksccks 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 55
AAV92011
ID AAV92011 standard; Protein; 112 AA.
```

```

XX
XX AC AAV92011;
XX
XX DT 19-JUL-2000 (first entry)
XX
XX DE Human transforming growth factor beta 2 monomer.
XX
XX KW human transforming growth factor beta 2 monomer; CKGF; mutant;
XX KW cystine knot growth factor; hairpin loop; infertility.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Misc-difference 1..20
XX FT /note= "optionally mutated to increase electrostatic
XX FT interaction between beta hairpin structure and
XX FT a receptor"
XX
XX FT Domain 21..40
XX FT /label= beta_hairpin_loop_1
XX FT /note= "mutant optionally comprises one or more
XX FT substitutions in these residues"
XX
XX FT Misc-difference 41..81
XX FT /note= "optionally mutated to increase electrostatic
XX FT interaction between beta hairpin structure and
XX FT a receptor"
XX
XX FT Domain 82..102
XX FT /label= beta_hairpin_loop_3
XX FT /note= "mutant optionally comprises one or more
XX FT substitutions in these residues"
XX
XX FT Misc-difference 103..112
XX FT /note= "optionally mutated to increase electrostatic
XX FT interaction between beta hairpin structure and
XX FT a receptor"
XX
XX PN WO200017360-A1.
XX
XX PD 30-MAR-2000.
XX
XX PF 19-MAR-1999; 99WO-US05908.
XX
XX PR 22-SEP-1998; 98WO-US19772.
XX
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Weintraub BD, Szkudlinski MW;
XX
XX WPI: 2000-283585/24.
XX
XX PT New mutant cystine knot growth factor proteins comprising one or more
XX mutant subunits, useful for treating or preventing diseases e.g.
XX hypothyroidism and thyroid cancer
XX
XX PS Claim 208; Page 301; 320pp; English.
XX
XX
XX CC This is the wild type human transforming growth factor beta 2 monomer.
XX Mutants comprise at least one electrostatic charge altering mutation in a
XX beta hairpin loop, resulting in increased bioactivity.
XX
XX CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more
XX mutant subunits and having novel properties or improved pharmacological
XX properties, compared to wild type CKGFs, are claimed. The CKGF
XX superfamily comprises at least four families of growth factors: the
XX glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
XX the neurotrophins and the transforming growth factor-beta family; the
XX families are known to be structurally similar (especially comprising the
XX cystine knot topology) and it was shown that mutations at certain
XX positions in the CKGF hairpin loops of family members and other members
XX of the CKGF superfamily could significantly alter the biological
XX activities of the CKGF.
XX
XX CC Mutant transforming growth factor family proteins or analogues are useful
XX for treatment of ovulatory dysfunction, luteal phase defect, unexplained
XX infertility, time-limited conception and in assisted reproduction.
XX
XX SQ Sequence 112 AA;
```


Query Match 84.4%; Score 535; DB 21; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 aldaaycfrrvqdnccrlplyidfrdlgkwwhepkgyanfcagacpylwsdtqhsr 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 vlslyntlnpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 56
AAB35938
ID AAB35938 standard; protein; 112 AA.
XX AC AAB35938;
XX DT 26-FEB-2001 (first entry)
XX DE TGF-beta 2 amino acid sequence.
XX KW Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
XX KW wound healing; dermal wound; wound healing; TGF-beta 2.
XX OS Unidentified.
XX PN WO200064481-A1.
XX PD 02-NOV-2000.
XX PF 22-APR-1999; 99WO-IB00800.
XX PR 22-APR-1999; 99WO-IB00800.
XX PA (ETH2-) ETH ZURICH & UNIV ZURICH.
XX PI Sakiyama SE, Hubbell JA;
XX WPI; 2001-024627/03.
XX Matrix for controlled release of growth factor for wound healing, has
PT substrate that attaches heparin binding peptide, protein growth factor
PT that bind heparin with low affinity, and heparin or heparin-like
PT polymer -
PS Example 5; Page 21; 48pp; English.
PS XX This invention relates to a matrix comprising a substrate capable of
CC providing attachment of a heparin binding peptide (HBP), a peptide
CC comprising a binding domain which binds heparin with high affinity,
CC heparin or heparin-like polymer, and a protein growth factor or peptide
CC fragment which has a domain that binds heparin with low affinity.
CC Included in the invention is a vascular graft comprising the matrix,
CC which is capable of supporting cell adhesion. The matrix is used for
CC delivering low heparin binding affinity growth factor proteins or
CC peptides in a controlled manner suitable for wound healing. The matrix
CC can be used in an article for treating dermal wounds, and in an
CC implantable sterilized composition capable of supporting cell adhesion.
CC The present sequence represents a growth factor protein. The protein is
CC used in an example illustrating that non-heparin-binding growth factors
CC can be released in a controlled manner from heparin-based drug delivery
CC systems based on their low affinity for heparin.
XX Sequence 112 AA;

Query Match 84.4%; Score 535; DB 22; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 1 ALDNTYCFNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 aldaaycfrrvqdnccrlplyidfrdlgkwwhepkgyanfcagacpylwsdtqhsr 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 vlslyntlnpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 57
AAB73205
ID AAB73205 standard; Protein; 115 AA.
XX AC AAB73205;
XX DT 11-MAY-2001 (first entry)
XX DE TGF-beta2 C-terminal sequence.
XX KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
XX KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
XX KW muscular dystrophy; musculodgenerative disease; tissue repair;
XX KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
XX KW traumatic injury; congestive obstructive pulmonary disease.
XX OS Unidentified.
XX PN WO200112777-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22884.
XX PR 19-AUG-1999; 99US-0378238.
XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Lee S, McPherron AC;
XX WPI; 2001-211209/21.
XX New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -
XX Example 2; Fig 3; 124pp; English.
PS The present invention relates to growth differentiation factor-8 (GDF-8)
PS CC coding sequences and proteins. The present sequence is a protein, which
CC was used in a sequence homology comparison with the GDF-8 protein
CC isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), musculodgenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.
XX Sequence 115 AA;

Query Match 84.4%; Score 535; DB 22; Length 115;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db      4 aldaaycfrnvqncclrpilyidfkrdlgkwkwhhepkgyanfcagacpylwsddtqhsr 63
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 115

RESULT  58
AAR20126
ID      AAR20126 standard; Protein; 390 AA.
XX      AC
XX      AAR20126;
XX      DT
XX      16-APR-1992 (first entry)
XX      DE
XX      Sequence of hybrid transforming growth factor (TGF) beta-1/beta2.
XX      KW
XX      Hypertension therapy; hypotensive agent; blood pressure modulator.
XX      OS
XX      Monkey and Homo sapiens.
XX      FH
XX      Key
XX      Peptide      8..21
XX      Protein      280...391
XX      W09119513-A.
XX      PD
XX      26-DEC-1991.
XX      PF
XX      20-JUN-1991; 91WO-US04449.
XX      PR
XX      20-JUN-1990; 90US-0541221.
XX      PA
XX      (BRIM ) BRISTOL-MYERS SQUIB.
XX      PI
XX      Oleson FB, Comereski CR;
XX      WPI; 1992-024199/03.
XX      DR
XX      N-PSDB; AAQ20291.
XX      PT
XX      Use of transforming growth factor (TGF)-beta and their
XX      PT antagonists - for modulating blood pressure, for treating
XX      PT hypertension and hypotension
XX      PS
XX      Disclosure; Fig 3; 42pp; English.
XX      CC
XX      A new method for treating hypertension comprises administering a
XX      CC transforming growth factor (TGF)-beta to an individual at a dose
XX      CC effective for lowering blood pressure; the TGF-beta may be e.g.
XX      CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX      CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX      CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX      CC complex.
XX      SQ
XX      Sequence 390 AA;

Query Match      84.4%; Score 535; DB 13; Length 390;
Best Local Similarity 79.5%; Pred. No. 4.8e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY      1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWWHEPKGYANFCSGPCPYLRSADTTHST 60
      ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      279 aldaaycfrnvqncclrpilyidfkrdlgkwkwhhepkgyanfcagacpylwsddtqhsr 338
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      339 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 390

RESULT  59
AAR83055
ID      AAR83055 standard; Protein; 414 AA.

```

```

XX      AAR83055;
XX      AC
XX      25-JUN-1996 (first entry)
XX      DT
XX      Transforming growth factor-beta 2.
XX      DE
XX      KW
XX      Macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
XX      KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
XX      KW nitric oxide production; hypotension; inflammation; septic shock;
XX      KW treatment.
XX      OS
XX      Mammalian sp.
XX      FH
XX      Key
XX      Protein      303..414
XX      FT
XX      /note= "represents the mature active TGF beta-1 mol."
XX      W09526745-A1.
XX      PN
XX      12-OCT-1995.
XX      PD
XX      05-APR-1994; 94WO-US03705.
XX      PF
XX      05-APR-1994; 94WO-US03705.
XX      PR
XX      (HARD ) HARVARD COLLEGE.
XX      PA
XX      Lee M, Perrella MA;
XX      PI
XX      WPI; 1995-358443/46.
XX      DR
XX      N-PSDB; AAT05877.
XX      PT
XX      Treatment of hypotension, esp. in septic shock - by administering
XX      PT transforming growth factor-beta e.g. to inhibit inducible nitric
XX      PT oxide synthase gene transcription
XX      PS
XX      Disclosure; Fig 18; 52pp; English.
XX      CC
XX      Transforming growth factor-beta 2 (TGF-beta 2) has been found to inhibit
XX      CC inducible nitric oxide synthase (iNOS) gene transcription, esp. in
XX      CC interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
XX      CC a dose which does not inhibit constitutive NOS. TGF-beta 1 (AAR83054) or
XX      CC 2 or their active fragments (esp. derived from the carboxy-terminal 112
XX      CC amino acids), can be used in the treatment of hypotension, such as that
XX      CC associated with severe inflammation or septic shock.
XX      SQ
XX      Sequence 414 AA;

Query Match      84.4%; Score 535; DB 16; Length 414;
Best Local Similarity 79.5%; Pred. No. 5.1e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY      1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWWHEPKGYANFCSGPCPYLRSADTTHST 60
      ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      303 aldaaycfrnvqncclrpilyidfkrdlgkwkwhhepkgyanfcagacpylwsddtqhsr 362
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      363 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 414

RESULT  60
AAR73597
ID      AAR73597 standard; Protein; 414 AA.
XX      AC
XX      AAR73597;
XX      DT
XX      20-DEC-1995 (first entry)
XX      DE
XX      Human TGF-beta 2 protein.

```



```
FT XX /label=Sinal peptide
PN XX
XX EP376785-A.
XX
XX 04-JUL-1990.
XX
XX 14-DEC-1989; 89EP-0403480.
XX
XX 16-DEC-1988; 89US-0285140.
XX
XX 05-DEC-1989; 89US-0446020.
XX
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX WPI; 1990-203127/27.
XX
XX N-PSDB; AAQ05126.
XX
XX Cloning and expression of transforming growth factor beta 2 -
XX used for treatment of tumors or for augmenting wound healing.
XX
XX Claim 1; Fig 1a; 58pp; English.
XX
XX TGF-Beta2 may be used in treatment of tumors at effective doses,
XX and may also be useful in augmenting wound healing by stimulating
XX cell proliferation. The growth factor can be produced at high
XX levels from a CHO expression system.
XX
XX Sequence 442 AA;

Query Match 84.4%; Score 535; DB 11; Length 442;
Best Local Similarity 79.5%; Pred. No. 5.5e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYGYANFCSCGPCPYLRSADTTHTST 60
DB 331 aldaaycfvrvqncclrlpyidfrkdlgwkwhepkgyanfcagacpylwsadtqhsr 390

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
DB 391 vlsyntlnpeasapccvsgdlepiltilyyigktpkieqlsnmivksckcs 442

RESULT 63
AAR20125
ID AAR20125 standard; Protein; 442 AA.
XX
XX AAR20125;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence of human transforming growth factor (TGF) beta-2-442.
XX
XX Hypertension therapy; hypotensive agent; blood pressure modulator.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 4..19
XX Protein 330..442
XX
XX W09119513-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
XX 20-JUN-1990; 90US-0541221.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comerreski CR;
```

```
XX WPI; 1992-024199/03.
XX N-PSDB; AAQ20290.
XX
XX Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX Disclosure; Fig 2; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta/beta2 hybrid, TGF-
XX beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta/TGF-
XX beta2 precursor, a latent TGF-beta complex or a latent TGF-beta2
XX complex.
XX
XX Sequence 442 AA;

Query Match 84.4%; Score 535; DB 13; Length 442;
Best Local Similarity 79.5%; Pred. No. 5.5e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYGYANFCSCGPCPYLRSADTTHTST 60
DB 331 aldaaycfvrvqncclrlpyidfrkdlgwkwhepkgyanfcagacpylwsadtqhsr 390

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
DB 391 vlsyntlnpeasapccvsgdlepiltilyyigktpkieqlsnmivksckcs 442

RESULT 64
AAR79922
ID AAR79922 standard; Protein; 442 AA.
XX
XX AAR79922;
XX
XX 28-MAY-1996 (first entry)
XX
XX Human transforming growth factor-2.
XX
XX TGF-beta1; TGF-beta2; transforming growth factor; protein;
XX cell differentiation; cell proliferation; CHO; Chinese hamster;
XX ovary; COS; monkey kidney; animal; mammal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 4..19
XX /note= "signal peptide"
XX
XX Cleavage-site 20..21
XX /note= "putative signal sequence cleavage site"
XX
XX Peptide 331..442
XX /note= "mature peptide"
XX
XX EP676474-A1.
XX
XX 11-OCT-1995.
XX
XX 14-DEC-1989; 89EP-0104223.
XX
XX 05-DEC-1989; 89US-0446020.
XX
XX 16-DEC-1988; 88US-0285140.
XX
XX (ONCO ) ONCOGEN LP.
XX
XX Madisen L, Purchio AF, Webb N;
XX
XX WPI; 1995-346094/45.
XX
XX N-PSDB; AAT04116.
```



```
AAR05666
ID AAR05666 standard; protein; 390 AA.
XX
AC AAR05666;
XX
DT 14-AUG-1990 (first entry)
XX
DE Hybrid transforming growth factor TGF-beta1/beta2.
XX
KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
XX factors; ds.
XX
FH Key Location/Qualifiers
FT Peptide 379..390
XX
PN EP356935-A.
XX
PD 07-MAR-1990.
XX
PF 25-AUG-1989; 89EP-0115719.
XX
PR 25-AUG-1988; 88US-0236698.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Brankovan V, Lioubin M, Purchio A;
XX
DR WPI; 1990-068723/10.
XX
DR N-PSDB; AAQ03511.
XX
PT Compsns. contg. transforming growth factor beta -
PT used for inhibitions of HIV infection and replication in vivo.
XX
CC TGF-beta may be used in vivo to prevent formation of synctia and
CC inhibit HIV infection. TGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
PS Disclosure; Fig 3; 20pp; English.
XX
SQ Sequence 390 AA;

Query Match 83.9%; Score 532; DB 11; Length 390;
Best Local Similarity 79.5%; Pred. No. 9.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSPCPYLRSADTTHST 60
   ||| |||||: |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 279 aldpaycfrrvghncclrplyidfrdlgkwihepkgyanfcagacpylwsdtqshr 338

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEOLSNMVKSKCS 112
   || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 339 vlslyntinpeasaspcvcsqdleptilyyigtkpkiedqslmivksckcs 390

RESULT 68
AAR05749
ID AAR05749 standard; protein; 390 AA.
XX
AC AAR05749;
XX
DT 02-NOV-1990 (first entry)
XX
DE Human TGF-Beta2 expressed by TGF-Beta1/TGF-Beta2 hybrid precursor.
XX
KW Human TGF-Beta2 precursor; cancer; tumorigenic; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Protein 279..390
FT Peptide 8..21
   /label=Signal peptide
```

```
XX EP376785-A.
XX
PN 04-JUL-1990.
XX
PD 14-DEC-1989; 89EP-0403480.
XX
PF 16-DEC-1988; 88US-0285140.
XX
PR 05-DEC-1989; 89US-0446020.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Purchio AP, Madisen L, Webb N;
XX
PN WPI; 1990-203127/27.
XX
DR N-PSDB; AAQ05127.
XX
PT Cloning and expression of transforming growth factor beta 2 -
PT used for treatment of tumors or for augmenting wound healing.
XX
PS Claim 15; Fig 1b; 58pp; English.
XX
CC TGF-beta2 may be used in treatment of tumors at effective doses,
CC and may also be useful in augmenting wound healing by stimulating
CC cell proliferation. The growth factor can be produced at high
CC levels from a CHO expression system.
XX
SQ Sequence 390 AA;

Query Match 83.9%; Score 532; DB 11; Length 390;
Best Local Similarity 79.5%; Pred. No. 9.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSPCPYLRSADTTHST 60
   ||| |||||: |||:|||||:|||||:|||||:|||||:|||||:|||||
Db 279 aldpaycfrrvghncclrplyidfrdlgkwihepkgyanfcagacpylwsdtqshr 338

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEOLSNMVKSKCS 112
   || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 339 vlslyntinpeasaspcvcsqdleptilyyigtkpkiedqslmivksckcs 390

RESULT 69
AAR27522
ID AAR27522 standard; Protein; 390 AA.
XX
AC AAR27522;
XX
DT 10-MAR-1993 (first entry)
XX
DE TGF-beta 1/beta 2 chimeric protein.
XX
KW Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
KW Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
KW vascular endothelial cell.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..29
   /note= "Signal peptide, pre-pro-protein"
FT Region 30..278
   /note= "Pro-protein"
FT Protein 279..390
   /note= "Mature TGF-5 beta"
FT Modified-site 82
   /note= "N-glycosylation site"
FT Modified-site 136
   /note= "N-glycosylation site"
FT Modified-site 176
   /note= "N-glycosylation site"
FT Misc-difference 287
```



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XX FH Key Location/Qualifiers
XX FT Misc-difference 287..298
XX FT /note="TGF-beta2 derived sequence"
XX PN EP374044-A.
XX PD 20-JUN-1990.
XX PF 13-DEC-1989; 89EP-0403463.
XX PR 15-DEC-1988; 88US-0284972.
XX PA (ONCO-) ONCOGEN LTD PARTNER.
XX PI Purchio AF, Madisen L;
XX DR WPI; 1990-187401/25.
XX DR N-PSDB; AAQ04908.
XX PT New chimeric transforming growth factor -
XX PT with TGF-beta biological activity and increased secretion
XX PS efficiency.
XX PS Claim 2; Fig 1; 18pp; English.
XX CC Chimeric gene has TGF activity and may be more desirable than its
XX CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
XX CC from a plasmid vector (pbeta/dhfr) are 2.5 times more bioactive
XX CC than normal. The product is useful in treatment of cancer and wound
XX CC healing.
XX CC See also EP-373994.
XX CC Sequence 390 AA;
XX SQ

Query Match 79.3%; Score 503; DB 11; Length 390;
Best Local Similarity 75.9%; Pred. No. 7.9e-43;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 279 aldtncyfrnqncclrlpyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 338
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 339 vlalynqhnpgasaapccvpqaleplpyvyvgrkpkveqlsnmivrsvkcs 390

RESULT 72
AAR04076
ID AAR04076 standard; protein; 112 AA.
XX AC AAR04076;
XX DT 31-MAY-1989 (first entry)
XX DE Sequence of mature human TGF-beta 1.
XX KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX KW inhibition.
XX PN W08912101-A.
XX PD 14-DEC-1989.
XX PF 08-JUN-1988; 88WO-US01945.
XX PR 08-JUN-1988; 88WO-0001945.
XX PA (GETH ) GENENTECH INC.
XX PI Dernyck RM, Goeddel DV;

```

```

XX WPI; 1990-007474/01.
XX Nucleotide sequence encoding transforming growth factor beta-3 used as a
XX probe, or to produce TGF beta 3, for inhibiting growth of certain normal
XX and neoplastic cells, eg A349.
XX Disclosure; Fig. 3; 61pp; English.
XX This sequence is that of mature human transforming growth factor-beta 1
XX (TGF-beta 1) polypeptide. It differs from human and porcine TGF-beta
XX subtype 3 sequences at positions 9-11,13,19,40,45,52,57,58,60,63,67,68,
XX 71,75,82,87, and 95. In addition porcine TGF-beta 3 has an AA substitution
XX at posn. 96. The N-terminal AA sequence of bovine TGF-beta 2 differs from
XX that of human TGF-beta 1 at posns 4,5,9,13, and 19.
XX The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
XX beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
XX neoplastic cell growth inhibition.
XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 11; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncyfssteknccvrlpyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhnpgasaapccvpqaleplpyvyvgrkpkveqlsnmivrsvkcs 112

RESULT 73
AAR08142
ID AAR08142 standard; protein; 112 AA.
XX AC AAR08142;
XX DT 28-FEB-1991 (first entry)
XX DE Platelet-derived human TGF-beta monomer.
XX KW Transforming growth factor; cartilages inducing factor; CIF;
XX KW polycythemia; thrombocytosis; splenomegaly.
XX OS Homo sapiens.
XX PN US4971952-A.
XX PD 20-NOV-1990.
XX PF 27-OCT-1988; 88US-0263635.
XX PR 06-MAR-1986; 86US-0836672.
XX PR 07-AUG-1985; 85US-0763337.
XX PA (CLGE ) COLLAGEN CORP.
XX PI Bentze H, Ellingsworth L, Armstrong R;
XX DR WPI; 1990-368150/49.
XX PT Treating inflammation associated with transplants, etc. - using
XX PT cartilage inducing factor polypeptide homodimer cpd.
XX PS Disclosure; Fig 1; 14pp; English.
XX CC The TGF-beta may be used to derive cartilage inducing factors (CIFs)
XX CC useful for inhibition of acute/chronic inflammation, treatment of red
XX CC blood cell dysfunction associated with polycythemia, thrombocytosis

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XX DT 01-APR-1994 (first entry)
XX DE Recombinant human TGF-beta.
XX KW Transforming growth factor beta; stable; treatment; wounds;
XX KW fractures; inflammation; autoimmune disease; tumours.
XX OS Homo sapiens (recombinant).
XX PN JP05252956-A.
XX PD 05-OCT-1993.
XX PF 11-JUL-1991; 91JP-0171280.
XX PR 11-JUL-1991; 91JP-0171280.
XX PA (PART ) EARTH SEIYAKU KK.
XX DR WPI; 1993-347572/44.
XX PT Prodn. of recombinant cell for high expression of polypeptide
XX PT such as human TGF-beta - for treatment of e.g. wounds, fractures,
XX PT inflammation, auto-immune diseases or tumours
XX PS Disclosure; Page 15; 18pp; Japanese.
XX CC Human transforming growth factor (TGF) -beta can be produced in
XX CC recombinant cells, and thus produced is stable in the presence of 50
XX CC microg/ml methotrexate. TGF-beta may be produced in large amounts
XX CC via recombinant means and has uses such a wound healing, treatment
XX CC of fractures, inflammation, autoimmune disease or tumours.
XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 14; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
   ||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : || :
Db 1 aldtncfsstekncvrrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 60

QY 61 VLGLNTLNPASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || ||| || ||||| ||| : ||||| ||||| : ||||| : |||||
Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 77
AAR92773
ID AAR92773 standard; Protein; 112 AA.
XX AC AAR92773;
XX DT 17-JUL-1996 (first entry)
XX DE Human TGF-beta 1.
XX KW Transforming growth factor type beta; TGF-beta 1;
XX KW protein renaturation; protein folding.
XX OS Homo sapiens.
XX PN WO9603433-A1.
XX PD 08-FEB-1996.
XX PF 12-JUL-1995; 95WO-EP02719.
XX PR 25-JUL-1994; 94EP-0810439.
XX PS Example 1; Page 33; 59pp; English.

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PA (CIBA ) CIBA GEIGY AG.
XX PI Cerletti N;
XX DR WPI; 1996-117000/12.
XX DR N-PSDB; AAT17235.
XX PT Prodn. of dimeric biologically active transforming growth factor -
XX PT by refolding denatured monomer in detergent-free folding buffer
XX PT contg. specific organic solvent to improve yield
XX PS Example 1B; Page 29-30; 54pp; English.
XX CC Non-soluble, monomeric transforming growth factor TGF-beta 1
XX CC (AAR92773) was recovered from E. coli LC 137 (DSM 5658) transformants
XX CC carrying plasmid pPLMu.TGF-beta 1, which includes the coding
XX CC sequence (AAT17235) for TGF-beta 1. A biologically active, dimeric
XX CC form of TGF-beta 1 was obtd. by refolding this monomer in detergent-
XX CC free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 2 (AAR92774)
XX CC and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-77),
XX CC were also produced.
XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 17; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
   ||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : || :
Db 1 aldtncfsstekncvrrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 60

QY 61 VLGLNTLNPASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || ||| || ||||| ||| : ||||| ||||| : ||||| : |||||
Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 78
AAR91956
ID AAR91956 standard; Protein; 112 AA.
XX AC AAR91956;
XX DT 10-JUN-1996 (first entry)
XX DE Human transforming growth factor beta 1.
XX KW Transforming growth factor beta; TGF; regulator; method;
XX KW proliferation; differentiation; wound healing; solvent.
XX OS Homo sapiens.
XX PN WO9603432-A1.
XX PD 08-FEB-1996.
XX PF 12-JUL-1995; 95WO-EP02718.
XX PR 25-JUL-1994; 94EP-0810438.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Cerletti N;
XX DR WPI; 1996-116999/12.
XX DR N-PSDB; AAT15462.
XX PT Prodn. of dimeric, biologically active transforming growth factor
XX PT beta - by refolding denatured monomer in buffer contg. mild
XX PT detergent and specific organic solvents to improve yields
XX PS Example 1; Page 33; 59pp; English.

```

XX AAR91956-P91958 are the amino acid sequences of human transforming
 CC growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to
 CC produce TGF beta-like proteins in dimeric form. The TGF beta-like
 CC proteins produced are hybrids of 2 different types of TGF beta e.g.
 CC TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g.
 CC BMP-2. The TGF beta hybrids were made using a new process of producing
 CC dimeric, biologically active TGF beta-like proteins. The new process
 CC involves treating denatured TGF beta monomers with folding buffer contg.
 CC a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
 CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF
 CC (dimethyl formamide). The detergent allows folding of the monomer such
 CC that, after dimerisation, the TGF beta-like protein retains biological
 CC activity and remains in soluble form. The method allows relatively high
 CC yields of biologically active TGF beta-like proteins in their native
 CC dimeric form. TGF-beta like proteins are multifunctional regulators of
 CC cellular activity and a typical use is to stimulate wound healing.

XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 17; Length 112;
 Best Local Similarity 76.8%; Pred. No. 3.9e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVCVRPLYIDFRDLGWKWHPEKGYANFCGPGPYLRSADTTHST 60

Db 1 aldtncfstsstekncvcvrqlyidfrkdlgwkwihpkgyhanfclgpcpyiwsldtqysk 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112

Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 79

AAW08173

ID AAW08173 standard; Peptide; 112 AA.

XX AC AAW08173;

XX DT 26-AUG-1997 (first entry)

XX TGF-beta1 active fragment of a TGF-beta fusion protein.

XX DE Transforming growth factor-beta fusion protein; wound healing;

XX KW artificial skin; surgery recovery time.

XX OS Homo sapiens.

XX XX WO9639430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMNI/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX DR WPI; 1997-043065/04.

XX DR N-PSDB; AAT42771.

XX XX

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to

XX PT reduce surgery recovery time and to prepare artificial skin

XX PS Claim 12; Page 45-46; 59pp; English.

XX XX

CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. The present
 CC sequence represents a specifically claimed TGF-beta1 active fragment.
 CC Additionally, the fusion protein may comprise proteinase-sensitive
 CC linker sites and binding domain so the protein sequence may contain
 CC some or all of the following elements: purification tag; proteinase
 CC site; ECM binding site; proteinase site; TGF-beta. TGF-beta promotes
 CC wound healing, and the fusion protein can be used to reduce surgery
 CC recovery time and in the preparation of artificial skin. The inclusion
 CC of a purification tag facilitates purification of the fusion protein.
 CC The proteinase site is included to permit cleavage and release of the
 CC purification tag after purification if desired. The extracellular
 CC matrix binding site facilitates delivery of the fusion protein to the
 CC desired site of action. Delivery of the TGF-beta to the site to be
 CC treated reduces the amount of TGF-beta required to be administered to
 CC be effective and reduces the concentration of circulating TGF-beta
 CC which may result in undesirable effects.

XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 18; Length 112;
 Best Local Similarity 76.8%; Pred. No. 3.9e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVCVRPLYIDFRDLGWKWHPEKGYANFCGPGPYLRSADTTHST 60

Db 1 aldtncfstsstekncvcvrqlyidfrkdlgwkwihpkgyhanfclgpcpyiwsldtqysk 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112

Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 80

AAW78781

ID AAW78781 standard; Protein; 112 AA.

XX AC AAW78781;

XX DT 21-DEC-1998 (first entry)

XX Human transforming growth factor-beta 1 N-terminal sequence.

XX DE Transforming growth factor-beta 1; TGF-beta 1; human.

XX KW Homo sapiens.

XX OS US5801231-A.

XX PN 01-SEP-1998.

XX PD 22-MAR-1985; 85US-0715142.

XX PF 13-MAR-1987; 87US-0025423.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PR 05-NOV-1993; 93US-0147364.

XX PR 30-MAY-1995; 95US-0454468.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX XX WPI; 1998-494840/42.

XX XX

XX PT DNA encoding transforming growth factor-beta precursor sequence -
 XX PT useful for analysis to perform manipulations to increase yield of
 XX PT recombinant production of the protein

XX PS Disclosure; Fig 3; 26pp; English.

XX XX

CC This is the amino acid sequence of human transforming growth factor
 CC beta-1 (TGF-beta 1, see also AAW78785). The sequence shows homology
 CC to human TGF-beta 3 (see AAW78782), porcine TGF-beta 3 (see AAW78783)
 CC and bovine TGF-beta 2 (see AAW78784), N-terminal sequences. The
 CC invention relates to the recombinant production of TGF-beta. DNA
 CC encoding TGF-beta has been isolated and cloned into vectors which
 CC are replicated in bacteria and expressed in eukaryotic cells.
 CC TGF-beta recovered from transformed cells can be used in known
 CC therapeutic applications.
 XX
 SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 19; Length 112;
 Best Local Similarity 76.8%; Pred. No. 3.9e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDGLGWKWHPEKGYANFCSGPCPYLRSADTHST 60
 DB 1 aldtncfsteckncvrglyidfrkdlgwkwhepkgyhanfclgpcpyiwsldtqysk 60
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMVKSCKS 112
 DB 61 vialynqhnpgasaapccvpqdaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 81
 AAY08299
 ID AAY08299 standard; Protein; 112 AA.
 XX
 AC AAY08299;
 DT
 DT 14-JUL-1999 (first entry)
 DE Human growth factor protein fragment TGF-Betal.
 XX
 KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
 KW pharmaceutical.
 XX Homo sapiens.
 XX
 PN DE19748734-A1.
 XX
 PD 06-MAY-1999.
 XX
 XX 05-NOV-1997; 97DE-1048734.
 XX
 PR 05-NOV-1997; 97DE-1048734.
 XX
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 XX
 PI Erdmann H, Kaerst U, Mueller C, Rinas U, Weich H;
 XX
 DR WPI; 1999-278785/24.
 XX
 PT Preparing active growth factor dimers from inclusion bodies in high
 PT yield
 XX
 PS Claim 14; Page 12; 14pp; German.
 XX
 CC This invention describes the novel preparation of biologically active
 CC dimers of recombinant human growth factors of the cysteine knot family
 CC starting from cellular inclusion bodies. Such dimers are useful in
 CC pharmaceutical compositions and the method provides yields of 31-39.7%,
 CC in examples, compared with about 10% for the conventional method (see
 CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
 CC protein fragments used in the method of the invention.
 XX
 SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 20; Length 112;
 Best Local Similarity 76.8%; Pred. No. 3.9e-43;

Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ALDNTYCFRNLENCVRLYIDFRDGLGWKWHPEKGYANFCSGPCPYLRSADTHST 60
 DB 1 aldtncfsteckncvrglyidfrkdlgwkwhepkgyhanfclgpcpyiwsldtqysk 60
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMVKSCKS 112
 DB 61 vialynqhnpgasaapccvpqdaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 82
 AAW97091
 ID AAW97091 standard; Protein; 112 AA.
 XX
 AC AAW97091;
 DT
 DT 28-APR-1999 (first entry)
 DE The mature form of transforming growth factor-beta-1.
 XX

KW Transforming growth factor-beta-1; TGF-beta-like protein;
 KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;
 KW bone repair; tissue repair; bone marrow protective agent;
 KW cardioprotection; anti-inflammatory; immunosuppressive;
 KW ulcer; bed sore.
 XX

OS Homo sapiens.
 XX
 PN EP891985-A1.
 XX
 PD 20-JAN-1999.
 XX
 PF 27-NOV-1990; 90EP-0810922.
 XX
 PR 06-DEC-1989; 89GB-0027546.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
 XX
 DR WPI; 1999-083520/08.
 DR N-PSDB; AAX15245.
 XX

Producing biologically active dimeric Transforming Growth
 Factor-beta - by refolding new monomeric Transforming Growth
 Factor-beta, useful for treatment of wounds and cancer
 XX
 PS Example 1; Page 28; 32pp; English.
 XX
 CC The present sequence represents the mature form of transforming growth
 CC factor-beta-1. Dimeric, biologically active TGF-beta-like protein
 CC can be produced by subjecting the denatured monomeric form to refolding
 CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
 CC useful for the production of the dimeric, biologically active
 CC TGF-beta-like protein, which is useful for the treatment of wounds
 CC (surface or internal) and cancer in a mammal, in bone and tissue
 CC repair, as a bone marrow protective agent, a mediator of
 CC cardioprotection, for the production of an anti-inflammatory or
 CC immunosuppressive preparation. Treatment is useful for animals,
 CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
 CC particularly useful for the elderly.
 XX
 SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 20; Length 112;
 Best Local Similarity 76.8%; Pred. No. 3.9e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDGLGWKWHPEKGYANFCSGPCPYLRSADTHST 60
 DB 1 aldtncfsteckncvrglyidfrkdlgwkwhepkgyhanfclgpcpyiwsldtqysk 60

Db 61 vlalynqhnpgasaapccvpqaleplivvyvqrkpkveqlsnm!vrsccks 112

RESULT	84
AAI92010	
ID	AAI92010 standard; Protein; 112 AA.
XX	
AC	AAI92010;
XX	
DT	19-JUL-2000 (first entry)
XX	
DE	Human transforming growth factor beta 1 monomer.
XX	
KW	human transforming growth factor beta 1 monomer; CKGF; mutant;
KW	cystine knot growth factor; hairpin loop; infertility.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	Misc-difference 1..20
FT	/note= "optionally mutated to increase electrostatic
FT	interaction between beta hairpin structure and
FT	a receptor"
FT	
Domain	21..40
FT	/label= beta_hairpin_loop_1
FT	/note= "mutant optionally comprises one or more
FT	substitutions in these residues"
FT	
Misc-difference	41..81
FT	/note= "optionally mutated to increase electrostatic
FT	interaction between beta hairpin structure and
FT	a receptor"
FT	
Domain	82..102
FT	/label= beta_hairpin_loop_3
FT	/note= "mutant optionally comprises one or more
FT	substitutions in these residues"
FT	
Misc-difference	103..112
FT	/note= "optionally mutated to increase electrostatic
FT	interaction between beta hairpin structure and
FT	a receptor"
FT	
PN	WO200017360-A1.
XX	
PD	30-MAR-2000.
XX	
PF	19-MAR-1999; 99WO-US05908.
XX	
PR	22-SEP-1998; 98WO-US19772.
XX	
PA	(UYMA-) UNIV MARYLAND BALTIMORE.
XX	
PI	Weintraub BD, Szkudlinski MW;
XX	
DR	WPI; 2000-293585/24.
XX	
PT	New mutant cystine knot growth factor proteins comprising one or more
PT	mutant subunits, useful for treating or preventing diseases e.g.
PT	hypothyroidism and thyroid cancer
XX	
PS	Claim 193; Page 300; 320pp; English.
XX	
CC	This is the wild type human transforming growth factor beta 1 monomer.
CC	Mutants comprise at least one electrostatic charge altering mutation in
CC	beta hairpin loop, resulting in increased bioactivity.
CC	Mutant cystine knot growth factor (CKGF) proteins comprising one or more
CC	mutant subunits and having novel properties or improved pharmacological
CC	properties, compared to wild type CKGFs, are claimed. The CKGF
CC	superfamily comprises at least four families of growth factors: the
CC	glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
CC	the neurotrophins and the transforming growth factor-beta family; the
CC	families are known to be structurally similar (especially comprising the
CC	cystine knot topology) and it was shown that mutations at certain
CC	positions in the CKGF hairpin loops of family members and other members
CC	of the CKGF superfamily could significantly alter the biological
CC	activities of the CKGF.
CC	Mutant transforming growth factor family proteins or analogues are used

CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
XX infertility, time-limited conception and in assisted reproduction.
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 21; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncfsstekncvvrqlyidfrkdigkwihpkgyhanfcigpcpylwsldtqysk 60
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhngpasaapccvpqaleplivyyvgrkpkveqlsnmivrskcs 112

RESULT 85
AAY67950
ID AAY67950 standard; protein; 112 AA.
XX
AC AAY67950;
XX
DT 03-APR-2000 (first entry)
XX
DE Human transforming growth factor SEQ ID NO:2.
XX
KW Human; transforming growth factor; Pax4 gene; expression; potentiator;
KW insulin; pancreatic beta cell; diabetes.
XX
OS Homo sapiens.
XX
PN WO9966073-A1.
XX
PD 23-DEC-1999.
XX
PF 15-JUN-1999; 99WO-JP03182.
XX
PR 16-JUN-1998; 98JP-0167976.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Ueda Y;
XX
DR WPI; 2000-097752/08.
XX
PT Screening potential Pax4 gene potentiators, used in treatment of, e.g.
PT diabetes -
XX
PS Disclosure; Page 29; 38pp; Japanese.
XX

CC The present invention describes the a method for screening potential
CC inhibitors of the expression of the Pax4 gene by contacting the
CC potential inhibitor with pancreatic beta cells and measuring the
CC expression of the gene in these cells is new. Substances identified
CC by the screening method potentiate the expression of the Pax4 gene in
CC pancreatic beta cells and accelerate the expression of insulin gene in
CC those cells. The method can be used in the treatment of disorders in
CC which the exhaustion of pancreatic beta cells is involved, such as
CC diabetes. The present sequence represents the human transforming growth
CC factor protein which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 21; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60

DB 1 aldtncfsstekncvvrqlyidfrkdigkwihpkgyhanfcigpcpylwsldtqysk 60
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhngpasaapccvpqaleplivyyvgrkpkveqlsnmivrskcs 112

RESULT 86
AAB35937
ID AAB35937 standard; protein; 112 AA.
XX
AC AAB35937;
XX
DT 26-FEB-2001 (first entry)
XX
DE TGF-beta 1 amino acid sequence.
XX
KW Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
KW wound healing; dermal wound; wound healing; TGF-beta 1.
XX
OS Unidentified.
XX
PN WO200064481-A1.
XX
PD 02-NOV-2000.
XX
PF 22-APR-1999; 99WO-IB00800.
XX
PR 22-APR-1999; 99WO-IB00800.
XX
PA (ETHZ-) ETH ZURICH & UNIV ZURICH.
XX
PI Sakiyama SE, Hubbell JA;
XX
DR WPI; 2001-024627/03.
XX

PT Matrix for controlled release of growth factor for wound healing, has
PT substrate that attaches heparin binding peptide, protein growth factor
PT that bind heparin with low affinity, and heparin or heparin-like
PT polymer -
XX
PS Example 5; Page 21; 48pp; English.
XX
CC This invention relates to a matrix comprising a substrate capable of
CC providing attachment of a heparin binding peptide (HBP), a peptide
CC comprising a binding domain which binds heparin with high affinity,
CC heparin or heparin-like polymer, and a protein growth factor or peptide
CC fragment which has a domain that binds heparin with low affinity.
CC Included in the invention is a vascular graft comprising the matrix,
CC which is capable of supporting cell adhesion. The matrix is used for
CC delivering low heparin binding affinity growth factor proteins or
CC peptides in a controlled manner suitable for wound healing. The matrix
CC can be used in an article for treating dermal wounds, and in an
CC implantable sterilized composition capable of supporting cell adhesion.
CC The present sequence represents a growth factor protein. The protein is
CC used in an example illustrating that non-heparin-binding growth factors
CC can be released in a controlled manner from heparin-based drug delivery
CC systems based on their low affinity for heparin.
XX
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 22; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncfsstekncvvrqlyidfrkdigkwihpkgyhanfcigpcpylwsldtqysk 60
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112

[illegible]

N.B. The present sequence is does not appear in the specification,
but is derived from the sequences mentioned above.

Sequence 122 AA;

Query Match 78.9%; Score 500; DB 18; Length 122;
Best Local Similarity 76.8%; Pred. No. 4.2e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLNCCVRRPLYIDFRQDLGKWKWHEPKGYANFCGPGCPYLRSADTTHST 60
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 aldnycfsstekccvrrqlyidfrkdlgwkwihpkgyhanfclgpcpylwsldtysk 70
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 VLGLYTLNLPASAPCCVPQDLPLTLILYYVGRTPKVEQLSNMVAACKCS 112
| | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 vlalynqhnpasapccvpqaleplivyyvgkpkveqlsnmivrskcs 122

RESULT 90
AAW08177
ID AAW08177 standard; Peptide; 124 AA.
AC AAW08177;
XX
XX 26-AUG-1997 (first entry)
XX TGF-beta fusion protein 22:15:30.
XX Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..6 /label= Purification_tag
FT Region 7..12 /label= Proteinase_site
FT Region 13..123 /label= TGF-beta1_active_fragment
XX W09639430-A1.
XX
XX 12-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US08973.
XX
XX 06-JUN-1995; 95US-0470837.
XX
XX (CHEU/) CHEUNG D T.
PA (HALL/) HALL F L.
FA (NIMN/) NIMNI M E.
PA (TUAN/) TUAN T.
XX (WULL/) WU L.
XX
PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
PT reduce surgery recovery time and to prepare artificial skin
XX
XX Example 1; Page -: 59pp; English.
XX
XX A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. Additionally,
CC the fusion protein may comprise proteinase-sensitive linker sites and
CC binding domain so the protein sequence may contain some or all of the
CC following elements: purification tag;proteinase site;ECM binding site:
CC proteinase site:TGF-beta. The present sequence represents a fusion
CC protein made up from a purification tag (AAW18225), a proteinase site

XX	05-JUN-1996;	96WO-US08973.
XX	06-JUN-1995;	95US-0470837.
XX	(CHEU/) CHEUNG D T.	
XX	(HALL/) HALL F L.	
XX	(NIMN/) NIMMI M E.	
XX	(TUAN/) TUAN T.	
XX	(WULL/) WU L.	
XX	Cheung DT, Hall FL, Nimmi ME, Tuan T, Wu L;	
XX	WPI; 1997-043065/04.	
XX	Prepn. of transforming growth factor-beta fusion protein - useful to	
XX	reduce surgery recovery time and to prepare artificial skin	
XX	Disclosure; Page -: 59pp; English.	
XX	A novel transforming growth factor-beta (TGF-beta) fusion protein	
XX	comprises a purification tag and a TGF active fragment. Additionally	
XX	the fusion protein may comprise proteinase-sensitive linker sites and	
XX	binding domain so the protein sequence may contain some or all of the	
XX	following elements: purification tag:proteinase site:ECM binding site	
XX	proteinase site:TGF-beta. The present sequence represents a fusion	
XX	protein made up from a purification tag (AAW18225), a proteinase site	
XX	(AAW08170), an extracellular matrix binding site (AAW08171) and a TGF	
XX	active fragment (AAW08173). TGF-beta promotes wound healing, and the	
XX	fusion protein can be used to reduce surgery recovery time and in	
XX	the preparation of artificial skin. The inclusion of a purification	
XX	tag facilitates purification of the fusion protein. The proteinase	
XX	site is included to permit cleavage and release of the purification	
XX	tag after purification if desired. The extracellular matrix binding	
XX	site facilitates delivery of the fusion protein to the desired site	
XX	of action. Delivery of the TGF-beta to the site to be treated reduces	
XX	the amount of TGF-beta required to be administered to be effective	
XX	and reduces the concentration of circulating TGF-beta which may	
XX	result in undesirable effects.	
XX	N.B. The present sequence is does not appear in the specification,	
XX	but is derived from the sequences mentioned above.	
XX	Sequence 130 AA;	
XX		

Query Match 78.9%; Score 500; DB 18; Length 130;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ALD	NYC	FRN	LENC	CCVR	PLYD	FRQD	IGWK	WH	HEP	KGY	ANFC	SGCP	YLRS	ADTT	HTST	60								
		:																:								
Db	19	ald	ny	cf	st	ek	nc	vr	qlyd	fr	kd	gwk	h	ep	kgy	h	an	fc	lpc	py	l	ws	ld	qy	sk	78

QY 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKS 112
||| || |:::||||| ||| :||| ||||| |:|:|
Dd 79 vlalynqhnpqasaapccvpqdaleplviyyvqrkpkvedlsmivrsckcs 130

RESULT 93

AAW08182
ID AAW08182 standard: Peptide: 131 AA.

XX AAW08182;

AX
DT 26-AUG-1997 (first entry)

XX DE TGF-beta fusion protein 22:13:20:30.

XX Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time.

XX	
OS	Homo sapiens.
OS	Synthetic.

Key	Location/Qualifiers
Region	1..6
	/label= Purification_tag
Region	7..10
	/label= Proteinase_site
Region	11..19
	/label= Extracellular_matrix_binding_site
Region	20..131
	/label= TGF-beta1_active_fragment

Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

WPI; 1997-043065/04.

Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin

Disclosure; Page - ; 59pp; English.

A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and a binding domain so the protein sequence may contain some or all of the following elements: purification tag; proteinase site; ECM binding site; proteinase site; TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAW18225), a proteinase site (AAW08170), an extracellular matrix binding site (AAW08171) and a TGF active fragment (AAW08173). TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.

N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.

Sequence 130 AA;

Query Match 78.9%; Score 500; DB 18; Length 130;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy	1 ALDTNYCFRNLEENCVRPLYIDFRQDGLGWKHVHEPKGYVANFCSGPCPYLRSDTTHST 60 : : : : : : : : :
Db	19 aldtncfcsstekncvrrqlyldfrkdlgwkhhepkgyhanfcgpcpyiwsldtqysk 78

QY 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKS 112
||| || |:::||||| ||| :||| ||||| |:|:|
Dd 79 vlalynqhnpcsaapccvpcaaleplviyyvqrkpkvedlsmivrsckcs 130

Query Match 78.9%; Score 500; DB 18; Length 131;
Best Local Similarity 76.8%; Pred. NO. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNL EENCVRPLYIDFRQDIGKWKVHEPKGYVANFCSGPCPYLRSDTTHST 60
 :
Dp 20 aldnvcfstekncvralvidfrklcwkwihepkavnaofclacpcviwslidtavsk 79

00V 61 VIGLYNTLNPEASASPCCVPODLEPLTILYVVGRTPKVEOLSNMVKSCKS 112

Db 80 vlalynghnpgtsaaapccvvpqaleplpivyyvgrkpkveqlsnmivrsckcs 131

RESULT 94

AAW08189
ID AAW08189 standard; Peptide; 132 AA.

XX AC AAW08189;

XX DT 26-AUG-1997 (first entry)

XX DE TGF-beta fusion protein 22:13:18:13:30.

XX KW Transforming growth factor-beta fusion protein; wound healing;
artificial skin; surgery recovery time.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..6
FT Region /label= Purification_tag
FT Region 7..10
FT Region /label= Proteinase_site
FT Region 11..16
FT Region /label= Extracellular_matrix_binding_site
FT Region 17..20
FT Region /label= Proteinase_site
FT Region 21..132
FT Region /label= TGF-beta1_active_fragment

XX PN W09639430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMN/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimmi ME, Tuan T, Wu L;

XX WPI; 1997-043065/04.

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin

XX PS Disclosure: Page -: 59pp; English.

XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinase-sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
following elements: purification tag; proteinase site; ECM binding site;
proteinase site; TGF-beta. The present sequence represents a fusion
protein made up from a purification tag (AAW18225), a proteinase site
(AAW08169), an extracellular matrix binding site (AAW08171), another
proteinase site (AAW08169) and a TGF active fragment (AAW08173).
TGF-beta promotes wound healing, and the fusion protein can be used to
reduce surgery recovery time and in the preparation of artificial skin.
The inclusion of a purification tag facilitates purification of the
fusion protein. The proteinase site is included to permit cleavage and
release of the purification tag after purification if desired. The
extracellular matrix binding site facilitates delivery of the fusion
protein to the desired site of action. Delivery of the TGF-beta to the
site to be treated reduces the amount of TGF-beta required to be
administered to be effective and reduces the concentration of circulating
TGF-beta which may result in undesirable effects.
N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.

XX Sequence 132 AA;

Query Match 78.9%; Score 500; DB 18; Length 132;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLNCCVRPLYIDFRQDLGWKWHPEKGYANFCSGPCPYLRSADTTHST 60
||||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 21 aldtncfsstekncvrlqyldfrkdldgkwkwhpekgynhanfclgpcpylwsldtgysk 80
QY 61 VLGLYNTLNPASAPCCVPQDLEPLTLYYVGRTPKVEQLSNMNVKSKCS 112
|| ||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 81 vlalynqhnpgasaapccvpqalepllvyyvgrkpkveqlsnmnlvrskcs 132

RESULT 95

AAW08178

ID AAW08178 standard; Peptide; 133 AA.

XX AC AAW08178;

XX DT 26-AUG-1997 (first entry)

XX DE TGF-beta fusion protein 22:15:20:30.

XX KW Transforming growth factor-beta fusion protein; wound healing;
artificial skin; surgery recovery time.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..6
FT Region /label= Purification_tag
FT Region 7..12
FT Region /label= Proteinase_site
FT Region 13..21
FT Region /label= Extracellular_matrix_binding_site
FT Region 22..133
FT Region /label= TGF-beta1_active_fragment

XX PN W09639430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMN/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimmi ME, Tuan T, Wu L;

XX WPI; 1997-043065/04.

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin

XX PS Example 1; Page -: 59pp; English.

XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinase-sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
following elements: purification tag; proteinase site; ECM binding site;
proteinase site; TGF-beta. The present sequence represents a fusion
protein made up from a purification tag (AAW18225), a proteinase site
(AAW08170), an extracellular matrix binding site (AAW08172) and a TGF
active fragment (AAW08173). TGF-beta promotes wound healing, and the


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PN WO639430-A1.
XX
XX PD
XX OS
XX PF 12-DEC-1996.
XX
XX PR 05-JUN-1996; 96WO-US08973.
XX
XX PR 06-JUN-1995; 95US-0470837.
XX
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX PT reduce surgery recovery time and to prepare artificial skin
XX
XX PS Disclosure; Page -: 59pp; English.
XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. Additionally,
XX CC the fusion protein may comprise proteinase-sensitive linker sites and
XX CC binding domain so the protein sequence may contain some or all of the
XX CC following elements: purification tag; proteinase site; ECM binding site;
XX CC proteinase site; TGF-beta. The present sequence represents a fusion
XX CC protein made up from a purification tag (AAW18225), a proteinase site
XX CC (AAW08169), an extracellular matrix binding site (AAW08171), another
XX CC proteinase site (AAW08170) and a TGF active fragment (AAW08173).
XX CC TGF-beta promotes wound healing, and the fusion protein can be used to
XX CC reduce surgery recovery time and in the preparation of artificial skin.
XX CC The inclusion of a purification tag facilitates purification of the
XX CC fusion protein. The proteinase site is included to permit cleavage and
XX CC release of the purification tag after purification if desired. The
XX CC extracellular matrix binding site facilitates delivery of the fusion
XX CC protein to the desired site of action. Delivery of the TGF-beta to the
XX CC site to be treated reduces the amount of TGF-beta required to be
XX CC administered to be effective and reduces the concentration of circulating
XX CC TGF-beta which may result in undesirable effects.
XX CC N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.
XX
XX SQ Sequence 134 AA;

Query Match 78.9%; Score 500; DB 18; Length 134;
Best Local Similarity 76.8%; Pred. No. 4.7e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFNRLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSPGCPYLRSDTTHST 60
Db 23 aldtncyfstekncvrrglyidfrkdlgkwihpkgyhanfclgpcpylwsldtqysk 82
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 83 vialynqhpgasapccvpqaleplivyyvgrpkpveqlsnmivrskcs 134

RESULT 98
AAW08183
ID AAW08183 standard; Peptide; 135 AA.
XX
XX AC AAW08183;
XX
XX DT 26-AUG-1997 (first entry)
XX
XX DE TGF-beta fusion protein 22:13:20:13:30.
XX
XX KW Transforming growth factor-beta fusion protein; wound healing;
XX artificial skin; surgery recovery time.

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XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key
XX FT Region 1..6
XX FT /label= Purification_tag
XX FT 7..10
XX FT /label= Proteinase_site
XX FT 11..19
XX FT /label= Extracellular_matrix_binding_site
XX FT 20..23
XX FT /label= Proteinase_site
XX FT 24..135
XX FT /label= TGF-beta1_active_fragment
XX
XX PN WO639430-A1.
XX
XX PD 12-DEC-1996.
XX
XX PF 05-JUN-1996; 96WO-US08973.
XX
XX PR 06-JUN-1995; 95US-0470837.
XX
XX CC (CHEU/) CHEUNG D T.
XX CC (HALL/) HALL F L.
XX CC (NIMN/) NIMNI M E.
XX CC (TUAN/) TUAN T.
XX CC (WULL/) WU L.
XX
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX PT reduce surgery recovery time and to prepare artificial skin
XX
XX PS Disclosure; Page -: 59pp; English.
XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. Additionally,
XX CC the fusion protein may comprise proteinase-sensitive linker sites and
XX CC binding domain so the protein sequence may contain some or all of the
XX CC following elements: purification tag; proteinase site; ECM binding site;
XX CC proteinase site; TGF-beta. The present sequence represents a fusion
XX CC protein made up from a purification tag (AAW18225), a proteinase site
XX CC (AAW08169), an extracellular matrix binding site (AAW08172), another
XX CC proteinase site (AAW08169), and a TGF active fragment (AAW08173).
XX CC TGF-beta promotes wound healing, and the fusion protein can be used to
XX CC reduce surgery recovery time and in the preparation of artificial skin.
XX CC The inclusion of a purification tag facilitates purification of the
XX CC fusion protein. The proteinase site is included to permit cleavage and
XX CC release of the purification tag after purification if desired. The
XX CC extracellular matrix binding site facilitates delivery of the fusion
XX CC protein to the desired site of action. Delivery of the TGF-beta to the
XX CC site to be treated reduces the amount of TGF-beta required to be
XX CC administered to be effective and reduces the concentration of circulating
XX CC TGF-beta which may result in undesirable effects.
XX CC N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.
XX
XX SQ Sequence 135 AA;

Query Match 78.9%; Score 500; DB 18; Length 135;
Best Local Similarity 76.8%; Pred. No. 4.8e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFNRLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSPGCPYLRSDTTHST 60
Db 24 aldtncyfstekncvrrglyidfrkdlgkwihpkgyhanfclgpcpylwsldtqysk 83
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112

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Db 84 vialynqhpasaapccvpqalepivyyvgrkpkveqlsnmivrsckcs 135

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RESULT 99
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ID AAW08186 standard; Peptide; 136 AA.
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AC AAW08186;
XX
DT 26-AUG-1997 (first entry)
XX
DE TGF-beta fusion protein 22:15:18:15:30.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..6
FT /label= Purification_tag
FT 7..12
FT /label= Proteinase_site
FT 13..18
FT /label= Extracellular_matrix_binding_site
FT 19..24
FT /label= Proteinase_site
FT 25..136
FT /label= TGF-beta1_active_fragment
XX
XX WO9639430-A1.
XX
XX 12-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US08973.
XX
XX 06-JUN-1995; 95US-0470837.
XX
XX (CHEU/) CHEUNG D T.
XX (HALL/) HALL F L.
XX (NIMN/) NIMNI M E.
XX (TUAN/) TUAN T.
XX (WULL/) WU L.
XX
XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
XX reduce surgery recovery time and to prepare artificial skin
XX
XX Disclosure; Page -: 59pp; English.
XX
XX A novel transforming growth factor-beta (TGF-beta) fusion protein
XX comprises a purification tag and a TGF active fragment. Additionally,
XX the fusion protein may comprise proteinase-sensitive linker sites and
XX binding domain so the protein sequence may contain some or all of the
XX following elements: purification tag; proteinase site; ECM binding site;
XX proteinase site; TGF-beta. The present sequence represents a fusion
XX protein made up from a purification tag (AAW18225), a proteinase site
XX (AAW08170), an extracellular matrix binding site (AAW08171), another
XX proteinase site (AAW08170) and a TGF active fragment (AAW08173).
XX TGF-beta promotes wound healing, and the fusion protein can be used to
XX reduce surgery recovery time and in the preparation of artificial skin.
XX The inclusion of a purification tag facilitates purification of the
XX fusion protein. The proteinase site is included to permit cleavage and
XX release of the purification tag after purification if desired. The
XX extracellular matrix binding site facilitates delivery of the fusion
XX protein to the desired site of action. Delivery of the TGF-beta to the
XX site to be treated reduces the amount of TGF-beta required to be
XX administered to be effective and reduces the concentration of circulating

```

CC TGF-beta which may result in undesirable effects.
 CC N.B. The present sequence is does not appear in the specification,
 CC but is derived from the sequences mentioned above.
 XX
 SQ Sequence 136 AA;

Query Match 78.9%; Score 500; DB 18; Length 136;
 Best Local Similarity 76.8%; Pred. No. 4.8e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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RESULT 100
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 ID AAW08180 standard; Peptide; 137 AA.
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 AC AAW08180;
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 DT 26-AUG-1997 (first entry)
 XX
 DE TGF-beta fusion protein 22:15:20:13:30.
 XX
 KW Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Region 1..6
 FT /label= Purification_tag
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 FT 26..137
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 XX 12-DEC-1996.
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 XX 05-JUN-1996; 96WO-US08973.
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 XX 06-JUN-1995; 95US-0470837.
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 XX (HALL/) HALL F L.
 XX (NIMN/) NIMNI M E.
 XX (TUAN/) TUAN T.
 XX (WULL/) WU L.
 XX
 XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 XX WPI; 1997-043065/04.

XX Prepn. of transforming growth factor-beta fusion protein - useful to
 XX reduce surgery recovery time and to prepare artificial skin
 XX
 XX Disclosure; Page -: 59pp; English.
 XX
 XX A novel transforming growth factor-beta (TGF-beta) fusion protein
 XX comprises a purification tag and a TGF active fragment. Additionally,
 XX the fusion protein may comprise proteinase-sensitive linker sites and
 XX binding domain so the protein sequence may contain some or all of the
 XX following elements: purification tag; proteinase site; ECM binding site;
 XX proteinase site; TGF-beta. The present sequence represents a fusion
 XX protein made up from a purification tag (AAW18225), a proteinase site
 XX (AAW08170), an extracellular matrix binding site (AAW08171), another
 XX proteinase site (AAW08170) and a TGF active fragment (AAW08173).
 XX TGF-beta promotes wound healing, and the fusion protein can be used to
 XX reduce surgery recovery time and in the preparation of artificial skin.
 XX The inclusion of a purification tag facilitates purification of the
 XX fusion protein. The proteinase site is included to permit cleavage and
 XX release of the purification tag after purification if desired. The
 XX extracellular matrix binding site facilitates delivery of the fusion
 XX protein to the desired site of action. Delivery of the TGF-beta to the
 XX site to be treated reduces the amount of TGF-beta required to be
 XX administered to be effective and reduces the concentration of circulating

Sequence 137 AA;

Search completed: October 30, 2001, 08:51:22
Job time: 151 sec

OM of: TGFB3P to: GenEmbl.* out_format : pfs

Date: Oct 30, 2001 9:34 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -GAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000
-FGAPEXT=7.000 -GAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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Search information block:
Query: TGFB3P
Query length: 113
Database: GenEmbl.*
Database sequences: 1344157
Database length: -856060004
Search time (sec): 1231.360000

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gb_r01:SLGTGFB2	+	516.00	955.42	5.6e-45	2724	X51817 Xenopus laevis TGF-b
gb_r01:SLGTGFB2	+	503.00	934.96	7.7e-44	1561	I08275 Sequence 3 from Pate
gb_r01:MUSTGRNA	+	503.00	934.88	7.8e-44	1579	M13177 Mouse transforming g
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gb_r01:MM0009862	+	503.00	932.79	1.0e-43	2094	AJ009862 Mus musculus mRNA
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gb_r01:AF191297	+	488.00	915.50	9.3e-43	469	X60296 M.auratus mRNA for tr
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gb_r01:AF276986	+	439.00	809.76	7.2e-37	2754	J05180 X.laevis transforming
gb_r01:AF161218	+	435.00	819.31	2.1e-37	273	AF276986 Capra hircus TGF be
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seq_documentation_block:
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DEFINITION H.sapiens TGF-beta 2 peptide seq ID No.3.
ACCESSION A18281
VERSION A18281.1 GI:513241
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE 1 (bases 1 to 339)

AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 6 19-JUN-1991;
CIBA-GEIGY AG
FEATURES Location/Qualifiers
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LOCUS A23753 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3 coding region.
ACCESSION A23753
VERSION A23753.1 GI:825587
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 339)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 3 19-MAY-1993;
CIBA-GEIGY AG
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Ratio: 5.652 Gaps: 0
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51 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCC 100
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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201 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGCTGCGTCCCGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCTTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
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DEFINITION Sequence 5 from Patent WO9603432.
ACCESSION A48553
VERSION A48553.1 GI:2302323
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
PROTEI
JOURNAL Patent: WO 9603432-A 5 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES Location/Qualifiers
source 1..339
/organism="unidentified"

CDS /db_xref="taxon:32644"
1..336
/note="Protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HUMAN TGF-BETA3"
/protein_id="CAA03115.1"
/db_xref="GI:2302324"
/translation="ALDNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFC SGPCPLRSADTHTSTVLGLYNLPEASPCCPQDLEPLTILYYVGRTPKVEQLS NMVVKSCKCS"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x A48553 ..

Align seg 1/1 to: A48553 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATTACTGCTTCGCCCAACTTGGAGGAGAAGTCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACATTCGACAGGATCTGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTCGACACACACCCAGCAGCGTGTGGGACTGTACACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAAGCATCTGCCTCGCCTTGTGCTGCCCGCAGGACCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTGCTATGTTGGGAGGACCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTGTAATGTAGC 336

seq_name: gb_pat1:A48567

seq_documentation_block:
LOCUS A48567 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent WO9603433.
ACCESSION A48567
VERSION A48567.1 GI:2302337
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 5 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES
Other publication AU 3109695 960222.
Location/Qualifiers
1..339
/organism="unidentified"

CDS /db_xref="taxon:32644"
1..336
/note="Protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HUMAN TGF-BETA3"
/protein_id="CAA03122.1"
/db_xref="GI:2302338"
/translation="ALDNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYANFC SGPCPLRSADTHTSTVLGLYNLPEASPCCPQDLEPLTILYYVGRTPKVEQLS NMVVKSCKCS"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x A48567 ..

Align seg 1/1 to: A48567 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATTACTGCTTCGCCCAACTTGGAGGAGAAGTCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACATTCGACAGGATCTGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTCGACACACACCCAGCAGCGTGTGGGACTGTACACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAAGCATCTGCCTCGCCTTGTGCTGCCCGCAGGACCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTGCTATGTTGGGAGGACCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTGTAATGTAGC 336

seq_name: gb_pat1:A59779

seq_documentation_block:
LOCUS A59779 339 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9705166.
ACCESSION A59779
VERSION A59779.1 GI:3715005
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Mittl,P., Gruetter,M. and Arvinde,T.
TITLE TRANSFORMING GROWTH FACTOR BETA CRYSTALS
JOURNAL Patent: WO 9705166-A 1 13-FEB-1997;
COMMENT CIBA GEIGY AG (CH)
FEATURES
Location/Qualifiers
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/organism="unidentified"
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CDS

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/db_xref="GI:3715006"
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SGPCPYLRASDTHSTVLGLYTLNPEASAPCCVPQDLPLTILYYVGRTPKVEQLS
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BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN

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alignment_scores:

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Quality: 633.00      Length: 112
Ratio: 5.652
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

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Align seg 1/1 to: A59779 from: 1 to: 339
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGCTGGAGTGGGTCC 100

34 isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACCCAGCAGCGTCTGGCTGGAGTGGGTCC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCTCGCTTGTGCTGGCTGGAGTGGGTCC 250

84 lArgProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGAGGAGCCCCAAAGTGGAGCAG 300

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

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seq_name: gb_pat1:AR036688
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seq_documentation_block:

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LOCUS      AR036688      339 bp      DNA      29-SEP-1999
DEFINITION Sequence 33 from patent US 5800811.
ACCESSION  AR036688
VERSION     AR036688.1 GI:5954544
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 339)
AUTHORS     Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE       Artificial skin prepared from collagen matrix containing
            transforming growth factor-beta having a collagen binding site
JOURNAL     Patent: US 5800811-A 33 01-SEP-1998;
FEATURES
            Location/Qualifiers
            source
            1. .339
            /organism="unknown"
BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN

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REFERENCE

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1 (bases 1 to 339)
AUTHORS     Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE       Artificial skin prepared from collagen matrix containing
            transforming growth factor-beta having a collagen binding site
JOURNAL     Patent: US 5800811-A 33 01-SEP-1998;
FEATURES
            Location/Qualifiers
            source
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            /organism="unknown"
BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN

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alignment_scores:

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Quality: 633.00      Length: 112
Ratio: 5.652
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

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TGFB3P x A59779
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Align seg 1/1 to: A59779 from: 1 to: 339
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

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alignment_scores:

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Quality: 633.00      Length: 112
Ratio: 5.652
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

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TGFB3P x AR036688
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Align seg 1/1 to: AR036688 from: 1 to: 339
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGCTGGAGTGGGTCC 100

34 isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACCCAGCAGCGTCTGGCTGGAGTGGGTCC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCTCGCTTGTGCTGGCTGGAGTGGGTCC 250

84 lArgProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGAGGAGCCCCAAAGTGGAGCAG 300

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

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seq_name: gb_pat2:I56856
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seq_documentation_block:

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LOCUS      I56856      339 bp      DNA      07-OCT-1997
DEFINITION Sequence 3 from patent US 5650494.
ACCESSION  I56856
VERSION     I56856.1 GI:2477269
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 339)
AUTHORS     Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE       Process for refolding recombinantly produced TGF-beta-like
            proteins
JOURNAL     Patent: US 5650494-A 3 22-JUL-1997;
FEATURES
            Location/Qualifiers
            source
            1. .339
            /organism="unknown"
BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN

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REFERENCE

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1 (bases 1 to 339)
AUTHORS     Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE       Process for refolding recombinantly produced TGF-beta-like
            proteins
JOURNAL     Patent: US 5650494-A 3 22-JUL-1997;
FEATURES
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            source
            1. .339
            /organism="unknown"
BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN

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alignment_scores:

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Quality: 633.00      Length: 112
Ratio: 5.652
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

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TGFB3P x I56856
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Align seg 1/1 to: I56856 from: 1 to: 339
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCTTTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCCCTCTACATTTGCTTCCGACAGGATCTGGCTGGAAGTGGGTCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ATGAACCTAAGGCTACTATGCCAATCTCTCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGCGAGTGCAGACACACACCCAGCAGCGTGTGGGACTGTACACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
201 TCTGAACCTGAAGCATCTGCTCGCTTGTGGAGGACCCCAAGTGGAGCAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCTCCCAACATGGTGGTGAAGCTCTTGAATGTAGC 336
seq_name: gb_rol:BC005513
seq_documentation_block:
LOCUS BC005513 2164 bp mRNA ROD 03-APR-2001
DEFINITION Mus musculus, similar to transforming growth factor, beta 3, clone
IMAGE:3492763, mRNA, partial cds.
ACCESSION BC005513
VERSION BC005513.1 GI:13529607
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2164)
Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 8 Row: f Column: 13.
FEATURES
source
Location/Qualifiers
1..2164
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3492763"
/tissue_type="Mammary tumor metastatized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clone) outgrowth infected with the virus MMV."
/clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
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/note="vector: pCMV-SPORT6"
<1..1090
/codon_start=2
/product="similar to transforming growth factor, beta 3"
/protein_id="AAH05513.1"
/db_xref="GI:13529608"
/translation="GRVGSPPSPVMTHTVQVLYALYNSTRLEEMHGEREGCTQE
TSESEYTAKEIHKFDMIOGLAEHNLAVCPKGIITSKVFRFNVSVEKNGTNLFRAEFR
VLVRPNSSKRTQRIELFQILRDEHIAKQRIIGKNLPTRGTAEWLSFDVTDVRE
WLLRNSNLGLEIISIHCPCHTFQPNGDILENNHEVMEIKFKGVNEDDHGDLGRLE
KOKDHNPHLILMMIPRILDSPGSGSKRRALDNTYCFNLEENCCVRPLYIDFRQ
DLGWKWHPEKGYVANSGPCPVLRSADTTTSHVIGLYNLINPEASASPCCVPDLE
PLTILYVGRTPKVEQLSNMVKSKCS"
BASE COUNT 634 a 541 c 550 g 439 t
ORIGIN
alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
TGF3P x BC005513 ..
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752 GCCCTGGACACCAATTAATGCTTCCGCAACCTGGAGGAGAACTGCTGTGT 801
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
802 AGCCCTCTTATATTGACTTCCGGCAGGATCTAGGCTGGAATGGTCC 851
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
852 AGCAACCTAAGGCTTACTATGCCAATCTTCTCAGGCCCTTGCCCATAC 901
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
902 CTCGCGAGCGCAGACACACCCATAGCAGCGTGTGGACTATACACAC 951
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
952 CCTGAACCCAGAGCGCTGCTGCCCATGCTGCGTCCGCCAGGACTGG 1001
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1002 AGCCCTTGACCATCTTGTACTATGTGGCAGAACCCCAAGTGGAGCAG 1051
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1052 CTGTCCACATGGTGGTGAAGTCGTGTAAGTGCAGC 1087
seq_name: gb_pr10:HUMTGF3A
seq_documentation_block:
LOCUS HUMTGF3A 2529 bp mRNA PRI 14-JAN-1995
DEFINITION Human transforming growth factor-beta 3 (TGF-beta3); mRNA, complete
cds.
ACCESSION J03241
VERSION J03241.1 GI:339551
KEYWORDS transforming growth factor.
SOURCE Human placental and umbilical cord (cell line A673), cDNA to mRNA,
from library lambda-gt10.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2529)
REFERENCE
AUTHORS ten Dijke, P., Hansen, P., Iwata, K.K., Pieler, C. and Foulkes, J.G.
TITLE Identification of another member of the transforming growth factor
type beta gene family
```

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988)
MEDLINE 88263019
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by C. Pieler 12-SEP-1988. The authors have found that this transforming growth factor contains multiple growth inhibitory elements.

FEATURES
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/db_xref="taxon:9606"
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263..1501
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/db_xref="GI:339552"
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KEIHKFDMIOGLAEHNEALVCPKGTISKVRENVSSEKRNRTNLFRAEFLRVNPDS
SKRNEQRIELFOILRPDEHIAKORYIGGKNLPTRGTAEWLSFDVDTVREWLLRRSN
LGLSISHCPCHTFQPGNDILENHEVMEIKFKGVNDDEHGRGDLGRLKKQKDHNP
HLILMMIPPHRLDNGQGGQRKRALDNTYCFRNLEENCCVRPLYIDFQDLGKRWVH
EPKGYANFCGCPGLRSADTTHSTVLGLYNTLNPEASASPCCVQDLEPLTILYY
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BASE COUNT 617 a 671 c 660 g 581 t
ORIGIN Chromosome 14.

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x HUMTGFB3A ..

Align seg 1/1 to: HUMTGFB3A from: 1 to: 2529

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1163 GCTTTGGACACCAATTAATGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 1212

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

|||||
1213 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGTCC 1262

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

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1263 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 1312

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

|||||
1313 CTCGCGAGTGCAGACACACACACACAGCGTCTGGGACTGTACAACAC 1362

67 rleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

|||||
1363 TCTGAACCCCTGAAGCATCTGCGCTTGGCTGCGTGGCCCGCAGGACCTGG 1412

84 lupProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

|||||
1413 AGCCCTTGACACCTCGTACTATGTTGGGAGGACCCCAAGAGTGGAGCAG 1462

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

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1463 CTCCTCAACATGGTGTGAAGTCTTCTAAATGTAGC 1498

seq_name: gb_pr9:HSTGFB3M

seq_documentation_block:

LOCUS HSTGFB3M 2574 bp mRNA PRI 12-SEP-1993

DEFINITION
X14149
VERSION
X14149.1 GI:37095
KEYWORDS
growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Chen, E.Y.
Direct Submission
Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San
Bruno Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 2574)
REFERENCE
Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L.,
Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and
Chen, E.Y.
A new type of transforming growth factor-beta, TGF-beta 3
EMBO J. 7 (12), 3737-3743 (1988)
MEDLINE 89091120
COMMENT See <J03241> for alternative sequence of TGF-beta 3.
FEATURES
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1..2574
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14q24"
/tissue_type="placenta, ovary glioblastoma"
/cell_line="A172 glioblastoma"
254..1492
/note="TGF-beta 3 (AA 1-412)"
/codon_start=1
/protein_id="CAA32362.1"
/db_xref="GI:37096"
/db_xref="SWISS-PROT:P10600"
/translation="MKHLQRLVLAALNFATVSLSTCTTLDLFGHIKKRVEAIR
GOILSKRLTSPPEPTVTHVPYQVLALYNSTRELLHEMHGEREGCTQENTSEYYA
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SKRNEQRIELFOILRPDEHIAKORYIGGKNLPTRGTAEWLSFDVDTVREWLLRRSN
LGLSISHCPCHTFQPGNDILENHEVMEIKFKGVNDDEHGRGDLGRLKKQKDHNP
HLILMMIPPHRLDNGQGGQRKRALDNTYCFRNLEENCCVRPLYIDFQDLGKRWVH
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BASE COUNT 629 a 680 c 666 g 599 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x HSTGFB3M ..

Align seg 1/1 to: HSTGFB3M from: 1 to: 2574

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1154 GCTTTGGACACCAATTAATGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 1203

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

|||||
1204 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTC 1253

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

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1254 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 1303

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

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1304 CTCGCGAGTGCAGACACACACACAGCGTCTGCTGGGACTGTACAACAC 1353

67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
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478 TCTGAACCTGAAGCATCTGCCTCGCTTCTGCTGATGCGCCAGGACTGG 527
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84 LuProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
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528 ACCCCTGACCATCTGCTACTATGTGGAGGAGACCCCAAGTGGAGCAG 577
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101 LeuSerAsnMetValLysSerCysLysCysSer 112
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578 CTCTCAACATGCTGTGAAGTCTTTGAAATGATAGC 613
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seq_name: gb_ro2:RRU03491

seq_documentation_block: 2633 bp mRNA ROD 06-JUN-1995
LOCUS RRU03491 Rattus norvegicus Wistar transforming growth factor beta-3 mRNA,
DEFINITION complete cds.
ACCESSION U03491
VERSION U03491.1 GI:424131
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2633)
AUTHORS Wang,J., Kuliszewski,M., Yee,W., Sedlackova,L., Xu,J., Tseu,I. and Post,M.
TITLE Cloning and expression of glucocorticoid-induced genes in fetal rat lung fibroblasts. Transforming growth factor-beta 3
J. Biol. Chem. 270 (6), 2722-2728 (1995)
MEDLINE 95155340
REFERENCE 2 (bases 1 to 2633)
AUTHORS Post,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1993) M. Post, The Hospital for Sick Children,
Paediatrics & Research Institute, 555 University Avenue, Toronto,
Ontario M5G 1X8, Canada

FEATURES
Location/Qualifiers
source 1..2633
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/strain="Wistar"
/db_xref="taxon:10116"
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/cell_type="fibroblast"
/tissue_type="lung"
/dev_stage="day 20 fetus"
399..1637
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SKRTEQRIELQILRPDEHIAKQYIGCKNLPTRGTAELWSFDVDTVREMLLRNS
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HLILMIPPHRLSPGGQGRKKRALDNTYCFRNLEENCCVRPLYIDFQDLGKWNH
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GRTPKVEQLSNMVKCKCS"

BASE COUNT 642 a 725 c 686 g 579 t
ORIGIN

alignment_scores:
Quality: 630.00 Length: 112
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1399 ACGAACCTAAGGGTACTATGCCAACTTCTGCTCAGGCCCTTGCCCTTAC 1448
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1449 CTCGGCAGCTCAGACACACACCCAGCAGCGTGTGGACTATACAACAC 1498
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67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
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1499 CTTGAACCCCGAGCATCGGCTCGCATCTGTGCTGCCCAAGACCTGG 1548
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84 LuProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1599 CTGTCCAACATGTTGTGTAAGTCTGTGTAAGTGCAGC 1634
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seq_name: gb_ov:CHKTFGB

seq_documentation_block: 2187 bp mRNA VRT 28-APR-1993
LOCUS CHKTFGB Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete
DEFINITION cds.
ACCESSION M31154
VERSION M31154.1 GI:212758
KEYWORDS transforming growth factor-beta.
SOURCE Chicken embryo chondrocyte, cDNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2187)
AUTHORS Jakowlew,S.B., Dillard,P.J., Kondaiah,P., Sporn,M.B. and Roberts,A.B.
TITLE Complementary deoxyribonucleic acid cloning of a novel transforming growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes
JOURNAL Mol. Endocrinol. 2, 747-755 (1988)
MEDLINE 89096966
FEATURES Location/Qualifiers
source 1..2187
/organism="Gallus gallus"
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/db_xref="GI:212759"
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SKRSQRIELFOILRPDEHIAKORYLSGRNVOTRGSPWLSFDVDTVREMLLRNS
LGLEISTHCPCHTFQNGDILENLEHVEIKFKGIDSDYDGRGLGRLLKQKQDHNH
HLILMPLPHRLSPGLGQGRKKRALDNTYCFRNLEENCCVRPLYIDFQDLGKWNH
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40..108
sig_peptide

/note="transforming growth factor beta signal peptide (pot.); putative"
40..93
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940..1275
/note="transforming growth factor beta (5' end could be at 109)"
BASE COUNT 525 a 587 c 608 g 467 t
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Quality: 629.00 Length: 112
Ratio: 5.616 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107
alignment_block:
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940 GCCTCGATACCACTACTGCTTCGGAACCTGGAGGAACTGCTGTGT 989
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
990 GCGTCTCTTTACATGACTTCCGACAGGACCTGGGCTGGAATGGTGCC 1039
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1040 ATGAGCCTAAGGCTACTTGTCAACTTCTGTTCGGGGCCCATGTCCTAC 1089
51 LeuArgSerAlaAspPheThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1090 CTTCCGAGTGCAGACACCACTTCACAGCAGCGTGTGGCTGTGACAAAC 1139
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1140 GCTGAACCCGAGGATCGCTTACCTGCTGTGCTCCACAGACCTGG 1189
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1190 AGCCACTGACGATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1239
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1240 CTCCTCAATATGGTGAATCCTGCAAGTGCAGC 1275
seq_name: gb_om:SSTGFB3M
seq_documentation_block:
LOCUS SSTGFB3M 2585 bp mRNA MAM 12-SEP-1993
DEFINITION Porcine mRNA for transforming growth factor-beta 3 (TGF-beta 3).
ACCESSION X14150
VERSION X14150.1 GI:2127
KEYWORDS growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Chen,E.Y.
Direct Submission
Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 2585)
Derynck,R., Lindquist,P., Lee,A., Wen,D., Tamm,J., Graycar,J.L., Rhee,L., Mason,A.J., Miller,D.A., Coffey,R.J., Moses,H.L. and Chen,E.Y.
A new type of transforming growth factor-beta, TGF-beta 3

JOURNAL EMBO J. 7 (12), 3737-3743 (1988)
MEDLINE 89091120
COMMENT See <X14149> and <J03241> for human TGF-beta 3 mRNA sequence.
FEATURES
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268..1497
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RSEQRTELFOITQPDDEHIAKQRYIDGNLPTRGAAEWLSESDVDTVREWLRLRESNLG
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LMMIPDRLDNPGLQAKRRLDITNYCFRNLSENCVRRPLYIDFRODLGKWKVHEPK
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BASE COUNT 620 a 705 c 699 g 561 t
ORIGIN
alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214
alignment_block:
TGFB3P x SSTGFB3M ..
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17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATGACTTCCGACAGATCTGGCTGGAAAGTGGTGCC 1258
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1259 ATGAACCTAAGGGCTACTATGCCAATCTGCTCAGGCCCTTGCCCGTAC 1308
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1309 CTCGCGAGTGCAGACACCAACCCACAGTTCGGTGTCTGGGGCTGTACAAC 1358
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCGAGGCTCGGCCCTCTCCGCTGCTGCTGCCCGCCAGACCTGG 1408
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1409 AGCCCTTGACCATCTGTACTACGTGGGAGGACCGCAAGTGGAGCAG 1458
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1459 CTCCTCAATATGGTGAAGTCTGCAAGTGCAGC 1494
seq_name: gb_pat2:I05432
seq_documentation_block:
LOCUS I05432 498 bp PAT
DEFINITION Sequence 2 from Patent EP 0267463.
ACCESSION I05432
VERSION I05432.1 GI:590974
KEYWORDS


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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 498)
AUTHORS      Iwata,K.K., Gold,L.I. and Stephenson,J.R.
TITLE        Tissue-derived tumor growth inhibitors, methods of preparation and
              uses thereof
JOURNAL      Patent: EP 0267463-A2 2 18-MAY-1988;
FEATURES     Location/Qualifiers
              source
              1..498
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BASE COUNT   122 a 137 c 129 g 110 t
ORIGIN

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  Quality: 620.00      Length: 112
  Ratio: 5.586         Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:
  TGF3P x I05432

Align seg 1/1 to: I05432 from: 1 to: 498

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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310 CTCGCGAGTGCAGACACACACCGAGCGGTGCTGGGACTGTACAACAC 359
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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360 TCTGAACCTGAAGCATCTGCTGGGCTTGTGCTGCCGTCGCCAGGACCTGG 409
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84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
410 AGCCCTTGACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 459
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460 CTCTCCACATGGTGTGAAGTCTTGTAAATGTAGC 495

seq_name: gb_pat2:I03319

seq_documentation_block:
LOCUS      I03319
DEFINITION Sequence 10 from Patent US 4886747.
ACCESSION  I03319
VERSION     I03319.1 GI:270713
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 1981)
AUTHORS      Derynck,R.M.A. and Goeddel,D.V.
TITLE        Nucleic acid encoding TGF-beta, and its uses
JOURNAL      Patent: US 4886747-A 10 12-DEC-1989;
              Genentech, Inc.;
              South San Francisco, CA
FEATURES     Location/Qualifiers
              source
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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 336)
AUTHORS      McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE        Novel hybrid transforming growth factors
JOURNAL      Patent: EP 0342679-A 5 19-MAY-1993;
              CIBA-GEIGY AG
FEATURES     Location/Qualifiers
              source
              1..336
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BASE COUNT   75 a 109 c 86 g 66 t
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  Quality: 595.00      Length: 112
  Ratio: 5.459         Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

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|||||
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|||||
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCGCGAGTGCAGACACACCGAGCTCGGCTGCTGGGCTGTACAACAC 1358
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_name: gb_pat1:A23755

seq_documentation_block:
LOCUS      A23755
DEFINITION TGF-beta1(4/45)beta3 hybrid coding region.
ACCESSION  A23755
VERSION     A23755.1 GI:825589
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    1 (bases 1 to 336)
AUTHORS      McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE        Novel hybrid transforming growth factors
JOURNAL      Patent: EP 0342679-A 5 19-MAY-1993;
              CIBA-GEIGY AG
FEATURES     Location/Qualifiers
              source
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              /organism="Homo sapiens"
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BASE COUNT   75 a 109 c 86 g 66 t
ORIGIN

alignment_scores:
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alignment_block:
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51 GCGCAGCTGTACATTGCTTCCGCAAGGACCTCGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGCGAGTGCAGACACACCCACAGCGGTGCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCCCTGAAGCATCTGCCTCGCTTGCCTGCCCGCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCCTCCAACTGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: gb_pat1:A48555
seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48555
DEFINITION Sequence 7 from Patent WO9603432.
ACCESSION A48555
VERSION A48555.1 GI:2302325
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti, N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEIN
JOURNAL Patent: WO 9603432-A 7 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES
source 1. .336
Location/Qualifiers
/organism="unidentified"
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mat_peptide 1. .132
CDS 1. .336
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/product="HYBRID TGF-BETA NAMED TGF-BETA1-3"
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/translation="ALDNTYCFSSSTEKNCCVRQLYIDFRKDLGKWKWIHEPKGYHANFC SGCPYLRSADTHTSTVLGLYNTLNPEASPCVQDLEPLTILYIVGRTPKRVEOLS NMVKSCKCS"
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGCGAGTGCAGACACACCCACAGCGGTGCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCCCTGAAGCATCTGCCTCGCTTGCCTGCCCGCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCCTCCAACTGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: gb_pat1:A48569
seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48569
DEFINITION Sequence 7 from Patent WO9603433.
ACCESSION A48569
VERSION A48569.1 GI:2302339
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti, N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 7 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES
source 1. .336
Location/Qualifiers
/organism="unidentified"
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mat_peptide 1. .132
CDS 1. .336
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA1"
/note="Protein sequence is in conflict with the conceptual translation"
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BASE COUNT 75 a 109 c 86 g 66 t
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alignment_scores:


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Ratio: 5.373          Gaps: 0
Percent Similarity: 98.214  Percent Identity: 91.071

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TGFB3P x A48557
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 GCITTTGGATGCGGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpValh 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 ACGAACCCAAAGGTACAAATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 CTCCGCGATGTCAGACACAAACCCAGCAGCGTGTGGGACTGTACAAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TCTGAACCCCTGAACATCTGCCTCGCCTTGTGGTGGCCCGAGACCTGG 250
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 AGCCCCGTGACCATCTGCTATGTTGGAGGAGCCCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 CTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: gb_pat1:A48571

seq_documentation_block:
LOCUS A48571 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 9 from Patent WO9603433.
ACCESSION A48571
VERSION A48571.1 GI:2302341
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 9 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
FEATURES
source
1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide
1..132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"
CDS
1..336
/note="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HYBRID TGF-BETA2-3"
/protein_id="CAA03124.1"
/db_xref="GI:2302342"
/translation="ALDAAYCFRNVDNCLRPlyIDFKRDLGKWKIHEPKGYANFPC
SGCPYLSADTHTSVLGLYTLNPEASASCCVPQDLEPLTILYVVGTPKVEQLS
NMVYSCKCS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 81 a 94 c 84 g 77 t
ORIGIN
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alignment_scores:
Quality: 591.00 Length: 112
Ratio: 5.373 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 91.071

alignment_block:
TGFB3P x A48571
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Align seg 1/1 to: A48571 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 GCTTTGGATGCGGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpValh 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 ACGAACCCAAAGGTACAAATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 CTCCGCGATGTCAGACACAAACCCAGCAGCGTGTGGGACTGTACAAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TCTGAACCCCTGAACATCTGCCTCGCCTTGTGGTGGCCCGAGACCTGG 250
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 AGCCCCGTGACCATCTGCTATGTTGGAGGAGCCCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 CTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: gb_pat1:A23759

seq_documentation_block:
LOCUS A23759 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3(44/45)beta2 hybrid coding region.
ACCESSION A23759
VERSION A23759.1 GI:825593
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 9 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
source
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0
Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x A23759
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Align seg 1/1 to: A23759 from: 1 to: 336

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTCTGTCTGGAGCATGCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
151 TTATGGAGTTCAGACACTCAGCACAGCAGGTCCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTATGCTGGAACCAACCCCAAGATTGATAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGCTTTGCAATGTCAGC 336
|||||
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seq_name: gb_pat1:A48559

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seq_documentation_block:
LOCUS A48559 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603432.
ACCESSION A48559
VERSION A48559.1 GI:2302329
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL PROTEI
PATENT: WO 9603432-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
FEATURES
Location/Qualifiers
1..336
/organism="unidentified"
/db_xref="taxon:32644"
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
mat_peptide
1..132
CDS
1..336
/translation="protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HYBRID TGF-BETA3-2"
/protein_id="CAA03118.1"
/db_xref="GI:2302330"
/translacion="ALDNYCFRNLNENCCVRPLYIDFRODLGKWKVHEPKGYANFC
AGACPYLWSSDTQHSRVLSTYNINPEASPCCVSQDLEPLTILYIGKTPKIEQLS
NMIVSKSCS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN
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alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0

Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x A48559

Align seg 1/1 to: A48559 from: 1 to: 336

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTCTGCTGCTGCTGCTGCTGCTGCTG 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
151 TTATGGAGTTCAGACACTCAGCACAGCAGGTCCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTATGCTGGAACCAACCCCAAGATTGATAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGCTTTGCAATGTCAGC 336
|||||
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seq_name: gb_pat1:A48573

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seq_documentation_block:
LOCUS A48573 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603433.
ACCESSION A48573
VERSION A48573.1 GI:2302343
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL PATENT: WO 9603433-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
FEATURES
Location/Qualifiers
1..336
/organism="unidentified"
/db_xref="taxon:32644"
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
mat_peptide
1..132
CDS
1..336
/translation="protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HYBRID TGF-BETA3-2"
/protein_id="CAA03125.1"
/db_xref="GI:2302344"
/translacion="ALDNYCFRNLNENCCVRPLYIDFRODLGKWKVHEPKGYANFC
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NMIVSKSCS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN
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alignment_scores:
  Quality: 577.00      Length: 112
  Ratio: 5.393        Gaps: 0
  Percent Similarity: 95.536      Percent Identity: 88.393

alignment_block:
  TGFB3P x A48573      ..

Align seg 1/1 to: A48573 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAACTATTGCTTTCAGCTCCACGGAGAAGAACTGCTCGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCCCTCTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCAATGCAACTTCTGCTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyTrpLysTrpValH 67
|||||
151 TTATGGAGTTCAGACACTCAGCACAGGCTCCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGACAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCNAATGCAGC 336

seq_name: gb_pat1:A23754

seq_documentation_block:
LOCUS      A23754      336 bp      mRNA      PAT      25-JAN-1995
DEFINITION TGF-beta1(44/45)beta2 hybrid coding region.
ACCESSION  A23754
VERSION    A23754.1 GI:825588
KEYWORDS   CIBA-GEIGY AG
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 336)
AUTHORS   McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE     Novel hybrid transforming growth factors
JOURNAL   Patent: EP 0542679-A 4 19-MAY-1993;
          CIBA-GEIGY AG
FEATURES   Location/Qualifiers
            source
              1..336
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT 90 a 92 c 72 g 82 t
ORIGIN

alignment_scores:
  Quality: 539.00      Length: 112
  Ratio: 5.183        Gaps: 0
  Percent Similarity: 92.857      Percent Identity: 81.250

alignment_block:
  TGFB3P x A23754      ..

Align seg 1/1 to: A23754 from: 1 to: 336
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAACTATTGCTTTCAGCTCCACGGAGAAGAACTGCTCGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCCCTCTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCAATGCAACTTCTGCTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyTrpLysTrpValH 67
|||||
151 TTATGGAGTTCAGACACTCAGCACAGGCTCCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGACAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCNAATGCAGC 336

seq_name: gb_pat1:A23758

seq_documentation_block:
LOCUS      A23758      336 bp      mRNA      PAT      25-JAN-1995
DEFINITION TGF-beta3(44/45)beta1 hybrid coding region.
ACCESSION  A23758
VERSION    A23758.1 GI:825592
KEYWORDS   CIBA-GEIGY AG
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 336)
AUTHORS   McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE     Novel hybrid transforming growth factors
JOURNAL   Patent: EP 0542679-A 8 19-MAY-1993;
          CIBA-GEIGY AG
FEATURES   Location/Qualifiers
            source
              1..336
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT 63 a 109 c 98 g 56 t
ORIGIN

alignment_scores:
  Quality: 538.00      Length: 112
  Ratio: 5.327        Gaps: 0
  Percent Similarity: 90.179      Percent Identity: 83.929

alignment_block:
  TGFB3P x A23758      ..

Align seg 1/1 to: A23758 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTG 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCCCTCTACATTGACTTCCGACAGGATCTGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
```

```
|||||
101 ATGAACCTAAGGCTACTATGCCAAGCTTCTGCGCTCGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
:: ||| |||| ::||| ::||| ::||| ::||| ::|||
151 ATTTGGAGCGCTGGACACGACGACAGCAAGGCTCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| ||||| ::||| ::||| ::||| ::||| ::|||
201 GCATAACCCGGGCGCTCGCGCGCGCGTCTGCTGCGCGCAGCGCTGG 250
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ::||| ::||| ::||| ::||| ::|||
251 AGCGGTGCCCATCGGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ::||| ::||| ::||| ::||| ::|||
301 CTGTCCAACATGATGCGCTGCGCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A18279
seq_documentation_block:
LOCUS A18279 339 bp mRNA PAT 17-MAY-1994
DEFINITION H.sapiens TGF-beta 2 peptide seq ID No:2.
ACCESSION A18279
VERSION A18279.1 GI:513239
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 3 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
Location/Qualifiers
source
1..339
/organism="synthetic construct"
/db_xref="taxon:32630"
CDS
1..339
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translation"
/codon_start=1
/transl_table=11
/product="TGF-beta 2"
/protein_id="CAA01386.1"
/db_xref="GI:4529904"
/translation="ALDAAYCFRNVDNCCLRLPLYIDPKRLDGLGWKWIHEPKRYNANFC
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NMIVKSKCS"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
..
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x A18279 ..
Align seg 1/1 to: A18279 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 100
..
Align seg 1/1 to: A18279 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 100
..
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||| ||||| ::||| ::||| ::||| ::||| ::|||
101 ACGAACCCAAAGGGTACAAATGCCAAGCTTCTGCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| ||||| ||||| ||||| ::||| ::||| ::||| ::|||
151 TTATGGAGTTCAGACACTCAGCACAGCAGGGTCTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| ||||| ::||| ::||| ::||| ::||| ::|||
201 CATAAATCCAGAAGCATCTGCTTCTCTCTGCTGCTGCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ::||| ::||| ::||| ::||| ::|||
251 AACCTCTAAACATTCCTACTACTACATTGGCAAAACACCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ::||| ::||| ::||| ::||| ::|||
301 CTTTCTAATATGATTGTTAAAGTCTTGCAAAATGCAGC 336
seq_name: gb_pat1:A23752
seq_documentation_block:
LOCUS A23752 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2 coding region.
ACCESSION A23752
VERSION A23752.1 GI:825586
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 339)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 2 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
Location/Qualifiers
source
1..339
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
..
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x A23752 ..
Align seg 1/1 to: A23752 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 100
..
Align seg 1/1 to: A23752 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 100
..
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201 CATAAATCCAGACATCTGCTTCTCTCTGCTGCGTGTCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTTAACCATCTCTACTACATTTGCCAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336

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seq_name: gb_pat1:A48551

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seq_documentation_block: 339 bp DNA PAT 07-MAR-1997
LOCUS A48551
DEFINITION Sequence 3 from Patent WO9603432.
ACCESSION A48551
VERSION A48551.1 GI:2302321
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL
COMMENT Patent: WO 9603432-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
FEATURES
location/Qualifiers
source
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/organism="unidentified"
/db_xref="taxon:32644"
CDS
1..336
/note="Protein sequence is in conflict with the conceptual
translation"
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/product="HUMAN TGF-BETA2"
/protein_id="CAA03114.1"
/db_xref="GI:2302322"
/translation="ALDAAYCFRNVDNCCLRPXYIDFKRDLGWKWIHEPKGYANFNC
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BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN

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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
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Align seg 1/1 to: A48551 from: 1 to: 339

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCTTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACGTCCACTTTACATTGATTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCAAGGGTACAAATGCCAACCTCTGCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACACTCAGCAGCAGGAGGTCCTGAGCTTATATATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

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1:::|||||
201 CATAAATCCAGACATCTGCTTCTCTCTGCTGCGTGTCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTTAACCATCTCTACTACATTTGCCAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336

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seq_name: gb_pat1:A48565

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seq_documentation_block:
LOCUS A48565 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9603433.
ACCESSION A48565
VERSION A48565.1 GI:2302335
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL
COMMENT Patent: WO 9603433-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
FEATURES
location/Qualifiers
source
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/db_xref="taxon:32644"
CDS
1..336
/note="Protein sequence is in conflict with the conceptual
translation"
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/db_xref="GI:2302336"
/translation="ALDAAYCFRNVDNCCLRPXYIDFKRDLGWKWIHEPKGYANFNC
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BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN

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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
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Align seg 1/1 to: A48565 from: 1 to: 339

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCTTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACGTCCACTTTACATTGATTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCAAGGGTACAAATGCCAACCTCTGCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACACTCAGCAGCAGGAGGTCCTGAGCTTATATATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

```



```
101 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGCTTCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336
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seq_name: gb_pat1:AR036687

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seq_documentation_block:
LOCUS AR036687 339 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 31 from patent US 5800811.
ACCESSION AR036687
VERSION AR036687.1 GI:5954543
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE Artificial skin prepared from collagen matrix containing
transforming growth factor-.beta. having a collagen binding site
JOURNAL Patent: US 5800811-A 31 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..339
/organism="unknown"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
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Align seg 1/1 to: AR036687 from: 1 to: 339

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1 GCCTTGATCGCGCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCC 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTTACATTGATTCAAGAGGGATCTAGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACACTCAGCACAGCAGGGTCTGTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336
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seq_name: gb_pat2:I56855

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seq_documentation_block:
LOCUS I56855 339 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 2 from patent US 5650494.
ACCESSION I56855
VERSION I56855.1 GI:2477268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for refolding recombinantly produced TGF-.beta.-like
proteins
JOURNAL Patent: US 5650494-A 2 22-JUL-1997;
FEATURES Location/Qualifiers
source 1..339
/organism="unknown"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x I56855 ..

Align seg 1/1 to: I56855 from: 1 to: 339

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCCTTGATCGCGCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCC 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTTACATTGATTCAAGAGGGATCTAGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACACTCAGCACAGCAGGGTCTGTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336
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seq_name: gb_pat1:A05306

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seq_documentation_block:
LOCUS A05306 342 bp DNA PAT 07-MAY-1993
DEFINITION Complete nucleotide sequence of mature human G-Tsf.
ACCESSION A05306
VERSION A05306.1 GI:345049
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 342)
AUTHORS
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JOURNAL Patent: WO 8803807-A 10 02-JUN-1988;
FEATURES Location/Qualifiers
source 1..342
/organism="synthetic construct"
/db_xref="taxon:32630"
gene 1..342 /gene="G-Tsf"
CDS <1..342 /gene="G-Tsf"
/codon_start=1
/transl_table=11
/product="glioblastoma-derived T-cell suppressor factor"
/protein_id="CAA00445.1"
/db_xref="GI:345050"
/translation="RALDAAYCFRNVDNCCLLRPLYIDFKRDIGKWIHEPKGYNNAF
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SNMIVSKCS"

BASE COUNT 98 a 78 c 71 g 95 t
ORIGIN

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x A05306 ..

Align seg 1/1 to: A05306 from: 1 to: 342

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1 AlaLeuAspThrAsnTyrcyspheArgasnLeuGluGlnAsnCysCysVa 17
|||||::: |||||::: |||||::: |||||::: |||||:::
4 GCTTTGGATCGCGCTATTGCTTTAGAAATCTGCAGGATAATTGCTGCCT 53

17 lArgProLeuTyrlleaspPheArGlnAspLeuGlyTrpLysTrpValH 34
:|||||::: |||||::: |||||::: |||||::: |||||:::
54 ACGTCCACTTTACATTGATTTCAGAGAGGATCTAGGGTGAATGGATAC 103

34 lsGluProLysGlyTyrrAlaasnPheCysSerGlyProCysProTyr 50
|||||::: |||||::: |||||::: |||||::: |||||:::
104 ACGAACCCAAAGGTGACAATGCCAACTTCTGTGTGGAGCATGCCCGPAT 153

51 LeuArgSerAlaAspThrThrsHisSerThrValLeuGlyLeuTyraSnTh 67
|||||::: |||||::: |||||::: |||||::: |||||:::
154 TTATGGAGTTTCAGACACTCACCAAGAGGCTCTGAGCTTATATAATAC 203

67 rLeuAsnProGluLaSerAlaSerProCysCysValProGlnAspLeuG 84
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
204 CATAAATCCAGAAGCATCTGCTTCTCTCTGCTGCGTGCCCAAGATTTAG 253

84 luProLeuThrIleLeuTyrrValGlyArgThrProLysValGlucIn 100
|||||::: |||||::: |||||::: |||||::: |||||:::
254 AACCTCTAACCAATTCTCTACATACATTGGCAAAACACCACCAAGATTGAACAG 303

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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304 CTTTCTATATGATTGTAAAGTCTTGCAATGCAGC 339
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seq_name: gb_pat1:A11707

seq_documentation_block:

	LOCUS	A11707	342 bp	DNA	PAT	26-NOV-1993
DEFINITION	mature H.sapiens G-Tsf gene.					
ACCESSION	A11707					
VERSION	A11707.1	GI:490099				
KEYWORDS	SOURCE	human.				
ORGANISM	Homo sapiens					
Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;	
Mammalia;	Eutheria;	Primates;	Catarrhini;	Hominidae;	Homo.	
REFERENCE	1 (bases 1 to 342)					
AUTHORS	De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.					


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1406 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1441
seq_name: gb_pat1:A05308

seq_documentation_block:
LOCUS A05308 1695 bp DNA PAT 07-MAY-1993
DEFINITION Nucleotide sequence for the human G-Tsf precursor.
ACCESSION A05308
VERSION A05308.1 GI:345051
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
sig_peptide
CDS
gene
mat_peptide
BASE COUNT 523 a 386 c 354 g 432 t
ORIGIN
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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x A05308
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Align seg 1/1 to: A05308 from: 1 to: 1695

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1088 GCTTTGGATCGGCCTATTGCTTTAGAAATGTCAGGATAATGCGCT 1137

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
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1138 ACGTCCACTTTACATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1188 ACGAACCCAAAGGTACAAATGCCAACTCTGCTGGAGCATGCCGTAT 1237

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1138 ACGTCCACTTTACATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1188 ACGAACCCAAAGGTACAAATGCCAACTCTGCTGGAGCATGCCGTAT 1237

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1238 TTATGGAGTTTACAGACTCAGCAGCAGCGGTCCTGAGCTTATATATAC 1287

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1288 CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 1337

84 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
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1138 ACGTCCACTTTACATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1238 TTATGGAGTTTACAGACTCAGCAGCAGCGGTCCTGAGCTTATATATAC 1287

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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1288 CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 1337

84 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 100
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1338 AACCTTAACCATCTCTACTACATGGCAAAACACCAAGATTGAACAG 1387

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1388 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1423

seq_name: gb_pat1:A11709

seq_documentation_block:
LOCUS A11709 1695 bp DNA PAT 10-DEC-1993
DEFINITION H sapiens G-Tsf gene precursor.
ACCESSION A11709
VERSION A11709.1 GI:490100
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
TITLE Production and use of a novel T-cell suppressor factor
JOURNAL Patent: EP 0268561-A 8 25-MAY-1988;
SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
Verwaltungsgesellschaft m.B.H
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 523 a 386 c 354 g 432 t
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Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x A11709
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Align seg 1/1 to: A11709 from: 1 to: 1695

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1088 GCTTTGGATCGGCCTATTGCTTTAGAAATGTCAGGATAATGCGCT 1137

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
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1138 ACGTCCACTTTACATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1188 ACGAACCCAAAGGTACAAATGCCAACTCTGCTGGAGCATGCCGTAT 1237

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1238 TTATGGAGTTTACAGACTCAGCAGCAGCGGTCCTGAGCTTATATATAC 1287

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1288 CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 1337

84 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1338 AACCTTAACCATCTCTACTACATGGCAAAACACCAAGATTGAACAG 1387

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1388 CTTCTAATGATGTTAAAGTCTTCAAAATGCAGC 1423
seq_name: gb_pr9:HSRTSF

seq_documentation_block:
LOCUS      HSGTSF      1695 bp      mRNA      PRI      27-MAR-1995
DEFINITION Human mRNA for glioblastoma-derived T-cell suppressor factor G-Tsf
            (transforming growth factor-beta2, tgfb-beta2).
ACCESSION  Y00083
VERSION    Y00083.1 GI:31959
KEYWORDS   T-cell suppressor factor; transforming growth factor-beta2.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1695)
AUTHORS    Hofer, E.
TITLE      Direct Submission
JOURNAL    Submitted (02-NOV-1987) Hofer, E., Sandoz AG, Department for
            Biotechnology, Preclinical Research, Building 386/328, Sandoz AG,
            CH-4002 Basel.
REFERENCE  2 (bases 1 to 1695)
            de Martin, R., Haendler, B., Hofer-Warbinek, R., Gaugitsch, H.,
            Wrann, M., Schlusener, H., Seifert, J.M., Bodmer, S., Fontana, A. and
            Hofer, E.
            Complementary DNA for human glioblastoma-derived T cell suppressor
            factor, a novel member of the transforming growth factor-beta gene
            family.
JOURNAL    EMBO J. 6 (12), 3673-3677 (1987)
MEDLINE    8811555
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                                /cell_line="glioblastoma 308"
                                /clone_lib="lambda gt10"
                                /clone="lambda SUP25, lambda SUP40, lambda SUP42"
                                182..1426
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                                VPEQRIELYQLKSKDLSPTQRYIDSKVVRABGEWLSDFTVDADVHFWLHDKRNL
                                GFKLSLHCPCCTFVPSNNYIIPNKESELEAFAGIDGTSTYSGDQKTIKSTRKNSG
                                KTHPLLMLPLSYLESQOTNRKRKRALDAAYCFRNVDNCLRLPYIDFKRDLGKW
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                                1088..1423
                                /product="put. mature G-Tsf"
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            misc_feature      523 a 386 c 354 g 432 t
            BASE COUNT      523 a 386 c 354 g 432 t
            ORIGIN

alignment_scores:
            Quality: 535.00      Length: 112
            Ratio: 5.095      Gaps: 0
            Percent Similarity: 93.750      Percent Identity: 79.464

alignment_block:
            TGFB3P x HSGTSF
            Align seg 1/1 to: HSGTSF from: 1 to: 1695

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1138 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187

34 iSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1188 ACGAACCAAGGGTACAAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 1237

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1238 TTATGGAGTTCAGACACTCAGCAGCAGGCTCTGAGCTTATATAATAC 1287

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1288 CATAAATCCAGAACATCTGCTCTCTGCTGCTGCTGCCCAAGATTAG 1337

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1338 AACCTCTAACCAATCTCTACTACATTGGCAAAACACCAAGATTGAACAG 1387

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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1388 CTTTCTAATATGATGTAAAGTCTTGCAAAATGCAGC 1423

seq_name: gb_pat2:108281
seq_documentation_block:
LOCUS      I08281      2569 bp      PAT      02-DEC-1994
DEFINITION Sequence 3 from patent EP 0376785.
ACCESSION  I08281
VERSION    I08281.1 GI:589009
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2569)
            Purchio, A.F., Madisen, L. and Webb, N.
            Cloning and expression of transforming growth factor beta 2
            Patent: EP 0376785-A2 3 04-JUL-1990;
            Location/Qualifiers
            source            1..2569
                                /organism="unknown"
            BASE COUNT      772 a 599 c 512 g 686 t
            ORIGIN

alignment_scores:
            Quality: 535.00      Length: 112
            Ratio: 5.095      Gaps: 0
            Percent Similarity: 93.750      Percent Identity: 79.464

alignment_block:
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            Align seg 1/1 to: I08281 from: 1 to: 2569

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1457 GCTTTGGATGGCGCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 1506

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1507 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1556

34 iSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1557 ACGAACCAAGGGTACAAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 1606

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1607 TTATGGAGTTCAGACACTCAGCAGCAGGCTCTGAGCTTATATAATAC 1656
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BASE COUNT      824 a      684 c      604 g      768 t
ORIGIN

alignment_scores:
    Quality: 530.00      Length: 112
    Ratio: 5.048      Gaps: 0
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alignment_block:
TGFBP3P x AF153012      ..

Align seg 1/1 to: AF153012 from: 1 to: 2880

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||::: |||||||::: |||||||::: |||||||::: |||||||:::
1298 GCTTTGGATGCCGCTATTGCTTTAGGAATGTCAGGATAATTGCTGCCT 1347

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||::: |||||||::: |||||||::: |||||||::: |||||||:::
1348 TCGCCCTCTTACATTGATTTTAAAGAGGATCTTGGATGGAATGCATCC 1397

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||::: |||||||::: |||||||::: |||||||::: |||||||:::
1398 ATGAACCCAAAGGATACAAATGCTAACTCTGCTGCTGGGCGATGCCCTTAT 1447

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||::: |||||||::: |||||||::: |||||||::: |||||||:::
1448 CTGTGGATTGACAGACACACACACCAAGTCTTCAGCGCTGTACAACAC 1497

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1498 CATAAACCCGAAGCTTCTGCTTCCCTTCCTGCTGTGTGCCAGGATCTGG 1547

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1548 AACCACTGACCATCTCTACTACATTTGGCAATACGCCCAAGATCGAACAG 1597

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_name: gb_rol:MMTGFb2

seq_documentation_block:
LOCUS      MMTGFb2      4267 bp      mRNA      ROD      14
DEFINITION      Mouse mRNA for transforming growth factor-beta2.
ACCESSION      X57413
VERSION      X57413.1 GI:54772
KEYWORDS      cell proliferation; transforming growth factor-beta2
SOURCE      mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; H
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
REFERENCE      Miller,D.A., Lee,A., Pelton,R.W., Chen,E.Y., Moses,H
AUTHORS      Derynck,R.
TITLE      Murine transforming growth factor-beta 2 cDNA sequen
JOURNAL      expression in adult tissues and embryos
MEDLINE      Mol. Endocrinol. 3 (7), 1108-1114 (1989)
FEATURES      90014832
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              /cell_type="carcinoma"
              /cell_line="PCC3"
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/gene="TGF-beta2"
/product="transforming growth factor-beta2"
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BASE COUNT 1139 a 1036 c 989 g 1103 t
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alignment_scores:
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  Ratio: 5.048        Gaps: 0
  Percent Similarity: 93.750  Percent Identity: 78.571
alignment_block:
  TGFb3P x MMTGFB2 ..
  Align seg 1/1 to: MMTGFB2 from: 1 to: 4267
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2124 GCTTTGGATGCGCTACTGCTTTAGAAATGTCAGGATAATTGCTGCCT 2173
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2174 TCGCCCTCTTACATGATTTAAGAGGATCTTGATGGAATGGATGCC 2223
34 lsgLuproLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2224 ATGAACCCAAAGGGTACATGCTTAACCTTCTGTGCTGGGCATGCCATAT 2273
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2274 CTATGGAGTTCAGACACTCAACACACACAAAGCTCAGCCTGTACAAAC 2323
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2324 CATAAATCCGAAGCTTCGCTTCCTCCCTTGTGTGTCCTCCAGGATCTGG 2373
84 lUpProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
2374 AACCACTGACCACTCTATTACATTGGAATACGCCCAAGATCGAACAG 2423
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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2424 CTTTCCAATATGATGTCAGTCTTGAATGCAAGC 2459
seq_name: gb_ro2:RNO132718
seq_documentation_block:
LOCUS RNO132718 1274 bp mRNA ROD 21-OCT-2000
DEFINITION Rattus norvegicus mRNA for TGF-beta2 protein.
ACCESSION AJ132718
VERSION AJ132718.1 GI:4753895
KEYWORDS tgf-beta2 gene; TGF-beta2 protein.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1274)
AUTHORS Konrad,L., Albrecht,M., Renneberg,H. and Aumuller,G.
```

```
TITLE Transforming growth factor-beta2 mediates mesenchymal-epithelial
interactions of testicular somatic cells
JOURNAL Endocrinology 141 (10), 3679-3686 (2000)
MEDLINE 20466150
REFERENCE 2 (bases 1 to 1274)
AUTHORS Konrad,L.
DIRECT SUBMISSION
TITLE Submitted (02-FEB-1999) Konrad L., Anatomy and Cell Biology,
JOURNAL Philipps University, Robert-Koch-Str. 6, 35033 Marburg, GERMANY
FEATURES
  Location/Qualifiers
1..1274
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/strain="Wistar"
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/sex="male"
/dev_stage="19-days-old"
/cell_type="peritubular myoid primary cells"
16..1260
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16..1260
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ORIGIN
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  Ratio: 5.029        Gaps: 0
  Percent Similarity: 93.750  Percent Identity: 78.571
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922 GCTTTGGATGCGCTACTGCTTTAGGAATGTCAGGATAATTGCTGCCT 971
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
972 TCGCCCTCTTACATGATTTAAGAGGATCTTGATGGAATGGATGCC 1021
34 lsgLuproLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1022 ATGAACCCAAAGGGTACAAATGCTAACCTTCTGTGCTGGGATGCCCTTAT 1071
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1072 CTGTGGAGTTCAGACACACACACCAAGTCTCTGAGCTGTACACAC 1121
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1122 CATAAACCCCGAAGCTTCTGCTTCCCTTGTGTGTCCTCCAGGATCTGG 1171
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1172 AACCACTGACCACTCTATTACATTGGAATACGCCCAAGATCGAACAA 1221
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1222 CTTTCCAAATGATGTCGAAGTCTGTGAATGCAGC 1257

seq_name: gb_om:SSTGFB2

seq_documentation_block:

LOCUS SSTGFB2 477 bp mRNA MAM 30-JUN-1993
DEFINITION S. scrofa mRNA for transforming growth factor beta 2.
ACCESSION X70142 S48994
VERSION X70142.1 GI:312949
KEYWORDS TGF-beta 2; transforming growth factor-beta2.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Mulheron,G.W., Mulheron,J.G., Danielpour,D. and Schomberg,D.W.
TITLE porcine granulosa cells do not express transforming growth
factor-beta 2 (TGF-beta 2) messenger ribonucleic acid: molecular
basis for their inability to produce TGF-beta activity comparable
to that of rat granulosa cells
JOURNAL Endocrinology 131 (6), 2609-2614 (1992)
MEDLINE 93076683
FEATURES Location/Qualifiers
source 1..477
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primer_bind 1..20
primer_bind 458..477
BASE COUNT 129 a 124 c 108 g 116 t
ORIGIN

alignment_scores:
Quality: 523.00 Length: 112
Ratio: 5.078 Gaps: 0
Percent Similarity: 91.964 Percent Identity: 77.679

alignment_block:

TGFB3P x SSTGFB2 ..

Align seg 1/1 to: SSTGFB2 from: 1 to: 477

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142 GCTTTGGATGCAGCCATTGCTTTAGAAATGTGCAGGATAATGCTGCCT 191
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValH 34
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192 GCGTCACATTACATTGATTCAAGAGGATCTGGGTGGAATGGATAC 241
34 isGluProLysGlyTyrValAlaAsnPheCysSerGlyProCysProTyr 50
|||||
242 ATGAGCCTTAAGGATACATGCCAATCTGTCGCGGGGCTGCCGCTAC 291
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnH 67
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292 CTGTGGAGCTTGGCACCAGCATAGCAGGGTCTCAGCTTATATAACAC 341
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGluAspLeuG 84
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342 CATAAACCCAGAGCTTCGCTTCCCTTGTCTCCGCTGCCAGGATTAG 391
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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392 ACCCGCTCACTCTCTACTACTACATCGGCAAAACGCCCAAGATCGAGCAG 441
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_name: gb_ov:XLTGFB2

seq_documentation_block:

LOCUS XLTGFB2 2724 bp mRNA VRT 08-NOV-1993
DEFINITION Xenopus laevis TGF-beta2 mRNA for transforming growth factor-beta2.
ACCESSION X51817
VERSION X51817.1 GI:414789
KEYWORDS growth factor; transforming growth factor.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2724)
AUTHORS Rebbert,M.L.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1990) Rebbert M.L., Laboratory of Molecular
Genetics, National Institute of Child, Health and Human
Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A
REMARK sequence revised by [3]
REFERENCE 2 (bases 1 to 2724)
AUTHORS Rebbert,M.L., Bhattia-Dey,N. and Dawid,I.B.
TITLE The sequence of TGF-beta 2 from Xenopus laevis
JOURNAL Nucleic Acids Res. 18 (8), 2185 (1990)
MEDLINE 90245678
REFERENCE 3 (bases 1 to 2724)
AUTHORS Rebbert,M.L.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1993) Rebbert M.L., Laboratory of Molecular
Genetics, National Institute of Child, Health and Human
Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A
COMMENT On Nov 9, 1993 this sequence version replaced gi:651136.
Data kindly reviewed (16-AUG-1990) by Rebbert .M.L.
FEATURES Location/Qualifiers
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/db_xref="SWISS-PROT:P17247"
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mat_peptide 982..1317

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  Percent Similarity: 91.964   Percent Identity: 76.786

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17 largProLeuTyriIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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34 iScLuPrOlySGLyTYrTYrAlaAsnPheCysSerGlyProCysProTYr 50
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51 LeuArgSerAlaAspThrrHisSerThrValLeuGlyLeuTyrrAsnTh 67
||| |||||:::|||||:::|||||:::|||||:::|||||:::
1132 CTGTGGAGCTCAGATACTAACATACCCGGGTGCTAAGCCTGTACAACAC 1181

67 rIeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
:: |||||:::|||||:::|||||:::|||||:::|||||:::
1182 CATTAATCGGAAGCATCTGCCTCCCCTGTTGCGGTCTCAAGATTTAG 1231

84 luProLeuThrlleLeuTyrrTYrValGlyArgThrProLysValGluGln 100
:: |||||:::|||||:::|||||:::|||||:::|||||:::
1232 ACTCCTTGACCATCTTGTTACTACATCGGAATAAGCCAAAATTGAACAG 1281

101 LeuSerAsnMetValVallYssSerCysLysCysSer 112
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1282 CTTCAAATATGATTGTAANAATCATGCAAGTCGACG 1317

seq_name: gb_pat2.I08275

seq_documentation_block:
LOCUS I08275 1561 bp PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent EP 0374044.
ACCESSION I08275
VERSION I08275.1 GI:589015
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Purchio,A.F. and Madisen,L.
TITLE TGF - beta 1 / beta 2 : a novel chimeric transforming growth factor-beta
JOURNAL Patent: EP 0374044-A2 3 20-JUN-1990;
FEATURES Location/Qualifiers
source 1..1561
/organism="unknown"
BASE COUNT 304 a 544 c 442 g 271 t
ORIGIN

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  Quality: 503.00          Length: 112
  Ratio: 5.030            Gaps: 0
  Percent Similarity: 89.286   Percent Identity: 75.893

alignment_block:
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Ratio: 5.133          Caps: 0
Percent Similarity: 87.500    Percent Identity: 77.679

alignment_block:
TGFB3p x MUSTGFRNA ..

Align seg 1/1 to: MUSTGFRNA from: 1 to: 1579

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1237 CGGCAGCTGTACATTGACTTTTAGGAAGACCTGGGTGGAAGTGGATCC 1286

34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1287 ACGAGCCCAAGGGCTACATGCCAACTTCTGTCTGGGACCTGCCCTAT 1336

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnth 67
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1337 ATTGGAGCCTGGACACACATACAGCAAGGTCCTGGCCCTCTACAAACA 1386

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1387 ACACAACCCGGGCGCTTCGGCGCTCACCGTGTGCGTGGCGCAGGCTTGG 1436

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1437 AGCCACTGCCCATCGTCTACTACGTGGGTGCGCAAGTGGAGCAG 1486

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

1487 TTGTCCAAACATGATTGTGCGCTCCTCGCAAGTGCAGC 1522

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seq_name: qb ro2:RNTGFB1

seq_documentation_block:					
LOCUS	INTGFB1	1585 bp	mRNA	ROD	23-MAR-1995
DEFINITION	Rat mRNA for transforming growth factor-beta 1.				
ACCESSION	X52498				
VERSION	X52498.1	GI:57341			
KEYWORDS	growth factor; TGF-beta 1; transforming growth factor-beta 1.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 1585)				
AUTHORS	Su Wen,Q.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-MAR-1990) Su Wen Q., National Cancer Institute NIH, Bldg 41 Room C629, Laboratory of Chemoprevention, NCI Bethesda MD 20892, U S A				
REFERENCE	2 (bases 1 to 1585)				
AUTHORS	Qian,S.W., Kondatiah,P., Roberts,A.B. and Sporn,M.B.				
TITLE	cDNA cloning by PCR of rat transforming growth factor beta-1				
JOURNAL	Nucleic Acids Res. 18 (10), 3059 (1990)				
MEDLINE	90272425				

LINE	00272423	Location/Qualifiers
JRES		
source	1. .1585	

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  Ratio: 5.133        Gaps: 0
  Percent Similarity: 87.500    Percent Identity: 77.679

alignment_block:
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Align seq 1/1 to: RNTGFB1 from: 1 to: 1585

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17 lAqgProLeuTyrIleAsppheAArgGlnAspLeuGlyTrpLvsTrpvalH 34

1297 ACGGCAGCTGTACATTGACTTTAGGAAGGACCTGGGTTGGAGTGGATCC 1346

34 isGluProIvsGlvTyrTyrAlaAsnpheCvssSergIvProCvssProTyr 50

1347 ACGAGCCCAAGGGCTACCATGCCAATTCTGTCTGGGGCCCTGCCCTAC 1396

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTrpAsnTh 67

1397 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGGCCCTCTACAACCA 1446

67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84

1447 ACACAACCCGGGGTGGTTCCGGCATCACCGTGGTGGCGGCGAGGGCTTGG 1496

84 **l**uProLeuThrIleLeuTyrT^rValGlyArgT^hrProLysValGluGln 100

1497 AGCCACTGCCCATCGTCTACTACGTGGGTCCGAAGCCCAAGGTGGAGCAG 1546

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name: qb rol:MMU009862

documentation block:

US NM0009862 2094 bp MRNA for transforming growth factor-beta

SESSION AJ009862
SESSION AJ009862.1 GT:3688423

KEY WORDS: TGF beta 1 gene; transforming growth factor-beta 1; house mouse

ORGANISM MUS MUSCULUS
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: P

REFERENCE 1 (bases 1 to 2094)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

AUTHORS
 Poirot, L.
 Direct Submission

JOURNAL Submitted (07-AUG-1998) Poirot L., Department of Immunology, Institut Pasteur, 28 rue du Dr Roux, 75013 Paris, FRANCE
T C R M C BP 163 67404 Illkirch FRANCE

REFERENCE 2 (bases 1 to 2094)

AUTHORS Poirrot,L., Benoist,C. and Mathis,D.
TITLE Transforming growth factor-beta 1 sequence and expression: no
JOURNAL difference between NOD/Lt and C57Bl/6 mouse strains
FEATURES Unpublished
source Location/Qualifiers
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/organism="Mus musculus"
/strain="NOD/Lt"
/strain="C57Bl/6"
/db_xref="taxon:10090"
/tissue_type="spleen"
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KSSVEQHVLYQKYSNNRWYLGKRLTPTDTPWLSFDVTGVVROWLNOGDGIGER
FSAHCSQDSKDKLHVEINGISPKRGLDGTIDMNRPLLLMATPLERAQHLHSSRH
BRALDYNCFSTENKCCVRQLYIDFRKDLGKWKIHEPKGTHANFCLGCPCTIWSLDT
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/product="transforming growth factor-beta 1"
BASE COUNT 421 a 734 c 574 g 365 t
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Quality: 503.00 Length: 112
Ratio: 5.133 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 77.679
alignment_block:
TGFB3P x MMU009862 ..
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1702 GCCTGGATACCAACTATGCTTCAGCTCCACAGAGAAGAACTGCTGT 1751
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1752 GCGGCAGCTGTACATTGACTTTAGGAGGACCTTGGTGGAGTGGATCC 1801
34 lGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
1802 ACAGCCCAAGGCTACCACTGACCACTTCTGCTGGGACCTGCCCTAT 1851
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1852 ATTTGGAGCTGGACACAGTACAGAGGCTCTTGCCTCTACAAACCA 1901
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1902 ACACAACCCGGGCGCTCGCGGTACCGTGTGCTGCGCGAGGCTTTGG 1951
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluIn 100
1952 AGCCATGCCCATGCTGTACTACGTGGGTGCGAAGCCCAAGGTGGAGC 2001
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
2002 TTGTCAACATGATTGTGGCTCTCTCAAGTGCAGC 2037
seq_name: gb_om:OCAF000133

seq_documentation_block:
LOCUS OCAF000133 339 bp mRNA MAM 06-MAY-1997
DEFINITION Oryctolagus cuniculus transforming growth factor beta-1 mRNA,
partial cds.
ACCESSION AF000133
VERSION AF000133.1 GI:2072531
KEYWORDS rabbit.
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Rabbit transforming growth factor beta-1 active region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Ophthalmology, Med.Univ. S.C., 171 Ashley
Avenue, Charleston, SC 29464, USA
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9986"
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NMIVRSCKCS"
BASE COUNT 71 a 114 c 97 g 57 t
ORIGIN
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Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGFB3P x OCAF000133 ..
Align seg 1/1 to: OCAF000133 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCCTGGACACCAACTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTGGGTGGAGTGGATCC 100
34 lGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
101 ACAGCCCAAGGCTACCACTGACCACTTCTGCTGGGACCTGCCCTTAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 ATCTGGAGCTGGACACCCAGTACAGCAAGGCTCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 GCACAACCCGGGCGCTCGCGAGCGCGTGTGTGTGCGCACAGCGGTGG 250
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluIn 100
251 AGCCATGCCCATGCTGTACTACGTGGGTGCGAAGCCCAAGGTGGAGC 300
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301 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A18277

seq_documentation_block:
LOCUS   A18277             339 bp      mRNA           PAT       17-MAY-1994
DEFINITION   H.sapiens TGF-beta 1 gene seq ID No:1.
ACCESSION   A18277
VERSION     A18277.1   GI:513237
KEYWORDS    .
SOURCE      synthetic construct.
            artificial sequence.
ORGANISM    1 (bases 1 to 339)
REFERENCE   1 (bases 1 to 339)
AUTHORS    Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE      Process for the production of biologically active protein (e.g.
            TGF)
JOURNAL    Patent: EP 0433225-A 1 19-JUN-1991;
CIBA-GEIGY AG
FEATURES             Location/Qualifiers
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     CDS              1..339
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                     translation"
                     /codon_start=1
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                     /protein_id="CAA01385.1"
                     /db_xref="GI:4529903"
                     /translation="ALDNYCYFSSTERNKCCVRLQYIDFRKDLGKWKIHEPKGYHANFC
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                     NMIVRSCKCS"
BASE COUNT      66 a 114 c 100 g 59 t
ORIGIN
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alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCCTGGACACCAACTATTGCTTCAGCTCCACGAGAGAACTGCTCGGT 50
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCGAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaSerPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
151 ATTTGGAGCGCTGGACACGACGACGACGACGACGACGACGACGACGAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGGCGCTCGGCGCGCGCTGCTGCGCTGCGCGCGCGCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCGTGCCTCATCGTGTACTACGTGGGCGGCAAGCCCAAGGTGGAGCAG 300
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A48549

seq_documentation_block:
LOCUS   A48549             339 bp      DNA           PAT       07-MAR-1997
DEFINITION   Sequence 1 from Patent WO9603432.
ACCESSION   A48549
VERSION     A48549.1   GI:2302319

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seq_name: gb_pat1:A23751

seq_documentation_block:
LOCUS   A23751             339 bp      mRNA           PAT       25-JAN-1995
DEFINITION   TGF-beta1 coding region.
ACCESSION   A23751
VERSION     A23751.1   GI:825585
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 339)
AUTHORS    McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE      Novel hybrid transforming growth factors
JOURNAL    Patent: EP 0542679-A 1 19-MAY-1993;
CIBA-GEIGY AG
FEATURES             Location/Qualifiers
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    Ratio: 5.102        Gaps: 0
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alignment_block:
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCGAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaSerPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCGTGCCTCATCGTGTACTACGTGGGCGGCAAGCCCAAGGTGGAGCAG 300
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seq_documentation_block:
LOCUS   A48549             339 bp      DNA           PAT       07-MAR-1997
DEFINITION   Sequence 1 from Patent WO9603432.
ACCESSION   A48549
VERSION     A48549.1   GI:2302319

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KEYWORDS      unidentified.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 339)
AUTHORS       Cerletti,N.
TITLE        NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL       PROTEI
PATENT:       WO 9603432-A 1 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT       Other publication AU 3109595 960222.
FEATURES     Location/Qualifiers
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BASE COUNT   66 a 114 c 100 g 59 t
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51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCAATCTTCTGCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block: 339 bp DNA PAT 07-MAR-1997
LOCUS A48563
DEFINITION Sequence 1 from Patent WO9603433.
ACCESSION A48563

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VERSION      A48563.1 GI:2302333
KEYWORDS     unidentified.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Cerletti,N.
TITLE        NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL      PATENT: WO 9603433-A 1 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT      Other publication AU 3109695 960222.
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              NMIVRSCKCS"
BASE COUNT   66 a 114 c 100 g 59 t
ORIGIN

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  Ratio: 5.102        Gaps: 0
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alignment_block:
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Align seg 1/1 to: A48563 from: 1 to: 339

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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCAATCTTCTGCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
151 ATTTGGAGCTGGACACGAGTACAGCAAGTCTTGGCCCTGTACAACCA 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block: 339 bp DNA PAT 29-SEP-1999
LOCUS AR036686
DEFINITION Sequence 29 from patent US 5800811.
ACCESSION AR036686

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VERSION      AR036686.1  GI:5954542
KEYWORDS
SOURCE
ORGANISM      Unknown.
               Uncl.
REFERENCE     1 (bases 1 to 339)
AUTHORS      Hall, F.L., Nimmi, M.E., Tuan, T., Wu, L. and Cheung, D.T.
TITLE        Artificial skin prepared from collagen matrix containing
              transforming growth factor- $\beta$ . having a collagen binding site
JOURNAL      Patent: US 5800811-A 29 01-SEP-1998;
FEATURES
SOURCE       1..339
              Location/Qualifiers
BASE COUNT   66 a 113 c 100 g 60 t
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  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 76.786
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGCTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 ATTTGGAGCTGGACAGCAGTACAGCAAGGTCTGCGCTGTACAAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCCAACATGATCGTGGCTCTGCAAGTGCAGC 336
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seq_documentation_block:
LOCUS      I56854
DEFINITION Sequence 1 from patent US 5650494.
ACCESSION  I56854
VERSION     I56854.1  GI:2477267
KEYWORDS
SOURCE
ORGANISM      Unknown.
               Uncl.
REFERENCE     1 (bases 1 to 339)
AUTHORS      Cerletti, N., McMaster, G. Kent, Cox, D., Schmitz, A. and Meyhack, B.
TITLE        Process for refeeding recombinantly produced TGF- $\beta$ .-like
              proteins
JOURNAL      Patent: US 5650494-A 1 22-JUL-1997;
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ACCESSION  I56854
VERSION     I56854.1  GI:2477267
KEYWORDS
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ORGANISM      Unknown.
               Uncl.
REFERENCE     1 (bases 1 to 339)
AUTHORS      Cerletti, N., McMaster, G. Kent, Cox, D., Schmitz, A. and Meyhack, B.
TITLE        Process for refeeding recombinantly produced TGF- $\beta$ .-like
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JOURNAL      Patent: US 5650494-A 1 22-JUL-1997;
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ACCESSION  M38449  M55656
VERSION     M38449.1  GI:339557
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ACCESSION M36271
VERSION M36271.1 GI:163747
KEYWORDS transforming growth factor-beta 1.
SOURCE Bovine fibropapilloma, cDNA to mRNA, (library of Okayama and Berg).
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1117)
AUTHORS Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
and Baker, C.C.
TITLE Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-beta-1
JOURNAL Mol. Endocrinol. 1, 693-698 (1987)
MEDLINE 91042552
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DEFINITION O.aries mRNA for transforming growth factor-beta 1.
ACCESSION X76916
VERSION X76916.1 GI:496648
KEYWORDS TGF-beta 1; transforming growth factor-beta 1.
SOURCE sheep.
ORGANISM Ovis aries
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Woodall, C.J., McLaren, L.J. and Watt, N.J.
TITLE Sequence and chromosomal localisation of the gene encoding ovine
latent transforming growth factor-beta 1
JOURNAL Gene 150 (2), 371-373 (1994)
MEDLINE 95121932
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DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete cds.
ACCESSION  L34956
VERSION    L34956.1 GI:516071
KEYWORDS   homologue; transforming growth factor-beta 1.
SOURCE     Canis familiaris adult jugular vein endothelial cDNA to mRNA.
ORGANISM   Canis familiaris
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REFERENCE  1 (bases 1 to 1369)
AUTHORS   Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.
TITLE     Cloning of a canine cDNA homologous to human transforming growth
factor-beta 1 (TGFBetal)
JOURNAL    Unpublished (1994)
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REFERENCE
AUTHORS Sharples,K., Plozman,G.D., Rose,T.M., Twardzik,D.R. and
Purchio,A.F.
TITLE Cloning and sequence analysis of simian transforming growth
factor-beta cDNA
JOURNAL DNA 6, 239-244 (1987)
MEDLINE 87246074
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DEFINITION Porcine mRNA for transforming growth factor-beta (TFG) precursor.
ACCESSION Y00111
VERSION Y00111.1 GI:2129
KEYWORDS transforming growth factor-beta.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 1605)
AUTHORS Derynck,R. and Rhee,L.
TITLE Sequence of the porcine transforming growth factor-beta precursor
JOURNAL Nucleic Acids Res. 15 (7), 3187 (1987)
MEDLINE 87174844
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LOCUS E03028
DEFINITION DNA encoding human prepro TGF-beta1.
ACCESSION E03028
VERSION E03028.1 GI:2171250
KEYWORDS JP 1991180192-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ohashi,H., Ishii,Y., Miyata,Y., Miyazono,K., Miyagawa,K. and
Takaku,F.
PRODUCTION OF HUMAN PRO-TGF-BETAL BY GENETIC RECOMBINATION
Patent: JP 1991180192-A 1 06-AUG-1991;
KIRIN BREWERY CO LTD
OS Homo sapiens (human)
PN JP 1991180192-A/1
PD 06-AUG-1991
PE 07-DEC-1989 JP 1989318243
PI OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI, PI MIYAZONO KOHEI,
PI MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
PC C12P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00,
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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sig_peptide 511..597
FT mat_peptide /note='human pro TGF-beta1'
FT mat_peptide 1345..1680
FT 3'UTR 1684..1820.
Location/Qualifiers
1..1821
/organism='Homo sapiens'
/db_xref='taxon:9606'
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BASE COUNT 326 a 679 c 508 g 308 t
ORIGIN
alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGFB3P x E03028
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Align seg 1/1 to: E03028 from: 1 to: 1821
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1346 GCCTGGACACCACTATTGCTTACGCTCCACGCGGAGAACTGCTGCGT 1395

17 LuProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1396 GCGCAGCTGTACTTACCTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1445

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1446 ACGAGCCCAAGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 1495

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1496 ATTTGGAGCTGGACACGACGACGACGACGACGACGACGACGACGAC 1545

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1546 GCATAACCCGCGCGCTCGCGCGCGCGTGTGCTGCGCGCGCGCGCTGG 1595

84 LuProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||::: ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1596 AGCGCTGCCCATGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAG 1645

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1646 CTGTCCACATGATGTGCTGCGCTCTGCAAGTGCAGC 1681

seq_name: gb_pat1:A06669
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seq_documentation_block: 2537 bp mRNA PAT 29-JUL-1993
LOCUS A06669
DEFINITION Synthetic mRNA for preTGF-beta1.
ACCESSION A06669
VERSION A06669.1 GI:412940
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2537)
AUTHORS NUCLEIC ACID CODING TGF- beta 3 AND ITS USE
TITLE Patent: WO 8912101-A 4 14-DEC-1989;
JOURNAL Location/Qualifiers
FEATURES
source
1..2537
/organism='synthetic construct'
/db_xref='taxon:32630'
842..2014
/codon_start=1
/transl_table=11
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/protein_id='CAA00588.1'
/db_xref='GI:412941'
/transl_table='MPPSGLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRK
RIFAIRGQILSKLRLASPPSGVEVPGPLPEAVLALYNSTRDRVAGSAEPEPEAD
LYAEVTRVLVETHNEIYDKFQSTHSITMFFNTSELREAVPEPVLSRAELRLRL
KLKVEHQVELYQKYSNNRWYLSNRLAPSDPEWLSFDVTGVVQRWLSRGGELGFR
LSAHCSDSRDNTLQVDINGTTGRGDLATIHGNRPFLLLMATPLERAGHLOSSRH
RRALDTNYCFSSTEKNCCKRQLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDT
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BASE COUNT      473 a      893 c      739 g      432 t
ORIGIN
      QYKVLALYNQHNPGASAAPCCVQQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS"

alignment_scores:
      Quality: 500.00      Length: 112
      Ratio: 5.102      Gaps: 0
      Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
      TGFB3P x A06669      ..

      Align seg 1/1 to: A06669 from: 1 to: 2537

      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1676 GCCCTGGACACCAACTATTGCTTCACGCTCCACGAGAGAAGAACTGCTCGGT 1725

      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1726 GGGCGACGCTGATCTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1775

      34 iSGLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1776 ACAGGCCCAAGGCTACCATGCAACTTCTGCTCGGCCCTCGCCCTAC 1825

      51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1826 ATTTGGAGCTGGACACGACGATACACAGGCTCTGGCCCTGTACCAACCA 1875

      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1876 GCATAACCCGGCGCGCTCGCGCGCGCTGCTGCGTGGCGAGCGCGTGG 1925

      84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1926 AGCCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975

      101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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      1976 CTGTCCAACATGATCGTGGCGCTCTGCAAGTGCAGC 2011

seq_name: gb_pr9:HSTGFB1

seq_documentation_block: 2745 bp mRNA PRI 27-MAR-1995
LOCUS HSTGFB1
DEFINITION Human mRNA for transforming growth factor-beta (TGF-beta).
ACCESSION X02812 J05114
VERSION X02812.1 GI:37092
KEYWORDS signal peptide; transforming growth factor-beta.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2745)
Derynck,R., Jarrett,J.A., Chen,E.Y., Eaton,D.H., Bell,J.R.,
Asolian,R.K., Roberts,A.B., Sporn,M.B. and Goeddel,D.V.
Human transforming growth factor-beta complementary DNA sequence
and expression in normal and transformed cells
Nature 316 (6030), 701-705 (1985)
JOURNAL 85296301
MEDLINE
COMMENT The sequence downstream from the translational stop codon
(2015-2017) was taken from a genomic clone.
FEATURES
source
1..2745
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
37..113
misc_feature
842..2017
/note="pot. hairpin loops-forming region"
CDS
/note="TGF-beta precursor"
/codon_start=1
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YVAKETRVLMVETHEINEIDYDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLR
LALKVQHVVELYQKYSNNRWLSNRLAPSDSEWLSTFDVTGVVQWLRSRGGEIEGF
RUSAHCSDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSR
HRRALDNTYCFSTERNKCCVRLYIDFKDLGWKWIHEPKGYHANFCLGCPYITWISLD
TOYSKVLALYNQHNPGASAAPCCVQQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS"
misc_feature      863..910
/note="pot. core sequence of signal peptide (aa -272 to
-257)"
misc_feature      953
/note="pot. altern. translation start site"
misc_feature      1035..1043
/note="put. glycosylation site"
misc_feature      1247..1255
/note="put. glycosylation site"
misc_feature      1370..1378
/note="put. glycosylation site"
mat_peptide      1679..2014
/product="mature TGF-beta (aa 1-112)"
misc_feature      2018..2096
/note="GC-rich region"
promoter          2097..2103
/note="TATA-box-like region"
misc_feature      2517..2522
/note="put. polyadenylation signal"
polyA_site        2539
/note="polyadenylation site"
BASE COUNT      527 a      938 c      801 g      479 t
ORIGIN

alignment_scores:
      Quality: 500.00      Length: 112
      Ratio: 5.102      Gaps: 0
      Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
      TGFB3P x HSTGFB1      ..

      Align seg 1/1 to: HSTGFB1 from: 1 to: 2745

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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1679 GCCCTGGACACCAACTATTGCTTCAGCTCCACGAGAGAAGAACTGCTCGGT 1728

      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1729 GCGCGACGCTGTACTTACATTCGCAAGGACCTCGGCTGGAAGTGGATCC 1778

      34 iSGLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1779 ACAGGCCCAAGGCTACCATGCCAACTTCTGCTGGGCCCTCGCCCTAC 1828

      51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1829 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTCGGCCCTGTACAACCA 1878

      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1879 GCATAACCCGGCGCGCTCGCGCGCGCTGCTGCGTGGCGAGCGCGTGG 1928

      84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1929 AGCCGCTGCCCATCGTGTACTTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1978

      101 LeuSerAsnMetValValLysSerCysLysCysSer 112
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1979 CTGTCCAACATGATCGTGGCGCTCTGCAAGTGCAGC 2014
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seq_name: gb_om:PIGTGFB1A
seq_documentation_block:
LOCUS PIGTGB1A 3206 bp mRNA MAM 31-MAR-1995
DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION M23703
VERSION M23703.1 GI:755044
KEYWORDS transforming growth factor-beta-1.
SOURCE Sus scrofa (strain miniature swine) cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS Kondaiah,P., Van Obberghen-Schilling,E., Ludwig,R.L., Dhar,R.,
Sporn,M.B. and Roberts,A.B.
TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation
J. Biol. Chem. 263 (34), 18313-18317 (1988)
JOURNAL
MEDLINE 89054010
COMMENT On Apr 1, 1995 this sequence version replaced gi:341017.
FEATURES
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1..3206
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/strain="miniature swine"
/db_xref="taxon:9823"
/cell_type="peripheral blood lymphocyte"
906..3191
/gene="TGF-beta-1"
906..2078
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/codon_start=1
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YKAEYTRVLMVDSGQIYDKFGTSPHLYMLFNTSELREAVPEPVLSSRAELRLRL
KLKVEQHVLYQKYSNDNSWYLSNRLPLSDSPWLSFDVTGVVROWLTRAIEGFR
LSAHCSDSKDNTLHVEINGNSRGREGDLATIHGMNRPFLLLMATPLERAQHLHSRRH
RRALDNTYCFSSTEKNCVRLYIDFRKDLGKWKIHEPKYGHANFCLGCPYIWSLDT
QYSKVALYNQHNPGASAPCCVPQALEPIVIYVGRKPKVEQLSNMIVRSCKS"
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3186..3191
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polyA_site
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BASE COUNT 645 a 1041 c 924 g 596 t
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Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
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Align seg 1/1 to: PIGTGB1A from: 1 to: 3206
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1740 GCCCTGGATACCACTACTGCTTCCAGTCCACGAGAGAACTGCTGCGT 1789
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1790 GCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGATTC 1839
|||||
34 isGluProLysGlyTyrTrpAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1840 ATGAACCAAGGGCTACCATCTTCTGCTGGGGCCCTGCTCCCTAC 1889
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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alignment_scores:
Quality: 499.00 Length: 112
Ratio: 5.092 Gaps: 0
Percent Similarity: 87.500 Percent identity: 76.786
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Align seg 1/1 to: ECRGBF1 from: 1 to: 1173
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
835 GCTCTGGACACCACTACTGTTTCAGCTCCACAGAGAAAGAACTGCTGGT 884
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
885 ACGGAGCTGTACATTGACTTTCGCAAGGACTTGGCTGGAAGTGGATCC 934
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
935 ACGAGCCCAAGGGGTACACGCCCACTTCTGCCCTGGGGCCCTGCCCTAC 984
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
985 ATTTGGAGCTGGACACGACAGTACAGCAAGTCTTGGCCCTGTACAACA 1034
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1035 GCACAACCCGGCGCGTGGCGGCGCGTGTGGTGGCGGAGTGGTGG 1084
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1085 AGCGGCTGCCATCGTGTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 1134
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1135 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGC 1170
seq_name: gb_pat2:E00973
seq_documentation_block:
LOCUS E00973 2527 bp RNA PAT 29-SEP-1997
DEFINITION cDNA encoding human TGF-beta.
ACCESSION E00973
VERSION E00973.1 GI:2169234
KEYWORDS JP 1986219395-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Riku,M.A.D.D. and Debitsudo,B.G.
NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
Patent: JP 1986219395-A 1 29-SEP-1986;
GENENTECH INC
COMMENT
OS human
PN JP 1986219395-A/1
PD 29-SEP-1986
PF 20-MAR-1986 JP 1986064661
PR 22-MAR-1985 US 85 715142
PI RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC
C12P21/00,C12N1/00,C12N5/00,C12N15/00,C12Q1/68,(C12P21/00, PC
C12R1:91),
PC (C12N1/00,C12R1:19),(C12N5/00,C12R1:91),(C12N15/00,C12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=placenta and glyoblastoma; FH Key
Location/Qualifiers
FH CDS 842..2014
FT FT /product='pre TGF-beta'

FT mat_peptide 1676..2011
FT 5'UTR /product='TGF-beta'
FT 1..841
FT 3'UTR 2015..2537
FT stem_loop 37..113
FT stem_loop 2015..2100
FT polyA_site 2514..2519.
FEATURES
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1..2527
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 472 a 888 c 735 g 432 t
ORIGIN
alignment_scores:
Quality: 497.00 Length: 112
Ratio: 5.071 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 75.893
alignment_block:
TGFB3P x E00973
Align seg 1/1 to: E00973 from: 1 to: 2527
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1726 GCGGAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1776 ACGAGCCCAAGGGGTACCATGCCCACTTCTGCCCTGGGGCCCTGCCCTAC 1825
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1826 ATTTGGAGCTGGACACGACAGTACAGCAAGTCTTGGCCCTGTACAACA 1875
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1876 GCATAACCCGGCGCGCTCGGCGGCGCGTGTGGTGGCGGAGTGGTGG 1925
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1926 AGCGGCTGCCATCGTGTACTAGTGGCGGCGCAAGCCCAAGTGGAGGAG 1975
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1976 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGC 2011
seq_name: gb_pat1:A23756
seq_documentation_block:
LOCUS A23756 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2(44/45)beta1 hybrid coding region.
ACCESSION A23756
VERSION A23756.1 GI:825590
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 6 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
source
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ORIGIN
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  Ratio: 5.010        Gaps: 0
  Percent Similarity: 88.393  Percent Identity: 75.000
alignment_block:
TGFB3P x A23756 ..
Align seg 1/1 to: A23756 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
1 GCTTGGATGGCGCCTATGCTTTAGAAATGTCAGGATTAATGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValh 34
:|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
51 ACGTCCACITTTACATTGATTTCAAGAGGATCTAGGGTGAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
101 ACGACCCAAAGGGTACAATGCGCAACTTCTGCTCGGGCGCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
151 ATTTGGAGCCTGGACACGCAAGTACGCAAGGCTCTGGCCCTGTACACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
201 GCATAACCCGGCGCCTCGCGCGCGCGTCTGCGTCCGCGCGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
251 AGCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCAAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
301 CTGTCCAACATGATGCTGCGCTCTCTGCAAGTGCAGC 336
seq_name: gb_om:SHPGFB1W
seq_documentation_block:
LOCUS SHPGFB1W 334 bp mRNA MAM 11-SEP-1994
DEFINITION Ovis aries transforming growth factor-beta 1 mRNA, partial cds.
ACCESSION L36038
VERSION L36038.1 GI:535759
KEYWORDS transforming growth factor-beta 1.
SOURCE Ovis aries (strain Merino) fetus dorsal skin cDNA to mRNA.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
REFERENCE
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IVRSCKCS"
BASE COUNT      70 a  106 c  94 g  64 t
ORIGIN
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  Quality: 492.00      Length: 110
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  Percent Similarity: 87.273  Percent Identity: 76.364
alignment_block:
TGFB3P x SHPGFB1W ..
Align seg 1/1 to: SHPGFB1W from: 1 to: 334
3 AspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgPr 19
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
3 GACACCAACTACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGTTCTGCA 52
19 oLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValHisGluP 36
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
53 GCTCTACATTGACTTCGGAAGAGACCTGGGCTGGAAGTGGATTTCATGAC 102
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
103 CCAAGGGTACCACGCCAATTTCTGCTGGGGCCCTGCCCTTACATCTGG 152
53 SerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAs 69
||| |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
153 AGCCTGGACAGCAGTACAGCAAGGTCTGCGCTGTACAAACAGCACAA 202
69 nProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProL 86
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
203 CCCGGGCGCATCGGCGCGCGTCTGCGTCCCTCAGCGCTGGAAACCC 252
86 euThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSer 102
||| |||||:  |||||:  |||||:  |||||:  |||||:  |||||:
253 TGCCCATCGTGTACTACTGTTGGCGCGCAAGCCCAAGGTGGAGCAGTTGCC 302
103 AsnMetValValLysSerCysLysCysSer 112
|||||:  |||||||:  |||||||:  |||||||:  |||||||:  |||||||:
303 AACATGATCGTGCCTCTCTGCAAGTGCAGC 332
seq_name: gb_om:AF175709
seq_documentation_block:
LOCUS AF175709 1187 bp mRNA MAM 15-AUG-1999
DEFINITION Equus caballus transforming growth factor beta 1 (TGFB1) mRNA, complete cds.
ACCESSION AF175709
VERSION AF175709.1 GI:5733113
KEYWORDS
SOURCE horse.
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
1 (bases 1 to 1187)
AUTHORS Nixon,A.J., Brower-Toland,B.T. and Sandell,L.J.
TITLE Molecular cloning of equine transforming growth factor beta 1 reveals a divergent nucleotide structure that encodes a novel bioactive peptide among mammalian species
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 1187)
AUTHORS Nixon,A.J., Brower-Toland,B.T. and Sandell,L.J.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1999) Clinical Sciences, Cornell University, P. O. Box 25, Ithaca, NY 14853, USA
FEATURES
1..1187
Location/Qualifiers
/organism="Equus caballus"
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15. .1187
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/translating="MPPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRK
RIARIGQILSKLRASPQSGVEPPGPLEAVLALYNSTRAOVAGSAETPEPEAD
YKAEYTRVLWEKENELIYVTGSHSYWFENASERLRAVPPMLLSRAELRLRL
KLSVEQHEVDIQTISNNWYLSNRLTSDSPSEWLSFDVTGVVQRLSOGAMEGLR
LSAHCDCSDNTLRVINGFSSRRGLDITDGMNPFLLMATPLERAQQLHSRR
RRALDPTKNCVKCVRQLYIDFKDLGKWIHEPKGYHANFCLGCPYIWSLDT
OYSKVLALYNOHNPASAAAPCCPVQVLEPLIVYVGRKPKVEQLSNMVRSCKS"
BASE COUNT 230 a 395 c 361 g 201 t
ORIGIN

alignment_scores:
Quality: 491.00 Length: 112
Ratio: 5.062 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893

alignment_block:
TGFB3P x AF175709 ..
Align seg 1/1 to: AF175709 from: 1 to: 1187

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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849 GCTCTGGACACCACTACTGTCTCCAGCTCCACAGAGAACACTGCTGCGT 898

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
899 ACGGCGAGTGTACATGTGCTTCGCAAGGATCTGGGCTGGAAGTGGATCC 948

34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
949 ACGACCCCAAGGCTACACGACCACTCTGCTGGGCGCCCTGCCCTAC 998

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
999 ATTTGGAGCTGGACACGAGTACAGCAAGGCTCTGGCCCTGTACACCA 1048

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1049 GCACAACCCGGCGCGTGGCGGCGCGTCTGCTGCGCGCAGGTGCTGG 1098

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1099 AGCCGCTGCCATCGTGTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 1148

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
1149 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 1184

seq_name: gb_ov:CCU66874
seq_documentation_block:
LOCUS CCU66874 1083 bp mRNA VRT 14-JUL-1997
DEFINITION Cyprinus carpio transforming growth factor-beta 2 mRNA, partial
cds.
ACCESSION U66874
VERSION U66874.1 GI:1519488
KEYWORDS
SOURCE
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
REFERENCE 1 (bases 1 to 1083)
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AUTHORS Sumathy,K., Desai,K.V. and Kondaiah,P.
TITLE Isolation of transforming growth factor-beta2 cDNA from a fish,
Cyprinus carpio by RT-PCR
JOURNAL Gene 191 (1), 103-107 (1997)
MEDLINE 97354301
REFERENCE 2 (bases 1 to 1083)
AUTHORS Sumathy,K., Desai,K.V. and Kondaiah,P.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1996) Center for Reproductive Biology and
Molecular Endocrinology, Indian Institute of Science, Bangalore,
Karnataka 560 012, India
FEATURES
source
1. .1083
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/db_xref="taxon:9796"
<1. >1083
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/protein_id="AAB62983.1"
/db_xref="GI:1519489"
/translating="OILCKLKLSCPEIYPEEVSRIIATYNSTRDLLOEKANERA
ATCERQRTGEEYVAKEVHKIDMQPEYPAENVLPYFRRLRFDVSSMEKNASNL
VKAELRIFRLQNPARKVSEQRLELYQLGHKDLTSTQRYIDSKVYRTTEGWLSPD
VTEAVSEWLLHRRNGPKLSLHCPCTFVPSNNYIPNKESELEAFAGIDDSFVHG
GDKMFKRRHSGQSPHLLMLLPSYRLSESHKSHKRALDAAFRCFRVQDNCCURS
LYIDFKDLGKWIHEPKGYNANFAGACPYLWSADTQHSNLTINPEASASPC
CVSQDLEPLTILYIGKTPKIEQLSNM"
BASE COUNT 282 a 310 c 281 g 210 t
ORIGIN

alignment_scores:
Quality: 489.00 Length: 104
Ratio: 5.041 Gaps: 0
Percent Similarity: 93.269 Percent Identity: 77.885

alignment_block:
TGFB3P x CCU66874 ..
Align seg 1/1 to: CCU66874 from: 1 to: 1083

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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772 GCTCTGGACGCGCTCTGCTTCAGAAATGTGCAGGACAACTGCTGTTT 821

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::: |||
822 ACCTCTCTCTACATCGACTTCAAGAAGGATCTGGGTGGAAGTGGATCC 871

34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
872 ACGACCCCAAGGATATACGCCCAACTCTGTCGGGAGCTGCTCCGTAT 921

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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922 CTGTGGAGTGCAGACACCCAGCAGCAATATCCTTGGCCTCTACACAC 971

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
::: |||
972 CATTAATCCAGAAGCATCTCCTGCTGTGTCTCAGGATCTGG 1021

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1022 AACCCCTTAAATCCCTTTACTACATCGGAAACGCCCAAAATCGAACAA 1071

101 LeuSerAsnMet 104
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1072 CTGTCCAACATG 1083

seq_name: gb_rol:MATGFB1
seq_documentation_block:
LOCUS MATGFB1 469 bp mRNA ROD 02-AUG-1993
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DEFINITION M.auratus mRNA for transforming growth factor beta-1.
ACCESSION X60296
VERSION X60296.1 GI:396177
KEYWORDS transforming growth factor-beta-1.
SOURCE golden hamster.
ORGANISM Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
REFERENCE 1 (bases 1 to 469)
AUTHORS Yang, J.T.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1991) J.T. Yang, Harvard School of Dental
Medicine, Laboratory of Molecular Carcinogenesis, Rm 122,
188 Longwood Avenue, Boston, MA 02115, USA
REFERENCE 2 (bases 1 to 469)
AUTHORS Wong, D.T., Donoff, R.B., Yang, J., Song, B.Z., Matossian, K.,
Nagura, N., Elovic, A., McBride, J., Gallagher, G., Todd, R., et, al.
TITLE Sequential expression of transforming growth factors alpha and beta
1 by eosinophils during cutaneous wound healing in the hamster
JOURNAL Am. J. Pathol. 143 (1), 130-142 (1993)
MEDLINE 93304479
FEATURES
Location/Qualifiers
source
1..469
/organism="Mesocricetus auratus"
/strain="LVG (Syr)"
/db_xref="taxon:10036"
/cell_type="DMBA transformed keratinocytes"
/cell_line="HCPC-1"
/clone_lib="oligodt primer-extended cDNA"
/clone="pJY-C"
misc_feature 1..18
/note="primer JV-2"
sig_peptide 24..77
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CDS 24..416
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PLPIVYVGRKKEVQLSNMIVRSKCS"
mat_peptide 78..413
/product="transforming growth factor-beta 1"
misc_feature 450..469
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BASE COUNT 87 a 167 c 133 g 82 t
ORIGIN
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alignment_scores:
Quality: 488.00 Length: 112
Ratio: 5.031 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGFB3P x MATGFB1
Align seg 1/1 to: MATGFB1 from: 1 to: 469
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78 GCCCTGGACACCACTATGCTTCCAGTCCACGGAGAACTGCTGCGT 127
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValH 34
|||||
128 GCGCAGCTGTACATTCACCTCCGAGGACCTCGGCTGGAGTGGATCC 177
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
178 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCCTAC 227

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
228 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCTTGGCCCTGTACAACCA 277
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| |||||:::||||| ||||| ||||| |||||
278 GCATAACCCGGGCGCTCGGCGGCCCTGCTGCTGCGCGCAGGCGCTGG 327
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| |||||:::||||| ||||| ||||| |||||
328 AGCCGCTCCCATCGTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAG 377
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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378 CTGTCCAACATGATGCTGCGCTCTTACCAAGTCAGC 413
seq_name: gb_rol:AF191297
seq_documentation_block:
LOCUS AF191297 1597 bp mRNA ROD 16-OCT-1999
DEFINITION Cavia porcellus transforming growth factor-beta (TGF-beta) mRNA,
complete cds.
ACCESSION AF191297
VERSION AF191297.1 GI:6049850
KEYWORDS domestic guinea pig.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 1597)
AUTHORS Jeevan, A., McMurray, D.N. and Yoshimura, T.
TITLE Guinea pig transforming growth factor-beta in peritoneal exudates
after BCG vaccination
JOURNAL Unpublished
AUTHORS Jeevan, A., McMurray, D.N. and Yoshimura, T.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1999) Medical Microbiology & Immunology, Texas
A&M Univ. System Hlth. Sci. Ctr., 407 Reynolds Medical Building,
College Station, TX 77843-1114, USA
FEATURES
source
1..1597
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/strain="Hartley"
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gene 1..1597
/gene="TGF-beta"
CDS 299..1471
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RFEAIRGOILSKLRLASPPQGDVPPGPPLEAVLALYNSTRDVRVAGSAPPEPEPD
YIAKEVTRVLVDNSHNIYSIETVAHSIYFNTSELRAVDPDLLSRAELRQRL
KLNVEQVELDIQYISNNWRYLSNQLTSPDPEWLSFDVTGVVQWLSQGELEGER
FSAHCSDKNDTLRVEINGIGPKRGDLAAIHGMNRPFLLLMATPLERAOHLHSSRH
RRGLDNTYCFSTTEKNCCVRQLYIDFRKDLGKWIHPKGFHANFCLGPGPYIWSLDT
QYSKVLALYNQHNPGASAAPCCVPOALEPLPIVYVGRKKEVQLSNMIVRSKCS"
BASE COUNT 318 a 542 c 436 g 301 t
ORIGIN
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alignment_scores:
Quality: 488.00 Length: 111
Ratio: 5.083 Gaps: 0
Percent Similarity: 86.486 Percent Identity: 75.676
alignment_block:
TGFB3P x AF191297
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1404 CTGTCACATGATCGTGGCTCTCGAAGTGCAGC 1439
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seq_name: gb_om:AF152592

seq_documentation_block: 244 bp mRNA MAM 28-MAR-2001
LOCUS AF152592
DEFINITION Capreolus capreolus transforming growth factor beta 3 (TGF-b3)
mRNA, partial cds.
ACCESSION AF152592
VERSION AF152592.1 GI:8132130
KEYWORDS
SOURCE roe deer.
ORGANISM Capreolus capreolus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
Cervidae; Odocoileinae; Capreolus.

REFERENCE 1 (bases 1 to 244)
Wagener,A., Blottner,S., Goeritz,F. and Fickel,J.
TITLE Detection of growth factors in the testis of roe deer (Capreolus capreolus)
JOURNAL Anim. Reprod. Sci. 64 (1-2), 65-75 (2000)
MEDLINE 20532861
PUBMED 11078967

REFERENCE 2 (bases 1 to 244)
Wagener,A. and Fickel,J.
AUTHORS Direct Submission
TITLE Submitted (19-MAY-1999) Evolutionary Genetics, Institute for Zoo
Biology and Wildlife Research, Alfred-Kowalke-Str. 17, Berlin
D-10315, Germany

FEATURES
source
1. .244
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CDS
1. .>244
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/db_xref="GI:8132131"
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THSTVLGLYTLNLPASASPCCPVQDLEPLTILYV"

BASE COUNT 52 a 84 c 57 g 51 t
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alignment_scores:
Quality: 463.00 Length: 81
Ratio: 5.716 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.765
alignment_block:
TGFB3P x AF152592 ..
Align seg 1/1 to: AF152592 from: 1 to: 244

12 GluGluAsnCysCysValArgProLeuThrIleAspPheArgGlnAspLe 28
1 GAGGAGAACTGCTGTGCGCCCTCTCTATATTGACTTCGACAGGATCT 50
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
51 GGGCTGGAATGGTCCATGAACCTTAGGGCTACTATGCCAACTTCTGCT 100
45 erglyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
101 CAGGCCCATGCCATACCTCCGACCTCAGACACACCCACAGCAGGTG 150
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||

151 CTGGGCGCTGTACAAACACCCCTGAACCCCTGAGCCTCAGCCTCCCTTGCTG 200
78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrVal 92
|||||

seq_name: gb_ov:CHKTGFB4

seq_documentation_block: 1256 bp mRNA VRT 05-AUG-1996
LOCUS CHKTGFB4
DEFINITION Chicken transforming growth factor beta 4 (TGF-beta 4) mRNA,
partial cds.

ACCESSION M31160 X08012 S41706
VERSION M31160.1 GI:1262437
KEYWORDS growth factor; transforming growth factor-beta 4.
SOURCE Chicken cDNA to mRNA.
ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 1256)
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 2 (bases 1 to 1256)
Jaworski,S.B., Dillard,P.J., Sporn,M.B. and Roberts,A.B.
TITLE Complementary deoxyribonucleic acid cloning of a messenger
ribonucleic acid encoding transforming growth factor beta 4 from
chicken embryo chondrocytes

JOURNAL Mol. Endocrinol. 2 (12), 1186-1195 (1988)
MEDLINE 89112198

REFERENCE 2 (bases 1 to 1256)
Burt,D.W. and Jakowlew,S.B.
AUTHORS Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA
JOURNAL Mol. Endocrinol. 6 (6), 989-992 (1992)
MEDLINE 92357039

COMMENT On Apr 12, 1996 this sequence version replaced gi:212760.
The sequence overlaps with that reported by Derynck et al. in
Nature 316:701-705(1985), X0812, and Derynck et al. in Nucl. Acids
Res.15:3187-3187(1987) Y00111, and Van Oberghen et al. in Mol.
Endocrin. 1:693-698(1987).

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1. .1256
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<1. .1124
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/db_xref="GI:1262438"

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LPDDVRLYNSQELLKQARLRPPDPDEYWKELRRIPMTTWDGMEHQPOSH
SIFVFNVSRRARGRPILLHRAELRMLRQKAADSAGTEQRLELYGGYGASWRILH
GRSVRATADDELSFDVDAHWLSELLGVFKLSVHCPCMGCPHAEMLRISIEG
FEQRQDMQSIAGKRRVYVLAALPAERANELHSARRRDLDTDYCFGPGTDEKNC
CVRLYIDFRKDLQWKIHEPKGYANFCSGCPYIWSADTQYTKVLALYNQHNPGAS
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780. .1121
/product="transforming growth factor beta 4"

BASE COUNT 231 a 450 c 379 g 196 t
ORIGIN
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Quality: 461.00 Length: 113
Ratio: 4.753 Gaps: 1
Percent Similarity: 85.841 Percent Identity: 71.681

alignment_block:
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SADQHSRVLSLYNTINPEASASCCVQDLEPLTILYIGNTPKIE"
BASE COUNT      73 a   67 c   63 g   70 t
ORIGIN

alignment_scores:
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Percent Similarity: 93.407 Percent Identity: 79.121

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      1 AGAAATGTCAGGAAATGCTGCTACGCCCACTTACATTGATTCAA 50
      25 gGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrlleAlaA 42
      51 GAGGGATCTTGGGTGGAAATGATTATCATGAGCCTAAAGGTCATGCCA 100
      42 snPheCysSerGlyProCysProTyrlleuArgSerAlaAspThrHis 58
      101 ACTTCTGTGCTGAGCGTCCCGTATCTGTGGAGCGCACACTCAGCAC 150
      59 SerThrValLeuGlyLeuTyrlleAsnThrLeuAsnProGluAlaSerAla 75
      151 AGTAGGGTCTCAGCTTATATAATACCAATAATCCAGAACGCTGCTTC 200
      75 ProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrlle 92
      201 CCCTTGTCTGCTGCCAGATTAGAGCGCTCACCATTCTCTACTACA 250
      92 alGlyArgThrProLysValGlu 99
      251 TTGGAATACGCCCAAGATCGAA 273

seq_name: gb_rol:AF161218

seq_documentation_block: 302 bp mRNA ROD 28-JUL-1999
LOCUS AF161218
DEFINITION Meriones unguiculatus transforming growth factor beta mRNA, partial
cds.
ACCESSION AF161218
VERSION AF161218.1 GI:5616326
KEYWORDS
SOURCE Mongolian gerbil.
ORGANISM Meriones unguiculatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Gerbillinae;
Meriones.
REFERENCE
1 (bases 1 to 302)
Rao,U.R. and Klei,T.R.
TITLE cDNA Cloning of Gerbil Transforming Growth Factor-beta by PCR
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 302)
Rao,U.R. and Klei,T.R.
AUTHORS
Direct Submission
TITLE Submitted (21-JUN-1999) Microbiology and Parasitology, School of
JOURNAL Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803,
USA
FEATURES
Location/Qualifiers

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misc_feature 7..18
/note="phosphorylated by casein kinase II; phosphorylation
site"
misc_feature 13..21
/note="phosphorylated by protein kinase C; phosphorylation
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misc_feature 73..99
/note="phosphorylated by tyrosine kinase; phosphorylation
site"
misc_feature 79..126
/note="Region: TGF-beta family signature"
misc_feature 256..267
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ORIGIN

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      1 TGCTTACAGCTCCACAGAGAGAACTGCTGTGGCGCAGCTGTACAGAGA 50
      23 pPheArgGluAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrl 40
      51 CTTTGGGAAGGACCTGGCTGGAGTGGATCCACGAGCCCAAGGGCTACC 100
      40 yrAlaAsnPheCysSerGlyProCysProTyrlleuArgSerAlaAspThr 56
      101 ACGCCAACTTCTGTCTGGGGCCCTGCCCTACATTGGAGTCTTCATACA 150
      57 ThrHisSerThrValLeuGlyLeuTyrlleAsnThrLeuAsnProGluAla 73
      151 CAGTACAGCAAGGTCTTGCCTCTACAAACCAACACACCCGGCGCTTC 200
      73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
      201 GGGTCTCCCTGTCTGCTGGCGCAGCGCTGGAGCCGCTGCCCATCGTCT 250
      90 yrTyrlleValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 106
      251 ACTACGTGGGGCCCAAGCCCAAGGTGGAGCAGTGTCCCAACATGTTCTG 300

seq_name: gb_rol:AF097509

seq_documentation_block: 358 bp DNA ROD 09-DEC-1998
LOCUS AF097509
DEFINITION Cavia porcellus interleukin TGF beta gene, partial cds.
ACCESSION AF097509
VERSION AF097509.1 GI:3983112
KEYWORDS
SOURCE domestic guinea pig.

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ORGANISM  Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 358)
AUTHORS  Wicher, V., Scarozza, A.M., Ramsingh, A.I., and Wicher, K.
TITLE  Cytokine gene expression in skin of susceptible guinea-pig infected
with Treponema pallidum
JOURNAL  Immunology 95 (2), 242-247 (1998)
MEDLINE  99069279
REFERENCE 2 (bases 1 to 358)
AUTHORS  Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
TITLE  Spontaneous cytokine gene expression in normal guinea pig blood and
tissues
JOURNAL  Cytokine 10 (11), 851-859 (1998)
MEDLINE  99144670
REFERENCE 3 (bases 1 to 358)
AUTHORS  Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
TITLE  Direct Submission
JOURNAL  Submitted (05-OCT-1998) New York State Dept of Health, David
Axelrod Institute, Wadsworth Center for Laboratories & Research,
120 New Scotland Ave, Albany, NY 12208, USA
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BASE COUNT 76 a 120 c 103 g 59 t
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Quality: 420.00 Length: 103
Ratio: 4.884 Gaps: 0
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|||||
48 CTGGACACCAACTATTGCTCCAGCTCCACGAGAGAACTGCTGTGCG 97
18 qProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
| |||||
98 GCAGCTCTACATTGACATCCGCAAGAGCTAGGATGGAGTGCCACG 147
35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
|||||
148 AGCCACAGGCTACATGCCAATCTCGCCCTGGGGCCCTGCCCTACATT 197
|||
52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
|||
198 TGGAGCTGGACACACAGTACAGCAAGTCTCGCCCTGTACACACGCA 247
68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP 85
|||||
248 CAACCCCGGGGTTTCGGGGGCTTGTGTGTCGCGCAGGCGTGGAGC 297
85 roLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeu 101
|||||
298 CACTGCCCATCGTGTACTAGCTGGGGCGCAAGCAAGGTGGAGCGTC 347
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102 SerAsnMet 104
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348 TCAACATG 356
seq_name: gb_on:CEU62111
seq_documentation_block:
LOCUS CEU62111 259 bp mRNA MAM 31-JUL-1996
DEFINITION Cervus elaphus transforming growth factor-beta-2 (TGF beta-2) mRNA,
partial cds.
ACCESSION U62111
VERSION U62111.1 GI:1470104
KEYWORDS
SOURCE red deer.
ORGANISM Cervus elaphus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
Cervidae; Cervinae; Cervus.
REFERENCE 1 (bases 1 to 259)
AUTHORS Francis, S.M. and Suttie, J.M.
TITLE Reverse-Transcriptase Polymerase Chain Reaction (RT-PCR) to measure
the expression of growth factors and proto-oncogenes in the tip of
the growing deer antler
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 259)
AUTHORS Francis, S.M. and Suttie, J.M.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1996) AgResearch, Invermay Agricultural Centre,
Puddle Alley, Mosgiel, New Zealand
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1..259
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Ratio: 5.150 Gaps: 0
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TGFB3P x CEU62111 ..
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2 CAGGATAATGTTGGCTAGCCCACTTTACATTGATTTCAAGAGGATCT 51
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||
52 TGGGTGGAAATGGATTGATGAGCCTAAAGGGTACAAATGCACTTCTGTG 101
45 exGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
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102 CTGGAGCGTGGCCCATATCTGTGAGCTCAGACACTCAGCAGTAGGTT 151
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
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78 svalProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95

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202 TGTGTCCCAAGATTAGAGCGCTACACATTCTTACTACATGGGCAAAA 251
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95 hrProLys 97
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252 CACCCAAG 259
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seq_documentation_block:
LOCUS AF169347 278 bp mRNA ROD 15-AUG-1999
DEFINITION Cavia porcellus transforming growth factor-beta mRNA, partial cds.
ACCESSION AF169347
VERSION AF169347.1 GI:5732935
KEYWORDS
SOURCE domestic guinea pig.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE
AUTHORS Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
Sekizawa,K.
TITLE Guinea-pig transforming growth factor-beta expression in injured
tracheal epithelium
JOURNAL Unpublished
REFERENCE
AUTHORS Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
Sekizawa,K.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1999) Department of Pulmonary Medicine, Institute
of Clinical Medicine, University of Tsukuba, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8575, Japan
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Ratio: 5.141 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 74.725

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4 CTGGACCAACCAATTCCTTTTCAGCTCCACGAGGAAGAACTGCTGTGCG 53
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18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
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54 GCAGCTCTACATTGACATTCGCGAAGGACCTAGGATGGAAGTGGATCCACG 103
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35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
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104 AGCCCAAGGCGCTACCATGCCCACTTCGTGCTGGGCGCTGCCCTCATTT 153
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52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
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154 TGGAGCGCTGGACACACAGTACAGCAAGGTCTGCGCCTGTACAAACGACA 203
|||||

68 uAsnProGluAlaSerAlaSerProCysValProGlnAspLeuGluP 85
||||| |||||:::||||| ||||| ||||| |||||
204 CAACCCCGCGCTTCGGCGCGCTTGTCTGTGTGCCGCGAGCGGTGGAGC 253
|||||

85 roLeuThrIleLeuTyrTyrVal 92
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254 CACTGCCCATCGTGTACTACGTG 276

seq_name: gb_htg17:AC079432

seq_documentation_block:
LOCUS AC079432 215287 bp DNA HTG 01-SEP-2000
DEFINITION Mus musculus chromosome 16 clone RP23-235H2, WORKING DRAFT
SEQUENCE, 43 unordered pieces.
ACCESSION AC079432
VERSION AC079432.1 GI:9958044
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

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Project Information
Center Project Name: 0
Center clone name: RPCI-23_235H2
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Summary Statistics
Consensus quality: 130929 bases at least Q40
Consensus quality: 155193 bases at least Q30
Consensus quality: 166143 bases at least Q20
Estimated insert size: 123300; agarose-fp estimation
Quality coverage: 4.98 in Q20 bases; agarose-fp estimation
Quality coverage: 2.91 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1221: contig of 1221 bp in length
* 1222 1321: gap of unknown length
* 1322 2450: contig of 1129 bp in length
* 2451 2550: gap of unknown length
* 2551 3734: contig of 1184 bp in length
* 3735 3834: gap of unknown length
* 3835 5248: contig of 1414 bp in length
* 5249 5348: gap of unknown length
* 5349 6444: contig of 1096 bp in length
* 6445 7871: gap of unknown length
* 7872 7971: contig of 1327 bp in length
* 7972 9199: contig of 1228 bp in length
* 9199 9200: gap of unknown length

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* 9300 10379: contig of 1080 bp in length
* 10380 10479: gap of unknown length
* 10480 11597: contig of 1118 bp in length
* 11598 11697: gap of unknown length
* 11698 12849: contig of 1152 bp in length
* 12850 12949: gap of unknown length
* 12950 14152: contig of 1203 bp in length
* 14153 14252: gap of unknown length
* 14253 15426: contig of 1174 bp in length
* 15427 15526: gap of unknown length
* 15527 16631: contig of 1105 bp in length
* 16632 16731: gap of unknown length
* 16732 17804: contig of 1073 bp in length
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* 17905 19077: contig of 1173 bp in length
* 19078 19177: gap of unknown length
* 19178 20507: contig of 1330 bp in length
* 20508 20607: gap of unknown length
* 20608 21763: contig of 1156 bp in length
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* 21864 23109: contig of 1246 bp in length
* 23110 23209: gap of unknown length
* 23210 24447: contig of 1238 bp in length
* 24448 24547: gap of unknown length
* 24548 25812: contig of 1265 bp in length
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* 25914 27151: contig of 1239 bp in length
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* 28394 29910: contig of 1517 bp in length
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* 31519 31618: gap of unknown length
* 31619 32733: contig of 1115 bp in length
* 32734 32833: gap of unknown length
* 32834 34632: contig of 1799 bp in length
* 34633 34732: gap of unknown length
* 34733 37157: contig of 2425 bp in length
* 37158 37257: gap of unknown length
* 37258 40264: contig of 3007 bp in length
* 40265 40364: gap of unknown length
* 40365 43087: contig of 2723 bp in length
* 43088 43187: gap of unknown length
* 43188 46514: contig of 3327 bp in length
* 46515 46614: gap of unknown length
* 46615 48688: contig of 2074 bp in length
* 48689 48788: gap of unknown length
* 48789 54008: contig of 5220 bp in length
* 54009 54108: gap of unknown length
* 54109 59084: contig of 4976 bp in length
* 59085 59184: gap of unknown length
* 59185 62589: contig of 3405 bp in length
* 62590 62689: gap of unknown length
* 62690 67662: contig of 4973 bp in length
* 67663 67762: gap of unknown length
* 67763 73470: contig of 5708 bp in length
* 73471 73570: gap of unknown length
* 73571 80059: contig of 6489 bp in length
* 80060 80159: gap of unknown length
* 80160 86065: contig of 5906 bp in length
* 86066 86165: gap of unknown length
* 86166 95152: contig of 8987 bp in length
* 95153 95252: gap of unknown length
* 95253 107209: contig of 11957 bp in length
* 107210 107309: gap of unknown length
* 107310 124400: contig of 17091 bp in length
* 124401 124500: gap of unknown length
* 124501 154709: contig of 30209 bp in length
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121718 TGTTTTCTTCATAGCAACCTGGAGGAGAACTGCTGTGTACGCCCTTTA 121669  
  
21 rIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG 38  
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121668 TATTGACTTCCGGCAGGATCTAGGCTGGAATGGTCCACGAACCTAAGG 121619  
  
38 lYTrpTrpAlaAsnPheCysSerGlyProCysProTyrlLeuArgSerAla 54  
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121618 GTTACTATGCACTTCTGTCTCAGGCCCTTGGCCATACCTCCGAGCGCA 121569  
  
55 AspThrThrHisSer..... 59  
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59 ..... 59  
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121268 AGCATGTGCACACATGCAGAGTTCACCACCATAGTTTCAAGCATCCTT 121219  
  
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63 GlyLeuTyAsnThrLeuAsnProGluAlaSerProCysCysVa 79
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1085 GCCGTGTATAGCATCAACCCAGAGCCTCTGCCAGCGCTGCTGTGT 1134

79 lProGlnAspLeuGluProLeuThrIleLeuTyTrpValGlyArgThrP 96
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1135 TCCCAGGCACCTGGAGCCACTGCCAATCTCTACTATGTGGCAGGCAC 1184

96 roLysValGluGlnLeuSerAsnMetValLysSerCysLysCysSer 112
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LOCUS AF046214 270 bp mRNA ROD 02-MAY-1998
DEFINITION Mesocricetus auratus transforming growth factor-beta mRNA, partial cds.
ACCESSION AF046214 GI:3005106
VERSION 98234044
KEYWORDS golden hamster.
SOURCE Mesocricetus auratus
ORGANISM Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
REFERENCE 1 (bases 1 to 270)
AUTHORS Melby,P.C., Tryon,V.V., Chandrasekar,B. and Freeman,G.L.
TITLE Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis
JOURNAL Infect. Immun. 66 (5), 2135-2142 (1998)
MEDLINE 98234044
REFERENCE 2 (bases 1 to 270)
AUTHORS Melby,P.C. and Tryon,V.V.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1998) Medicine, UTHSCSA, 7703 Floyd Curl Drive,
San Antonio, TX 78284, USA
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ORIGIN

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Quality: 389.00 Length: 90
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1 TTCACCTCCACGAGCAAGAACTGCTGTGTGGCGCAGCTGTACATCGACT 50

24 eArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyTrpA 41
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51 TCGCAAGGACCTGGGCTGGAAGTGGATTCAACGAGCCAGGCGCTACCA 100

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58 HisSerThrValLeuGlyLeuTyAsnThrLeuAsnProGluAlaSerAl 74
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151 TACAGTAAGGTCTCTGGCCCTCTACAACCAACACACACCCGGGTGCTTGGC 200

74 asrProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyTr 91
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201 GTCTCGTGTGTGTGCCCCAGGCGCTGGAGCGCTGCCCATCGTGTACT 250

91 yrValGlyArgThrProLys 97
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251 ACGTGGGTGCCAAGCCCAAG 270

seq_name: gb_ov:OMTGFB

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LOCUS OMTGFB 1152 bp mRNA VRT 17-JUL-1998
DEFINITION O.mykiss mRNA for transforming growth factor beta.
ACCESSION X99303
VERSION X99303.1 GI:1478246
KEYWORDS tgf-beta; transforming growth factor beta.
SOURCE rainbow trout.
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Hardie,L.J., Laing,K.J., Daniels,G.D., Grabowski,P.S.,
Cunningham,C. and Secombes,C.J.
TITLE Isolation of the first piscine transforming growth factor B gene:
analysis reveals tissue specific expression and a potential
regulatory sequence in rainbow trout (Oncorhynchus mykiss)
Cytokine in press
REFERENCE 2 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
AB24 2Tz, UK
REMARK revised by [3]
REFERENCE 3 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
AB24 2Tz, UK
COMMENT On Aug 2, 1996 this sequence version replaced gi:1438515.
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ORIGIN
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  Ratio: 4.687        Gaps: 0
  Percent Similarity: 83.000  Percent Identity: 66.000

alignment_block:
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Align seg 1/1 to: OMTGFB from: 1 to: 1152
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308 GAGAGTGTGTGTGGAAACATTACATTGACTCCGTAAGGACCTGGG 357

29 yTrpLysTyrValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
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358 CTGGAAGTGGATCCATGAACCCACTGGCTACTTGTCTAAGTACTGCTG 407

46 lyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeu 62
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408 GCCCTGACCTATATATGACACACAGAAAAACAAGTATTTCCAGGTACTG 457

63 GlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysVa 79
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458 GCTCTGTATAAGCACACACACCCCGGAGCCTCTGCCACCCCTGCTGT 507

79 lProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrp 96
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508 TCACAGGCTTGGAGCCCTCCCAATTAATATATGTTGGGAGACAC 557

96 roLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
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558 ACAAGGTGGAGCAGGTGCCCAATATGTTATGTTCTCTCAGGTGTAGC 607
```


OM of: TGFB3P to: N_Geneseq_0601:* out_format : pfs

Date: Oct 30, 2001 9:13 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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-DB=N_Geneseq_0601 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosome2
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
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Search information block:

Query: TGFB3P

Query length: 113

Database: N_Geneseq_0601.*

Database sequences: 730101

Database length: 313950809

Search time (sec): 76.040000

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seq_documentation_block:

ID AAQ11995 standard; DNA; 339 BP.

XX AAQ11995;

XX AC

DT 29-AUG-1991 (first entry)

DE Encodes Transforming Growth Factor beta 3.

XX TGF-beta3; biologically active protein production; ss.

XX OS Homo sapiens.
XX PN EP433225-A.
XX PD 19-JUN-1991.
XX PF 27-NOV-1990; 90EP-0810922.
XX PR 06-DEC-1989; 89GB-0027546.
XX PA (CIBA) CIBA GEIGY AG.
XX PI Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;
XX WPI; 1991-180005/25.
XX DR P-PSDB; AAR12404.
XX PT Prodn. of Transforming Growth Factor type-beta-like proteins - by
XX PT subjecting denaturated monomeric form to refolding conditions
XX PS Example; Page 27; 35pp; English.
XX CC This coding sequence was isolated from the CI-215 human glioma cell
XX CC line. It was incorporated into an appropriate vector to transform
XX CC Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
XX CC denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M NaCl, 5mM EDTA,
XX CC 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps.
XX CC After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
XX CC conc. 10 times. The conc. soln was diluted to the original vol. with
XX CC 10mM HCl and conc to a final vol of 10 ml. The supernatant from
XX CC centrifugation at 5000g for 30 min contained disulphide-linked dimeric
XX CC TGF-beta3.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

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Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATGTGACTTCCGACAGGATCTGGGCTGGAAAGTGGGTCC 100
34 lSgLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGACCTTAAGGCTACATATGCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 CTCGCGAGTGCAGACACACACACACAGCAGCGGTGCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCTCTGAAGCATCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCCCTGACCATCTGTACTATGTGTGGAGGAGACCCCAAGAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTCTCCAAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
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seq_documentation_block:
ID AAQ41601 standard; cDNA; 339 BP.
XX AC AAQ41601;
XX DT 26-AUG-1993 (first entry)
XX DE Mature human Transforming Growth Factor-beta3.
XX KW hTGF-beta3; hybrid protein; wound healing; cancer treatment;
XX KW bone repair; growth regulation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..336
XX FT /*tag= a
XX PN EP542679-A.
XX PD 19-MAY-1993.
XX PF 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX PA (CIBA) CIBA GEIGY AG.
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
XX DR P-PSDB; AAR39640.
XX PT New hybrid transforming growth factor-beta molecules - comprise
XX PT portions of mature TGF-beta isoforms; useful as wound healants,
XX PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 4; Page 24; 48pp; English.
XX CC The invention covers hybrid TGF-beta molecules consisting of parts
XX CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX CC derived from different parent isoforms are pref. between amino acids
XX CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
XX CC molecules promote cell migration, inhibit the growth of A375
XX CC melanoma cells, accelerate the healing of partial-thickness burn
XX CC wounds and full-thickness incisional wounds and increase formation
XX CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

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Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATGTGACTTCCGACAGGATCTGGGCTGGAAAGTGGGTCC 100

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34 iscluproLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAACAC 200
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
|||||
84 luProLeuThrLeuLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCTGACCATCCCTGCTATGTTGGGAGGACCCCAAGTGGAGCAG 300
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seq_documentation_block:

ID AAT17234 standard; cDNA to mRNA; 339 BP.

XX AC AAT17234;

XX DT 17-JUL-1996 (first entry)

XX DE Human TGF-beta 3 cDNA.

XX KW Transforming growth factor type beta; TGF-beta 3;
XX KW protein renaturation; protein folding; ds.

XX OS Homo sapiens.

XX PN WO9603433-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02719.

XX PR 25-JUL-1994; 94EP-0810439.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI: 1996-117000/12.

XX DR P-PSDB; AAR92772.

XX PT Prodn. of dimeric biologically active transforming growth factor -
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. specific organic solvent to improve yield

XX PS Example 1B; Page 34; 54pp; English.

XX CC The coding sequence (AAT17234) of human transforming growth factor
CC TGF-beta 3 (AAR92772) was cloned into plasmid pGEM-52E(+) (Promega)
CC and the construct used to transform E. coli Y1090. Subcloning in
CC pPLMu yielded plasmid pPLMu.hTGF-beta 3. Non-soluble, monomeric
CC TGF-beta 3 was recovered from E. coli LC 137/pPLMu.hTGF-beta 3 (DSM
CC 5658) transformants. A biologically active, dimeric form of
CC TGF-beta 3 was obtd. by refolding this monomer in detergent-free
CC buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and
CC TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were
CC also produced.

XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent identity: 100.000

alignment_block:

TGFB3P x AAT17234 ..

Align seg 1/1 to: AAT17234 from: 1 to: 339

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAlaAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAATCTGCTTCCGCAACTTGGAGGAGAACTGCTGTG 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGCCCTCTCTACATTGACTTCCGACAGATCTGGCTGGAGTGGGTCC 100
|||||
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCCCTGCTATGTTGGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTCTGAATGTAGC 336
|||||

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15464

seq_documentation_block:

ID AAT15464 standard; cDNA to mRNA; 339 BP.

XX AC AAT15464;

XX DT 10-JUN-1996 (first entry)

XX DE Human transforming growth factor beta 3 encoding cDNA.

XX KW Transforming growth factor beta; TGF; regulator; method;
XX KW proliferation; differentiation; wound healing; solvent; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 1..339

XX FT /*tag= a

XX FT /product= human_TGF-beta-3

XX PN WO9603432-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02718.

XX PR 25-JUL-1994; 94EP-0810438.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI: 1996-116999/12.

XX DR P-PSDB; AAR91958.

PT Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
XX Example 1; Page 36-37; 59pp; English.
XX
XX AAT15462-T15464 encode transforming growth factor (TGF) beta-1,
CC TGF beta-2 and TGF beta-3 which are produced using recombinant
CC DNA technology and used to produce TGF beta-like proteins in
CC dimeric form. The TGF beta-like proteins produced are hybrids of
CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
CC made using a new process of producing dimeric, biologically active
CC TGF beta-like proteins. The new process involves treating denatured
CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CC CHAPS or digitonin) and at least one of the solvents DMSO (dimethyl
CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
CC The detergent allows folding of the monomer such that, after
CC dimerisation, the TGF beta-like protein retains biological activity
CC and remains in soluble form. The method allows relatively high yields
CC of biologically active TGF beta-like proteins in their native dimeric
CC form. TGF-beta like proteins are multifunctional regulators of
CC cellular activity and a typical use is to stimulate wound healing.
XX
XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAT15464 ..

Align seg 1/1 to: AAT15464 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTTACTGCTCCGCAACTTGGAGGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCCGCACTGCAGACACACACACAGCAGCGTGTGGGACTGTACACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250

84 lProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCCCTGACCATCTGTACTATGTGTGGAGGAGCCCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCCACATGGTGGTGAAGTCTGTAAATGTAGC 336

seq_name: /SDSL/gcdata/geneseq/geneseq/NA197.DAT:AAT80110

seq_documentation_block:

ID AAT80110 standard; cDNA to mRNA; 339 BP.

XX
AC AAT80110;

XX
DT 28-NOV-1997 (first entry)

XX Mature transforming growth factor beta3 coding sequence.
DE
XX

KW Transforming growth factor beta3; TGF-beta3; human; mature protein;
KW acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation;
KW cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis;
KW bone disease; bone repair; therapy; ds.
XX

XX Homo sapiens.

XX W09705166-A1.

XX 13-FEB-1997.

XX 17-JUL-1996; 96WO-EP03140.

XX 25-JUL-1995; 95EP-0810484.

XX (CIBA) CIBA GEIGY AG.

XX Arvinde T, Grutter M, Mittl P;

XX WPI: 1997-145621/13.

XX P-PSDB; AAW26173.

XX Crystalline form of transforming growth factor beta-3 - useful in
PT compns. as slow release form of TGF, e.g. for wound healing, and
PT for structure determ. in rational drug design

XX Example 1; Page 25-26; 34pp; English.

XX This sequence represents the coding sequence for human transforming
CC growth factor beta3 (TGF-beta3). TGF-beta3 is one of five distinct
CC homodimeric TGF-beta's. TGF-beta3 is an acid-stable and heat-stable
CC disulphide linked homodimer. All the TGF-beta's are produced as 390-412
CC amino acid precursors, which undergo proteolytic cleavage to produce
CC mature forms which consist of the C-terminal 112 amino acids. Depending
CC upon cell and tissue type, and the presence of other growth factors,
CC TGF-beta may either stimulate mitogenesis, cell proliferation and growth,
CC or inhibit these processes. Many of the actions of TGF-beta are related
CC to the response of cells or tissues to stress or injury, and to the
CC repair of resultant damage. A crystalline form of TGF-beta3 can be
CC produced by a method of the invention. Crystalline TGF-beta3 is useful in
CC slow release compositions for treatment of conditions such as wounds,
CC oral or intestinal mucositis, osteoarthritis, bone disease and repair,
CC generally wherever TGF-beta3 is normally used. The crystalline form is
CC also used for structure determination in rational drug design.

XX Crystalline TGF-beta3 shows lower tendency than the dissolved protein to
CC adsorb on the walls of vials and is more stable against oxidation.
CC Variation of the properties, e.g. size, of the crystals allows control
CC over the rate at which active TGF is released in vivo.

XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x AAT80110 ..

Align seg 1/1 to: AAT80110 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTTACTGCTCCGCAACTTGGAGGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

```
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACTAAGGCTACTATGCCAACTTCGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGGCAGTGCAGACACACCCACAGCAGCGTGTGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCCCTGAAGCATCTCGCTCGCTGCTGCTGCCCGCAGGACCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTGTAAATGTAGC 336
|||||
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT.AAT42773

```
seq_documentation_block:
ID AAT42773 standard; cDNA; 339 BP.
XX
AC AAT42773;
XX
DT 26-AUG-1997 (first entry)
XX
DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..339
FT /tag= a
FT /function= TGF active fragment
XX
PN WO9639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US08973.
XX
PR 06-JUN-1995; 95US-0470837.
XX
PA (CHEU/) CHEUNG D T.
PA (HALL/) HALL F L.
PA (NIMN/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WULL/) WU L.
XX
PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX
WPI: 1997-043065/04.
DR P-P5DB; AAW08175.
XX
```

Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin

Disclosure; Page 48; 59pp; English.

A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery

CC recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. CC The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the CC desired site of action. Delivery of the TGF-beta to the site to be CC treated reduces the amount of TGF-beta required to be administered to CC be effective and reduces the concentration of circulating TGF-beta CC which may result in undesirable effects.

XX

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAT42773 ..

Align seg 1/1 to: AAT42773 from: 1 to: 339

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTACTGCTTCGCCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTCCGACAGAGATCTGGGCTGGAAGTGGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGCAGTGCAGACACCAACCCACAGCAGCGTGTGGAGCTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCCCTGAAGCATCTCGCTCGCTGCTGCTGCCCGCAGGACCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTGTAAATGTAGC 336
|||||
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT.AAX15247

seq_documentation_block:
ID AAX15247 standard; cDNA; 339 BP.

XX
AC AAX15247;
XX
DT 28-APR-1999 (first entry)
XX

DE cDNA encoding the mature form of transforming growth factor-beta-3.

XX Transforming growth factor-beta-3; TGF-beta-like protein;

KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

KW bone repair; tissue repair; bone marrow protective agent;

KW cardioprotection; anti-inflammatory; immunosuppressive;

KW ulcer; bed sore; ds.

XX Homo sapiens.

XX

PN EP891985-A1.

XX

PD 20-JAN-1999.

```
XX PF 27-NOV-1990; 90EP-0810922.
XX PR 06-DEC-1989; 89GB-0027546.
XX XX (NOVS ) NOVARTIS AG.
XX XX
XX PI Carletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX DR WPI; 1999-083520/08.
XX DR P-PSDB; AAW97093.
XX XX
XX PT Producing biologically active dimeric Transforming Growth
XX PT Factor-beta - by refolding new monomeric Transforming Growth
XX PT Factor-beta, useful for treatment of wounds and cancer
XX PS
XX PS Example 1; Page 30; 32pp; English.
XX CC
XX CC The present sequence encodes the mature form of transforming growth
XX CC factor-beta-3. Dimeric, biologically active TGF-beta-like protein
XX CC can be produced by subjecting the denatured monomeric form to refolding
XX CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
XX CC useful for the production of the dimeric, biologically active
XX CC TGF-beta-like protein, which is useful for the treatment of wounds
XX CC (surface or internal) and cancer in a mammal, in bone and tissue
XX CC repair, as a bone marrow protective agent, a mediator of
XX CC cardioprotection, for the production of an anti-inflammatory or
XX CC immunosuppressive preparation. Treatment is useful for animals,
XX CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
XX CC particularly useful for the elderly.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
    Quality: 633.00      Length: 112
    Ratio: 5.652        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAX15247 ..

Align seg 1/1 to: AAX15247 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCTTTGGACACCAATACTGCTTCGCCAATTGGAGGAAGTCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCCCTCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 100
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ATGAACCTTAAGGCTACTATGCCAATCTGCTCAGGCCCTTGGCCATAC 150
51 lLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCCGCGAGTGCAGACACACACCCACAGCGGTGCTGGGACTGTACAAAC 200
67 lLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGCGTGGCCAGGACCTGG 250
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 lLeuSerAsnMetValValLysSerCysLysCysSer 112
301 CFTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: /SIDSl/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV99377
```

```
seq_documentation_block:
ID AAV99377 standard; cDNA; 339 BP.
XX AC AAV99377;
XX XX
XX DT 25-MAR-1999 (first entry)
XX DE cDNA encoding a transforming growth factor beta active fragment.
XX KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
XX KW bone morphogenetic protein; transforming growth factor beta;
XX KW active fragment; wound healing; bone growth; purification tag; ds.
XX OS Homo sapiens.
XX PN WO9855137-A1.
XX PD 10-DEC-1998.
XX PF 02-JUN-1998; 98WO-US11189.
XX PR 03-JUN-1997; 97US-0868452.
XX PA (HALL/) HALL F L.
XX PA (HANB/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX WPI; 1999-059875/05.
XX DR P-PSDB; AAW84209.
XX PT New bone morphogenetic fusion proteins - comprising a purification
XX PT tag and a bone morphogenetic active fragment, used for enhancing
XX PT wound healing or bone growth
XX PS Disclosure; Page 43; 64pp; English.
XX CC
XX CC The present sequence encodes a transforming growth factor beta active
XX CC fragment. The protein can be used in place of a bone morphogenetic
XX CC active fragment to create the fusion proteins of the invention. When a
XX CC bone morphogenetic active fragment is used, the fusion proteins are
XX CC designated bone morphogenetic fusion proteins. The bone morphogenetic
XX CC fusion protein may contain some or all of the following elements: a
XX CC purification tag, a proteinase site, an ECM/bone binding site, a second
XX CC proteinase site, and a bone morphogenetic protein active fragment.
XX CC The bone morphogenetic fusion proteins can be used for enhancing wound
XX CC healing or bone growth.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
    Quality: 633.00      Length: 112
    Ratio: 5.652        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAV99377 ..

Align seg 1/1 to: AAV99377 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCTTTGGACACCAATACTGCTTCGCCAATTGGAGGAAGTCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCCCTCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 100
```

```
34 isGluProLysGlyTyrAlaAsnPhcCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCCGAGTCGAGACACACACCCAGCAGCGGTGCTGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCTGCCCTTCTGCTGCCCGACGACCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCCTCCACATGGTGGTGAAGCTCTGTAAATGTAGC 336
|||||
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05774

seq_documentation_block:
ID AAQ05774 standard; cDNA; 609 BP.

XX AAQ05774;

DT 03-JAN-1991 (first entry)

DE Sequence encoding protein with tumour growth inhibitory activity.

KW Cancer; carcinoma; melanoma; leukaemia; arteriosclerosis; psoriasis;
KW TGF-alpha; ds;

OS Homo sapiens.

XX EP384494-A.

PD 29-AUG-1990.

XX 20-OCT-1987; 87EP-0106772.

PR 01-JAN-1990; 90EP-0106772.

PR 20-OCT-1986; 86US-0922121.

XX (ONCO-) ONCOGENE SCI INC.

XX Iwata KK, Stephenson JR, Gold LI;

DR WPI; 1990-262507/35.

DR P-PSDB; AAR06348.

XX Tissue-derived tumour growth inhibitors - used in diagnosis and
PT treatment of tumours and treatment of proliferative type
PT disorders, burns and wounds

XX Disclosure; Fig 29; 81pp; English.

CC Gene product may be used to inhibit growth of tumour cells, to
CC treat proliferative type disorders, burns and other wounds, and may
CC also be used as an immune modulator. Detection of proteins and of
CC TGF-alpha can indicate presence of a tumour.

CC Proteins may be produced from a bacterial or eukaryotic expression
CC system.

XX Sequence 609 BP; 154 A; 172 C; 158 G; 125 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112

Ratio: 5.652 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAQ05774 ..

Align seg 1/1 to: AAQ05774 from: 1 to: 609

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
271 GCTTTGGACACCAATTACTTCCGCAACTTGGAGGAGAACTGCTGTGT 320
|||||
```

```
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
321 GGGCCCCCTCTACATTGACTCCGACAGGATCTGGGCTGGAAGTGGGTCC 370
|||||
```

```
34 isGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyr 50
|||||
371 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 420
|||||
```

```
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
421 CTCCTCCAGTGCAGACACACACCCAGCAGCGTGTGGACTGTACAACAC 470
|||||
```

```
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
471 TCTGAACCTGAAGCATCTGCTGCCCTTCTGCTGCCCGACGACCTGG 520
|||||
```

```
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
521 AGCCCTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 570
|||||
```

```
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
571 CTCCTCCACATGCTGTGAAGTCTGTAAATGTAGC 606
|||||
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20576

seq_documentation_block:

ID AAQ20576 standard; cDNA; 2529 BP.

XX AAQ20576;

DT 05-MAY-1992 (first entry)

DE Transforming Growth Factor beta 3 coding sequence.

XX TGF-beta 3; homodimer; ss.

XX Synthetic.

XX WO9200318-A.

XX 09-JAN-1992.

XX 25-JUN-1991; 91WO-US04541.

XX 25-JUN-1990; 90US-0543348.

XX (ONCO-) ONCOGENE SCI INC.

XX Iwata KK, Foulkes JG, Tendijke P, Haley JD;

XX WPI; 1992-041510/05.

XX P-PSDB; AAR20621.

XX Transforming growth factor beta 3 proteins, precursors and
PT mutants - obt'd. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence

XX Example 2; Fig 1; 107pp; English.

XX This 2529bp full-length TGF-beta3 gene sequence was obtained from
CC three shorter overlapping clones derived from human placental, human
CC umbilical cord and A673 cells cDNA libraries, respectively. The
CC predicted amino acid sequence of the gene encoding TGF-beta3 shows

CC extensive homology to TGF-beta 1 and beta 2.
XX See also AAQ22229 and AAR20622.
SQ Sequence 2529 BP; 617 A; 670 C; 661 G; 581 T; 0 other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAQ20576 ..

Align seg 1/1 to: AAQ20576 from: 1 to: 2529

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
1163 GCTTTGGACACCAATACCTGCTCCGCAACTTGGAGGAACTGCTGTGT 1212

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1213 GCGCCCTCTCACTTACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1262

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1263 ATGAACCTAAGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCATAC 1312

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1313 CTCCCGAGTGCAGACACACCCACAGCGTGTGGGACTGTACAACAC 1362

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1363 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGCGTGGCCCGAGGACCTGG 1412

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1413 AGCCCTTGACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 1462

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1463 CTCTCCACATGGTGTGAAGTCTGTGTAATGTAGC 1498

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT:AAV63209

seq_documentation_block:
ID AAV63209 standard; DNA; 2574 BP.
AC AAV63209;

14-JAN-1999 (first entry)

DE Nucleic acid sequence of human transforming growth factor-beta 3.

XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; ss.
XX Homo sapiens.
XX

Key Location/Qualifiers
CDS 254..1492
FT /*tag= a
FT /product= TGF-beta3

WO9840747-A1.
XX
XX
PD 17-SEP-1998.
XX
XX 05-MAR-1998; 98WO-CA00180.
XX

PR 07-MAR-1997; 97US-0039919.
XX
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
PI Caniggia I, Lye S, Post M;
XX
XX WPI; 1998-520837/44.
DR P-PSDB; AAW80417.
XX
PT Regulation of trophoblast invasion - by, e.g. transforming growth
PT factor-beta3 inhibitor, useful for detecting or treating
PT preeclampsia in pregnant women
XX
PS Disclosure: Fig 1; 59pp; English.
XX
CC The present sequence encodes human transforming growth factor-beta 3
CC (TGF-beta3). The specification describes a composition for regulating
CC trophoblast invasion which comprises an inhibitor of TGF-beta3,
CC TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
CC (HIF-1 alpha) or oxygen tension. The composition is used in methods of
CC diagnosing, monitoring, preventing or treating conditions requiring
CC regulation of trophoblast invasion, especially preeclampsia in pregnant
CC women or choriocarcinomas.
XX
SQ Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAV63209 ..

Align seg 1/1 to: AAV63209 from: 1 to: 2574

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
1154 GCTTTGGACACCAATACCTGCTCCGCAACTTGGAGGAACTGCTGTGT 1203

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1204 GCGCCCTCTCACTTACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1253

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1254 ATGAACCTAAGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCATAC 1303

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1304 CTCCGAGTGCAGACACACCCACAGCGTGTGGGACTGTACAACAC 1353

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1354 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGCGTGGTGGCCCGAGGACCTGG 1403

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1404 AGCCCTTGACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 1453

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1454 CTCTCCACATGGTGTGAAGTCTGTGTAATGTAGC 1489

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF55131

seq_documentation_block:
ID AAF55131 standard; DNA; 4382 BP.
XX
XX
AC AAF55131;
XX

DT 29-MAY-2001 (first entry)
 XX Nucleotide sequence of the vector puhld0-3-tgf.
 DE
 KW Stem cell; gene therapy; cell therapy; stem cell disorder; ss.
 XX
 OS Synthetic.
 XX
 PN WO200114530-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 24-AUG-2000; 2000WO-EP08247.
 XX
 PR 24-AUG-1999; 99EP-0116533.
 XX
 PA (CHEN/) CHEN U.
 XX
 PI Chen U;
 XX
 XX WPI; 2001-218440/22.
 DR
 XX Growing stem cells useful as therapeutic, involves providing stem cells
 PT with supporters which are genetically modified to provide externally
 PT regulatable interactions, and applying an external signal -
 XX
 PS Disclosure; Fig 26; 92pp; English.
 XX
 CC The specification describes a method for growing stem cells. The method
 CC involves providing stem cells with supporters which are genetically
 CC modified in order to provide externally regulatable interactions between
 CC the supporters and the stem cells, and applying an external signal for
 CC starting or stopping the interactions. The cells are useful for curing
 CC diseases by gene therapy and/or cell therapy in combination with tissue
 CC engineering, when the functional expression of stem cells is helped
 CC with engineered architecture of the tissue, which diseases are related
 CC to insufficient and/or lack and/or disorders of stem cells. The present
 CC sequence represents a vector, which is used in the method of the
 CC invention.
 XX
 SQ Sequence 4382 BP; 1153 A; 1120 C; 1091 G; 1018 T; 0 other;

alignment_scores:
 Quality: 633.00 Length: 112
 Ratio: 5.652 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x AAF55131 ..

Align seg 1/1 to: AAF55131 from: 1 to: 4382

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
 1358 GCCCTGGACACCAATTAATCTCCGCAACCTGGAGGAGACTGCTGT 1407
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 1408 ACGCCCCCTTTATATTGACTTCGCGGAGGATCTAGGCTGGAAATGGGTCC 1457
 34 lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 1458 AAGCAACTAAGGGTTACTATGCGCAACTTCGCTCAGGCGCCCTGCCCATAC 1507
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 1508 CTCGGCAGCGCACACACACCCATAGCAGCGTCTGGACTATACACAC 1557
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 1558 CCTGAACCCAGAGGGCTGTCTCCCTCGCATCTGCTGCTCCCGCCAGACCTGG 1607

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 1608 AGCCCTTACCCTATCTGTACTATGTGGCAGAACCCCAAGGTGGAGCAG 1657
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 1658 CTGTCCACACATGGTGTGAAGTCGTGTAAAGTCGAGC 1693

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1994.DAT:AAQ56926

seq_documentation_block:

ID_ AAQ56926 standard; cDNA; 2157 BP.

XX
 AC AAQ56926;

XX
 DT 09-JUL-1994 (first entry)

XX
 XX Human TGF-beta-3.

XX
 KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
 KW transforming growth factor beta-3; recombinant; wound healing;
 KW vulnerary; ss.

XX
 OS Homo sapiens.

XX
 PN US284763-A.

XX
 XX 08-FEB-1994.

XX
 XX 22-MAR-1985; 85US-0715142.

XX
 XX 22-MAR-1985; 85US-0715142.

XX
 PR 13-MAR-1987; 87US-0025423.

XX
 PR 04-AUG-1989; 89US-0389929.

XX
 PR 04-MAR-1992; 92US-0845893.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Derynk RMA, Goeddel DV;

XX
 XX WPI; 1994-056343/07.

DR
 DR P-PSDB; AAR46229.

XX
 PT Nucleic acid sequences encoding transforming growth factor-beta -
 PT diagnostic probes, and for use in therapeutics

XX
 PS Disclosure; Fig 4a-c; 25pp; English.

XX
 CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
 CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
 CC corresponding amino acid sequences were determined (AAR46227-29,
 CC respectively). A genomic fragment corresponding to a human TGF-
 CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
 CC determined (AAR46230). The sequences have been used in the
 CC construction of vectors for the expression of recombinant TGF-
 CC beta.

XX
 SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

alignment_scores:

Quality: 630.00 Length: 112

Ratio: 5.625 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:

TGFB3P x AAQ56926 ..

Align seg 1/1 to: AAQ56926 from: 1 to: 2157

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
 278 GCTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGT 327

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
328 GGGCCCCCTCTACATTGACTTCGACAGGATCGGCTGGAGTGGGTCC 377
|||||
34 isGluProLysGlyTyrTrpAlaAsnPheCysSerGlyProCysProTyr 50
|||||
378 ATGAACCTAAGGCTACTATGCCAATCTGCTCAGGCTTGCCCATAC 427
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
428 CTCGCGAGTGCAGACACACACACAGCAGCGGTGCTGGGACTGTACAAAC 477
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||
478 TCTGAACCTGAAGCATCTGCTCGCTTGTGATGCCGCCAGGACCTGG 527
|||||
84 lUpProLeuThrIleLeuTyrTrpValGlyArgThrProLysValGluGln 100
|||||
528 AGCCCTTGACCATCTCTGCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 577
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
578 CTCTCCACATGGTGTGAAGTCTTGTAAATGTAGC 613
|||||

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52935

seq_documentation_block:
ID AAV52935 standard; cDNA: 2157 BP.

XX AC AAV52935;
XX DT 21-DEC-1998 (first entry)

XX DE Human transforming growth factor-beta 3 cDNA.
XX KW Transforming growth factor-beta 3; TGF-beta 3; human; ss.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 2..616

FT /*tag= a
FT /transl_except= (pos:50..52, aa:Thr)

XX US5801231-A.
XX PD 01-SEP-1998.

XX 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 22-MAR-1985; 85US-0715142.

XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PR 05-NOV-1993; 93US-0147364.
XX PR 30-MAY-1995; 95US-0454468.

XX (GETH) GENENTECH INC.
XX PI Derynck RMA, Goeddel DV;
XX DR WPI: 1998-494840/42.
XX DR P-PSDB; AAW8787.

XX DNA encoding transforming growth factor-beta precursor sequence -
XX useful for analysis to perform manipulations to increase yield of
XX recombinant production of the protein

XX Example 6; Fig 4a-c; 26pp; English.
XX This nucleotide sequence, hu4, codes for a human partial
XX transforming growth factor-beta 3 (TGF-beta 3) sequence including

CC all of the mature sequence. Clone hu4 was isolated from a human
CC ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934)
CC as probe. The inventory relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiased anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
XX
SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

alignment_scores:
Quality: 630.00 Length: 112
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:
TGF3P x AAV52935 ..

Align seg 1/1 to: AAV52935 from: 1 to: 2157

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
278 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGT 327

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
328 GCGCCCTCTACATTGACTTCGACAGGATCTGGGCTGGAGTGGGTCC 377

34 isGluProLysGlyTyrTrpAlaAsnPheCysSerGlyProCysProTyr 50
|||||
378 ATGAACCTAAGGCTACTATGCCAATCTGCTCAGGCTTGCCCATAC 427

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
428 CTCGCGAGTGCAGACACACACACAGCAGCGGTGCTGGGACTGTACAAAC 477

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
478 TCTGAACCTGAAGCATCTGCTCGCTTGTGATGCCGCCAGGACCTGG 527

84 lUpProLeuThrIleLeuTyrTrpValGlyArgThrProLysValGluGln 100
|||||
528 AGCCCTTGACCATCTCTGCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 577

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
578 CTCTCCACATGGTGTGAAGTCTTGTAAATGTAGC 613

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ02820

seq_documentation_block:
ID AAQ02820 standard; DNA: 2158 BP.

XX AC AAQ02820;
XX DT 31-MAY-1989 (first entry)

XX DE cDNA sequence encoding human TGF-beta 3.
XX KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX inhibition.

XX PN WO8912101-A.
XX PD 14-DEC-1989.
XX PF 08-JUN-1988; 88WO-US01945.

```

PR 08-JUN-1988; 88WO-U001945.
PA (GETH ) GENENTECH INC.
PI DERNYCK RM, Goeddel DV;
XX WPI; 1990-007474/01.
XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT probe; or to produce TGF beta 3, for inhibition of growth of normal
PT and neoplastic cells, eg A549.
XX Disclosure; Fig. 4; 6lpp; English.
PS
XX This sequence encodes human transforming growth factor-beta 3 (TGF-
CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
CC cell growth inhibition.
XX
SQ Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0 other;

alignment_scores:
    Quality: 630.00      Length: 112
    Ratio: 5.625        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:
TGFB3P x AAQ02820 ..

Align seg 1/1 to: AAQ02820 from: 1 to: 2158
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
278 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 327

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
328 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 377

34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
378 ATGAACCTAAGGCTACTATGCCAACTTCCTGCACAGGCCCTTGCCCATAC 427

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
428 CTCGCGAGTCAGACACCAACCCAGCAGCGGTCTGGGACTGTACACAC 477

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
478 TCTGAACCTGAAGCATCTGCCTGCCTCTGCTGCATGCCCCAGACCTGG 527

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
528 AGCCCTTGACCATCTCTACTATGTTGGAGGAGCCGCCAAAGTGGAGCAG 577

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
578 CTCTCCAACTGTGGTGAAGTCTTGTAATGTAGC 613

seq_name: /SIDSI/gcgdata/geneseq/geneseq/NA1992.DAT:AAQ22229
seq_documentation_block:
ID AAQ22229 standard; cDNA; 1239 BP.
XX
XX AC AAQ22229;
XX
DT 05-MAY-1992 (first entry)
XX
DE Mutant transforming growth Factor beta 3 coding sequence.
XX
XX TGF-beta 3; homodimer; ss.
XX

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..888 /*tag= a
FT /*note= "nucleotides 263-1150 of TGF-beta3"
FT misc_feature 889..903 /*tag= b
FT /*note= "encodes Factor Xa cleavage site
FT followed by a methionine residue"
FT misc_feature 904..1212 /*tag= c
FT /*note= "nucleotides 1163-1471 of TGF-beta3"
FT misc_difference 1213..1215 /*tag= d
FT /*note= "wild-type codon = ATG. May be replaced by
FT any other codon to give mutant sequence"
FT misc_feature 1216..1239 /*tag= e
FT /*note= "nucleotides 1475-1498 of TGF-beta3"
XX
XX WO9200318-A.
XX
XX 09-JAN-1992.
XX
XX 25-JUN-1991; 91WO-US04541.
XX
XX 25-JUN-1990; 90US-0543348.
XX
XX (ONCO-) ONCOGENE SCI INC.
XX
XX Iwata KK, Foulkes JG, Tendijke P, Haley JD;
XX
XX WPI; 1992-041510/05.
XX P-PSDB; AAR22038.
XX
XX Transforming growth factor beta 3 proteins, precursors and
PT mutants - obt'd. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence
XX
XX Claim 12; Page 66; 107pp; English.
XX
XX This sequence has been compiled from the description of a mutant TGF-
CC beta3 contained in the claims. The sequence coding for the Factor Xa
CC cleavage site may be replaced by one encoding a similar protease
CC recognition site, e.g. for collagenase. The coding sequence may
CC also include a region encoding a hydrophobic transmembrane amino
CC acid sequence, e.g. from c-erbB2 cDNA and a "stop transfer"
CC sequence. The protease recognition site is located between the
CC C-terminal of the transmembrane region and the N-terminal of the
CC TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently
CC cleaved from the membrane. See also AAQ20576 and AAR20622.
XX
XX Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;

```

```

alignment_scores:
    Quality: 627.00      Length: 112
    Ratio: 5.649        Gaps: 0
Percent Similarity: 99.107 Percent Identity: 99.107

alignment_block:
TGFB3P x AAQ22229 ..

Align seg 1/1 to: AAQ22229 from: 1 to: 1239
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
904 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 953

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
954 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 1003

```

```
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1004 ATGAACCTAAGGCTACTATGCCAATCTTGCTCAGGCCCTTGCCCATAC 1053
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1054 CTCGCGAGTGCAGACACACACACAGCAGCGGTGCTGGGACTGTACAAC 1103
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1104 TCTGAACCTGAAGCATCTGCTCGCTTGTCTGCGTCCCGCCAGGACCTG 1153
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1154 AGCCCTGTACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1203
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1204 CTCCTCAACNNGTGGTGAAGTCTTGTAAATGTAGC 1239
|||||
```

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52934

seq_documentation_block:

ID AAV52934 standard; cDNA; 2639 BP.

XX AC AAV52934;

XX 21-DEC-1998 (first entry)

XX Pig transforming growth factor-beta 3 cDNA.

XX Transforming growth factor-beta 3; TGF-beta 3; pig; ss.

XX Sus scrofa.

XX Key Location/Qualifiers

XX CDS 127..1497

XX /*tag= a

XX /transl_except= (pos:481..483, aa:Met)

XX US5801231-A.

XX 01-SEP-1998.

XX 22-MAR-1985; 85US-0715142.

XX 13-MAR-1987; 87US-0025423.

XX 22-MAR-1985; 85US-0715142.

XX 04-AUG-1989; 89US-0389929.

XX 04-MAR-1992; 92US-0845893.

XX 05-NOV-1993; 93US-0147364.

XX 30-MAY-1995; 95US-0454468.

XX (GETH) GENENTECH INC.

XX Derynck RNA, Goeddel DV;

XX WPI; 1998-494840/42.

XX P-PSDB; AAW78786.

XX DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein

XX Example 6; Fig 4a-c; 26pp; English.

XX This nucleotide sequence, termed 10+11.3, codes for the porcine
CC transforming growth factor-beta 3 precursor (prefGF-beta 3, see
CC AAW78786). A porcine ovarian cDNA library was screened using human
CC TGF-beta 1 cDNA (see AAV52933) as probe. A hybridising clone,
CC designated lambda 11.3, was used to rescreen the library to
CC identify clone lambda 10. The was combined with clone lambda 11.3

CC to provide the 10+11.3 sequence. The invention relates to the
CC recombinant production of TGF-beta. Biologically active TGF-beta
CC is defined as being capable of inducing EGF-potentiated anchorage
CC dependent growth of target cell lines and/or growth inhibition of
CC neoplastic cell lines. Nucleic acids encoding TGF-beta have been
CC isolated and cloned into vectors which are replicated in bacteria
CC and expressed in eukaryotic cells. TGF-beta recovered from
CC transformed cells is used in known therapeutic applications.
CC TGF-beta nucleic acids are also useful in diagnosis and
CC identification of TGF-beta clones.

XX
SQ Sequence 2639 BP; 677 A; 702 C; 697 G; 563 T; 0 other;

alignment_scores:

Quality: 621.00 Length: 112

Ratio: 5.595 Gaps: 0

Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:

TGFB3P x AAV52934 ..

Align seg 1/1 to: AAV52934 from: 1 to: 2639

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
1159 GCCCTGGACACCAACTACTGCTTCGCAATTGGAGGAGAACTGCTGTG 1208
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATTGACTTCGACAGGATCTGGCTGGAAAGTGGGTCC 1258
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGCTACTATGCCAATCTTGCTCAGGCCCTTGCCCATAC 1308
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCGCGAGTGCAGACACACACACAGCTCGGTGCTGGGGCTGTACAAC 1358
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCCGAAGCCTCGGCCCTCTCGTGTCTGCGTCCCGCCAGGACCTGG 1408
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTGTACCATCTGTACTATGCTGGGAGGACCCCAAGTGGAGCAG 1458
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1459 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1494
|||||
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seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56925

seq_documentation_block:

ID AAQ56925 standard; cDNA; 2669 BP.

XX AC AAQ56925;

XX 09-JUL-1994 (first entry)

XX Pig TGF-beta-3.

XX TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnerable; ss.

XX Sus scrofa.

XX US284763-A.

XX 08-FEB-1994.

XX

```

PF 22-MAR-1985; 85US-0715142.
PR 22-MAR-1985; 85US-0715142.
PR 13-MAR-1987; 87US-0025423.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynk RMA, Goeddel DV;
XX
XX WPI; 1994-056343/07.
XX P-PSDB; AAR46228.
XX
XX Nucleic acid sequences encoding transforming growth factor-beta -
XX diagnostic probes, and for use in therapeutics
XX
XX Disclosure; Fig 4a-c; 25pp; English.
XX
XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
XX pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
XX corresponding amino acid sequences were determined (AAR46227-29,
XX respectively). A genomic fragment corresponding to a human TGF-
XX beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
XX determined (AAR46230). The sequences have been used in the
XX construction of vectors for the expression of recombinant TGF-
XX beta.
XX
XX Sequence 2669 BP; 706 A; 702 C; 697 G; 564 T; 0 other;

alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:
TGFB3P x AAQ56925 ..
Align seg 1/1 to: AAQ56925 from: 1 to: 2669
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1159 GCCCTGGACACCACTACTGCTCCGCAATTTGGAGGAGAACTGCTGTG 1208
17 lArqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1209 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 1258
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1259 ATGAACCTAAGGCTACTATGCCAATTCGCTCAGGCCCTTGGCCGTAC 1308
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1309 CTCGGAGTGCAGACACACCCAGCTCGGTGCTGGGGCTGTACAACAC 1358
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1359 CCTGAACCCGGAAGCCTTCGCTCTCCGCTGCTGGTGGCCCGAGACCTGG 1408
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
1409 AGCCCTTGACATCTCTACTAGCTCGGGAGGACCCCAAGGTGGAGCAG 1458
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1459 CTCTTAACATGTGTGTGAAGTCTCTGCAAGTGCAGC 1494

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03303
seq_documentation_block:
ID AAQ03303 standard; DNA; 2671 BP.

```

```

XX AAQ03303;
XX
XX 05-AUG-1990 (first entry)
XX
XX Entire porcine transforming growth factor (TGF) beta-3 cDNA sequence.
XX
XX Porcine transforming growth factor (TGF) beta-3; human ovarian cDNA;
XX human transforming growth factor (TGF) beta-3.
XX
XX Porcine.
XX
XX US4886747-A.
XX
XX 12-DEC-1989.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX 13-MAR-1987; 87US-0025423, US-715142.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1990-051338/07.
XX
XX Nucleic acid encoding transforming growth factor-beta -
XX cloned into expression vectors for expression in eukaryotic host
XX calls for therapeutic use
XX
XX Disclosure; Fig 4a-c; 28pp; English.
XX
XX It was used to screen plaques from a human ovarian cDNA library to find
XX human TGF-beta-3.
XX
XX Sequence 2671 BP; 706 A; 705 C; 699 G; 561 T; 0 other;

alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:
TGFB3P x AAQ03303 ..
Align seg 1/1 to: AAQ03303 from: 1 to: 2671
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1159 GCCCTGGACACCACTACTGCTCCGCAATTTGGAGGAGAACTGCTGTG 1208
17 lArqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1209 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 1258
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1259 ATGAACCTAAGGCTACTATGCCAATTCGCTCAGGCCCTTGGCCGTAC 1308
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1309 CTCGCCAGTGCAGACACACCCAGCTCGGTGCTGGGGCTGTACAACAC 1358
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1359 CCTGAACCCGGAAGCCTTCGCTCTCCGCTGCTGGTGGCCCGAGACCTGG 1408
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1409 AGCCCTTGACATCTCTACTAGCTCGGGAGGACCCCAAGGTGGAGCAG 1458
101 LeuSerAsnMetValValLysSerCysLysCysSer 112

```

1459 CTCTTAACATGCTGTGAAGTCTCTCAAGTCGACG 1494

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA06496

seq_documentation_block:

ID AA06496 standard; cDNA; 498 BP.

XX AC AA06496;

XX DT 12-JUN-1996 (first entry)

XX DE Tissue-derived tumour growth inhibitor-1 coding sequence.

XX KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
XX KW arteriosclerosis; inflammation; psoriasis; therapy; vulnery;

XX KW immunomodulator; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT CDS 1..498

XX FT /*tag= a

XX FT /product= tumour_growth_inhibitor_precursor

XX FT /note= "see AAR86771"

XX FT misc_feature 159..160

XX FT /*tag= b

XX FT /note= "the codons at positions -40 to -1 (i.e. 117
nucleotides) are not given in the
specification"

XX FT mat_peptide 160..495

XX FT /*tag= c

XX FT /product= mature_tumour_growth_inhibitor

XX FT /note= "see AAR86770"

XX PN EP684260-A2.

XX XX 29-NOV-1995.

XX XX 20-OCT-1987; 87EP-0109866.

XX XX 20-OCT-1986; 86US-0922121.

XX XX (ONCO-) ONCOGENE SCI INC.

XX XX Gold LI, Iwata KK, Stephenson JR;

XX XX WPI; 1996-000991/01.

XX XX P-PSDB; AAR86770, AAR86771.

XX XX Tissue-derived growth inhibitor and corresponding genes - useful for
XX PT detection of tumours, inhibition of tumour growth, treatment of
XX PT proliferative disorders and healing of burns and wounds.

XX PS Claim 6; Fig 29; 83pp; English.

XX CC The sequence encodes a 112 amino acid tumor growth inhibitor (TGI)
XX CC (AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an
XX CC additional 93 amino acid residues at the N-terminus. However, the
XX CC nucleotides representing codons -40 to -1 of the precursor TGI are
XX CC not specified in Figure 29, i.e. the cDNA is 498 nucleotides in
XX CC length, but should be 615 nucleotides long. The DNA is used to
XX CC produce the inhibitors by recombinant methods i.e. vector
XX CC expression in bacterium or eukaryotic host cells. The proteins can
XX CC be used to inhibit the growth of human tumour cells, e.g.
XX CC carcinoma, melanoma or leukaemia cells, in the treatment of
XX CC proliferative disorders e.g. arteriosclerosis, inflammation and
XX CC psoriasis, or for the treatment of burns to facilitate wound
XX CC healing. They can also be used as immunomodulators. Although the
XX CC proteins have tumour growth inhibitory activity, they are not
XX CC transforming growth factor-beta-1 or -beta-2.

XX SQ Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;

alignment_scores:
Quality: 620.00 Length: 112
Ratio: 5.586 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214
alignment_block:
TGFB3P x AAT06496 ..
Align seg 1/1 to: AAT06496 from: 1 to: 498
1 AlAlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
160 GCTTTGGACCACTTACTGCTTCGCAACTTGGAGGAGAACTGTTGT 209
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIysTrpValH 34
210 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 259
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
260 ATCAACCTAAGGCTACTATGCCAACTTCCTCAGCCCTTGCCCATAC 309
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
310 CTCGGCAGTGCACACACCAACCCACAGCAGCGTCTGGGACTGTACAAC 359
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
360 TCTGAACCCCTGAAGCATCTGCCTGGCCTTCTGCGTCCCGCCAGACCTGG 409
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
410 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 459
101 LeuSerAsnMetValLysSerCysLysCysSer 112
460 CTCCTCAACATGCTGCTGAAGTCTTGTAAATGTAGC 495

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AA006845

seq_documentation_block:

ID AA006845 standard; cDNA; 2530 BP.

XX AC AA006845;

XX DT 05-MAR-1991 (first entry)

XX DE Sequence encoding tumour growth inhibitor.

XX KW TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
XX KW psoriasis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT CDS 263..1501

XX FT /*tag= a

XX FT polyA_signal 2506..2511

XX FT /*tag= b

XX FT polyA_site 2529

XX FT /*tag= c

XX PN WO9014360-A.

XX XX 29-NOV-1990.

XX XX 17-MAY-1990; 90WO-US02753.

XX XX 17-MAY-1989; 89US-0353410.

XX XX 19-APR-1985; 85US-0725003.

XX XX 07-APR-1986; 86US-0847931.

```
PR 20-OCT-1986; 86US-0992121.
PR 20-OCT-1987; 87US-0111022.
PR 20-APR-1988; 88US-0183224.
XX
XX (ONCO-) ONCOGENE SCI INC.
XX
XX Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX
XX WPI; 1990-375949/50.
DR P-PSDB; AAR08264.
XX
XX Tissue-derived tumour growth inhibitors - comprise specified
PT protein sequences used to detect, and treat tumours, burns and
PT wounds.
XX
XX Claim 10; Fig 41; 190pp; English.
XX
XX The plasmid was isolated from a human cDNA library prepd. from the
CC DNA of a chronic myelocytic leukaemia cell line (K562). The
CC sequence can be used to produce the tumour growth inhibitor (TGI)
CC by recombinant techniques. The protein may also be isolated from
CC human umbilical cord and placental tissues. It can be used to
CC inhibit tumour cell growth, to treat burns, to facilitate the
CC healing of wounds or to treat proliferative disorders. The
CC protein and Abs raised to it can be used for detection and typing
CC of tumours. The Abs can also be used to inhibit the activity of
CC the TGI.
XX
XX Sequence 2530 BP; 619 A; 671 C; 659 G; 581 T; 0 other;

alignment_scores:
Quality: 617.00 Length: 112
Ratio: 5.559 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 97.321

alignment_block:
TGFB3P x AAQ06845 ..
Align seg 1/1 to: AAQ06845 from: 1 to: 2530
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1163 GCTTTGGACACCAATTAATGCTTCGCAACTTGGAGGAGAACTGCTGTGT 1212
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1213 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 1262
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1263 ATGAACCTAAGGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCATAC 1312
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1313 CTCGCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAAAC 1362
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1363 TCTGAACCTGAAGCATCTGCTTCGCTTGTCTGCTGCGTGGCCCGAGACCTGG 1412
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1413 AGCCCTGTGACCTCCCTGTACTATGTTGGGAGGACCCCAAGAGTGGAGCAAG 1462
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1463 CTCCTCAACATGGTGTGAAGTCTTGTAAATGTAGC 1498
seq_name: /SID81/gcgdata/geneseq/geneseq/NA1990.DAT:AAQ02819
seq_documentation_block:
ID AAQ02819 standard; DNA; 2676 BP.
```

```
XX
AC AAQ02819;
XX
XX 31-MAY-1989 (first entry)
XX
XX cDNA sequence encoding porcine TGF-beta 3.
XX
XX Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.
KW
XX WO8912101-A.
XX
XX 14-DEC-1989.
XX
XX 08-JUN-1988; 88WO-US01945.
XX
XX 08-JUN-1988; 88WO-UO01945.
XX
XX (GETH ) GENENTECH INC.
XX
XX Dernyck RM, Goeddel DV;
XX
XX WPI; 1990-007474/01.
XX
XX P-PSDB; AAR04080.
XX
XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT probe, or to produce TGF beta 3, for inhibition of growth of normal
PT and neoplastic cells, eg A549.
XX
XX PS Disclosure; Fig. 4; 61pp; English.
XX
XX This sequence encodes porcine transforming growth factor-beta 3 (TGF-
CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
CC cell growth inhibition.
XX
XX Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other;

alignment_scores:
Quality: 612.00 Length: 112
Ratio: 5.564 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 97.321

alignment_block:
TGFB3P x AAQ02819 ..
Align seg 1/1 to: AAQ02819 from: 1 to: 2676
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1175 GCCCTGGACACCACTACTCTCTCCGCAATTTGGAGGAGAACTGCTGTGT 1224
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1225 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 1274
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1275 ATGAACCTAAGGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCATAC 1324
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1325 CTCGCGAGTGCAGACACACCAACACAGCAGCGTCTGGGACTGTACAAAC 1374
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1375 TCTGAACCTGAAGCATCTGCTTCGCTTGTCTGATGCCCGCCAGGACCTGG 1424
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1425 AGCCCTGACCATCTCTGTACTACTACGTGCGGAGGACCCCAAGTGGAGCAG 1474
```

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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1475 CTTCTAATGCTGGTGAAGTCCGCAAGTCGACG 1510

seq_name: /SIDSL/gcgdata/geneseq/NA1993.DAT:AAQ41603
seq_documentation_block:
ID AAQ41603 standard; cDNA; 336 BP.
XX
XX AAQ41603;
XX
XX 26-AUG-1993 (first entry)
XX
XX Transforming Growth Factor-beta1(44/45)beta3 hybrid.
XX
XX hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
XX cancer treatment; bone repair; growth regulation; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX mat_peptide 1..336
XX /*tag= a
XX /note= "TGF-beta1=1-132, TGF-beta3=133-336"
XX
XX EP542679-A.
XX
XX 19-MAY-1993.
XX
XX 03-NOV-1992; 92EP-0810845.
XX
XX 11-NOV-1991; 91EP-0810870.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
XX
XX P-PSDB; AAR39642.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
XX portions of mature TGF-beta isoforms; useful as wound healants,
XX cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 8; Page 26-27; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
XX of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX derived from different parent isoforms are pref. between amino acids
XX 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
XX possible hybrids using these hinge points and one part each
XX from two of the isoforms, 6 are preferred including the hybrid
XX TGF-beta1(44/45)beta3. The hybrid molecules promote cell migration,
XX inhibit the growth of A375 melanoma cells, accelerate the healing of
XX partial-thickness burn wounds and full-thickness incisional wounds and
XX increase formation of fibrous granular tissue.
XX See AAQ41602-Q41607 for the most pref. hybrids.
XX
XX Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:
Quality: 595.00 Length: 112
Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:
TGFB3P x AAQ41603 ..
Align seg 1/1 to: AAQ41603 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

```

```

|||||
1 GCCTGGACACCAACTATTGCTTTCAGCTCCACGAGAAAGAACTGCTCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 CGGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGGCAGTGCAGACACACACCCACAGCACGCTGCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCCCTGAAGCATCTGCCCTTGTGCGTCCCGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCTCCAACATGCTGGTGAAGTCTTGTAAATGTAGC 336

```

seq_name: /SIDSL/gcgdata/geneseq/NA1996.DAT:AA17237

seq_documentation_block:

```

ID AA17237 standard; DNA; 336 BP.
XX
XX AA17237;
XX
XX 17-JUL-1996 (first entry)
XX
XX Hybrid TGF-beta 1-3 DNA.
XX
XX Transforming growth factor type beta; TGF-beta 1; TGF-beta 3;
XX protein renaturation; protein folding; ds.
XX
XX Synthetic.
XX
XX WO9603433-A1.
XX
XX 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02719.
XX
XX 25-JUL-1994; 94EP-0810439.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Cerletti N;
XX
XX WPI; 1996-117000/12.
XX
XX P-PSDB; AAR92775.
XX
XX Prodn. of dimeric biologically active transforming growth factor
XX by refolding denatured monomer in detergent-free folding buffer
XX contg. specific organic solvent to improve yield
XX
XX Example 10; Page 36-37; 54pp; English.
XX
XX A DNA sequence (AA17237) codes for a recombinant hybrid of human
XX transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which
XX the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773)
XX and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772).
XX The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
XX 1(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was
XX recovered from E. coli transformants. A biologically active,
XX dimeric form of the hybrid was obtd. by refolding the monomer in
XX detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers

```


CC TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR92777) were similarly
CC produced.
XX
SQ Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:
Quality: 595.00 Length: 112
Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:
TGFB3P x AAT17237 ..

Align seg 1/1 to: AAT17237 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCGAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCTACCACTTGTCTCAGGCGCTTCCGCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACACGACGCTGCTGGACTGTACAAAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAGCATCTGCGCTTGTCTGCGTGGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGTGACCTCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG 300
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGTGAAGTCTTGTAAATGTAGC 336

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1996.DAT:AAT15465

seq_documentation_block:

ID AAT15465 standard; cDNA to mRNA; 336 BP.

XX AAT15465;

AC 10-JUN-1996 (first entry)

DE cDNA encoding human TGF-beta-like protein, TGF-beta-1-3.

XX Transforming growth factor beta; TGF; regulator; method;
KW proliferation; differentiation; wound healing; solvent; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..336

FT /*tag= a
FT /product= hybrid_TGF-beta-1-3
FT 1..132

FT /*tag= b
FT /note= "encodes N-terminal 44 amino acids of
FT TGF-beta-1"

FT mat_peptide 133..336

FT /*tag= c
FT /note= "encodes C-terminal 68 amino acids of
FT TGF-beta-3"

XX

PN WO9603432-A1.
XX
PD 08-FEB-1996.
XX
PF 12-JUL-1995; 95WO-EP02718.
XX
PR 25-JUL-1994; 94EP-0810438.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Cerletti N;
XX
DR WPI; 1996-116999/12.
DR P-PSDB; AAR91959.
XX
PT Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
PS Claim 17; Page 39-40; 59pp; English.
XX
CC AAT15465 encodes transforming growth factor (TGF) beta-like protein,
CC TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta
CC hybrids were made using a new process of producing dimeric,
CC biologically active TGF beta-like proteins. The new process involves
CC treating denatured TGF beta monomers with folding buffer contg. a
CC mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC DMF (dimethyl formamide). The detergent allows folding of the monomer
CC such that, after dimerisation, the TGF beta-like protein retains
CC biological activity and remains in soluble form. The method allows
CC relatively high yields of biologically active TGF beta-like proteins
CC in their native dimeric form. TGF-beta like proteins are multifunctional
CC regulators of cellular activity and a typical use is to stimulate wound
XX healing.
SQ Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:

Quality: 595.00 Length: 112
Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:

TGFB3P x AAT15465 ..

Align seg 1/1 to: AAT15465 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCGAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCTACCACTTGTCTCAGGCGCTTCCGCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACGACGCTGCTGGACTGTACAAAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAGCATCTGCGCTTGTCTGCGTGGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGTGACCTCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG 300

```
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGTGAAGTCTTGTAATAATGTCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41605
seq_documentation_block:
ID AAQ41605 standard; cDNA; 336 BP.
XX AC
XX AAQ41605;
XX DT
XX 26-AUG-1993 (first entry)
DE Transforming Growth Factor-beta2(44/45)beta3 hybrid.
XX DE
XX KW hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX OS
XX Homo sapiens.
XX FH Key Location/Qualifiers
FT mat_peptide 1..336
FT FT /*tag= a
FT FT /note= "TGF-beta2=1-132, TGF-beta3=133-336"
XX PN EP542679-A.
XX PD 19-MAY-1993.
XX PF 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX PS (CIBA ) CIBA GEIGY AG.
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX DR WPI; 1993-161126/20.
XX DR P-PSDB; AAR39644.
XX PT New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 8; Page 29-30; 48pp; English.
XX CC The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-Q41607 for the most pref. hybrids.
XX SQ Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;

alignment_scores:
Quality: 591.00 Length: 112
Ratio: 5.373 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 91.071

alignment_block:
TGFβ3P x AAQ41605 ..
Align seg 1/1 to: AAQ41605 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
```


CC TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were similarly
XX produced.
SQ Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0
Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x AAT17239 ..

Align seg 1/1 to: AAT17239 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCATTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGGCTACTATGCCAACTCTGTGCTGGAGCATGCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| |
151 TTATGGAGTTTCACACACTCAGCACAGGAGTCTTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|:::|
201 CATAAATCCAGAGCATCTGCTCTCTGCTGCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTGCAAAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT.AAT15467

seq_documentation_block:

ID AAT15467 standard; cDNA to mRNA; 336 BP.

XX AC AAT15467;

XX DT 10-JUN-1996 (first entry)

XX DE cDNA encoding human TGF-beta-like protein, TGF-beta-3-2.

XX KW Transforming growth factor beta: TGF; regulator; method;
KW proliferation; differentiation; wound healing; solvent; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..336

FT /*tag= a

FT /product= hybrid_tgf-beta-3-2

FT mat_peptide 1..132

FT /*tag= b

FT /note= "encodes N-terminal 44 amino acids of
FT TGF-beta-3"

FT mat_peptide 133..336

FT /*tag= c

FT /note= "encodes C-terminal 68 amino acids of
FT TGF-beta-2"

PN W09603432-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02718.

XX PR 25-JUL-1994; 94EP-0810438.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-116999/12.

XX DR P-PSDB; AAR91961.

XX PT Prodn. of dimeric, biologically active transforming growth factor
XX beta - by refolding denatured monomer in buffer contg. mild
XX detergent and specific organic solvents to improve yields

XX PS Claim 17; Page 44-45; 59pp; English.

XX AAT15467 encodes transforming growth factor (TGF) beta-like protein,
CC TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta
CC hybrids were made using a new process of producing dimeric,
CC biologically active TGF beta-like proteins. The new process involves
CC treating denatured TGF beta monomers with folding buffer contg. a
CC mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC DMF (dimethyl formamide). The detergent allows folding of the monomer
CC such that, after dimerisation, the TGF beta-like protein retains
CC biological activity and remains in soluble form. The method allows
CC relatively high yields of biologically active TGF beta-like proteins
CC in their native dimeric form. TGF-beta like proteins are multifunctional
CC regulators of cellular activity and a typical use is to stimulate wound
XX healing.

SQ Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0
Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x AAT15467 ..

Align seg 1/1 to: AAT15467 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

1 GCATTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||

51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 100
|||||

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||

101 ATGAACCTAAGGGCTACTATGCCAACTCTGTGCTGGAGCATGCCGTAT 150
|||||

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| |

151 TTATGGAGTTTCACACACTCAGCACAGGAGTCTTGAGCTTATATAATAC 200
|||||

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|:::|

201 CATAAATCCAGAGCATCTGCTCTCTGCTGCTGCTGCCAAGATTAG 250
|||||

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||

251 AACCTCTAACCATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
|||||

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTATATGATTGTAAGTCTTGCAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41602

seq_documentation_block:
ID_AAQ41602 standard; cDNA; 336 BP.

XX AAQ41602;

XX 26-AUG-1993 (first entry)

XX Transforming Growth Factor-beta1(44/45)beta2 hybrid.

XX hTGF-beta1; hTGF-beta2; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH 1..336
FT mat_peptide /*tag= a
FT /note= "TGF-beta1-1-132, TGF-beta2=133-336"
XX EP542679-A.
XX 19-MAY-1993.
XX 03-NOV-1992; 92EP-0810845.
XX 11-NOV-1991; 91EP-0810870.
XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39641.
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX Claim 8; Page 25-26; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See also AAQ41603-041607 for the other pref. hybrids.
XX Sequence 336 BP; 90 A; 92 C; 72 G; 82 T; 0 other;

SQ

alignment_scores:
Quality: 539.00 Length: 112
Ratio: 5.183 Gaps: 0
Percent Similarity: 92.857 Percent Identity: 81.250

alignment_block:

TGFB3P x AAQ41602 ..

Align seg 1/1 to: AAQ41602 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

|||||
1 GCCTTGACACCACCACTATTGCTTCAGCTCCACGGAGAAAGACTGCTCGGT 50
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||
51 GCGGACAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGTGTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
151 TTATGGAGTTTCAGACACTCAGCAGCAGGGTCTGTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41606

seq_documentation_block:

ID_AAQ41606 standard; cDNA; 336 BP.

XX AAQ41606;

XX 26-AUG-1993 (first entry)

XX Transforming Growth Factor-beta3(44/45)beta1 hybrid.

XX hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH 1..336
FT mat_peptide /*tag= a
FT /note= "TGF-beta3-1-132, TGF-beta1-133-336"
XX EP542679-A.
XX 19-MAY-1993.
XX 03-NOV-1992; 92EP-0810845.
XX 11-NOV-1991; 91EP-0810870.
XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39645.
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX Claim 8; Page 30-31; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids


```

1  GCTTTGGATCGCGCTATTGCTTTAGAAATGTCAGGATAAATGCTGCCT 50
17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  ACCTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAATGGATAC 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  ACGAACCCAAAGGGTACAATGCCAACTTCTGCTGGAGCATGCCCGTAT 150
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151  TTATGGAGTTCAGACACTCAGCACAGCAGGGTCTGAGCTTATATATAC 200
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201  CATAAATCCAGAAGCATCTGCTTCTGCTGCGTGTCCCAAGATTAG 250
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251  AACCTCTAACCATTTCTACTACTGATTGGCAAAACACCCCAAGATTGAAC 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  LeuSerAsnMetValValLysSerCysLysCysSer 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301  CTTTCTAATATGATTGTAAGTCTTGCAAATGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA15463

seq_documentation_block:

ID AA15463 standard; cDNA to mRNA; 339 BP.

XX AC AA15463;

XX DT 10-JUN-1996 (first entry)

XX DE Human transforming growth factor beta 2 encoding cDNA.

XX KW Transforming growth factor beta; TGF; regulator; method;
XX KW proliferation; differentiation; wound healing; solvent; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..339

XX FT /*tag= a

XX FT /product= human_TGF-beta-2

XX FN W09603432-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02718.

XX PR 25-JUL-1994; 94EP-0810438.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-116999/12.

XX DR P-PSDB; AAR91957.

XX PT Prodn. of dimeric, biologically active transforming growth factor
XX PT beta - by refolding denatured monomer in buffer contg. mild
XX PT detergent and specific organic solvents to improve yields

XX PS Example 1; Page 34-35; 59pp; English.

XX CC AA15462-T15464 encode transforming growth factor (TGF) beta-1,

XX CC TGF beta-2 and TGF beta-3 which are produced using recombinant

XX CC DNA technology and used to produce TGF beta-like proteins in

XX CC dimeric form. The TGF beta-like proteins produced are hybrids of

XX CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc.

CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
CC made using a new process of producing dimeric, biologically active
CC TGF beta-like proteins. The new process involves treating denatured
CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CC CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
CC The detergent allows folding of the monomer such that, after
CC dimerisation, the TGF beta-like protein retains biological activity
CC and remains in soluble form. The method allows relatively high yields
CC of biologically active TGF beta-like proteins in their native dimeric
CC form. TGF-beta like proteins are multifunctional regulators of
CC cellular activity and a typical use is to stimulate wound healing.

XX SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

alignment_scores:

Quality: 535.00 Length: 112

Ratio: 5.095 Gaps: 0

Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:

TGFB3P x AA15463 ..

Align seg 1/1 to: AA15463 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

1 GCTTTGGATCGCGCTATTGCTTTAGAAATGTCAGGATAAATGCTGCCT 50

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

101 ACGAACCCAAAGGGTACAATGCCAACTTCTGCTGGAGCATGCCCGTAT 150

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

151 TTATGGAGTTCAGACACTCAGCACAGCAGGGTCTGAGCTTATATATAC 200

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

201 CATAAATCCAGAAGCATCTGCTTCTGCTGCGTGTCCCAAGATTAG 250

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

251 AACCTCTAACCATTTCTACTACTGATTGGCAAAACACCCCAAGATTGAAC 300

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

301 CTTTCTAATATGATTGTAAGTCTTGCAAATGCAGC 336

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AA142772

seq_documentation_block:

ID AA142772 standard; cDNA; 339 BP.

XX XX

XX AC AA142772;

XX XX

XX DT 26-AUG-1997 (first entry)

XX XX

XX DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX XX

XX KW Transforming growth factor-beta fusion protein; wound healing;

XX KW artificial skin; surgery recovery time; ss.

XX XX

XX OS Homo sapiens.

XX XX

XX FH Key Location/Qualifiers

XX FT CDS 1..339

XX FT /*tag= a


```

alignment_block:
TGFB3P x AAX15246 ..
Align seg 1/1 to: AAX15246 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
1 GCCTTGGATGCGCGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 50
17 lArgProLeuThrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAAATGCCAACTTCTGTCTGGAGCATGCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TATGGAGTTCAGACACTCAGCAGCAGAGGGTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAAAGCATCTGCTTCTCTTGTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACTATGTCACAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336
seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1999.DAT:AAV99376
seq_documentation_block:
ID AAV99376 standard; cDNA; 339 BP.
XX AC AAV99376;
XX DT 25-MAR-1999 (first entry)
DE cDNA encoding a transforming growth factor beta active fragment.
KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW bone morphogenetic protein; transforming growth factor beta;
KW active fragment; wound healing; bone growth; purification tag; ds.
XX OS Homo sapiens.
XX PN WO9855137-A1.
XX PD 10-DEC-1998.
XX PF 02-JUN-1998; 98WO-US11189.
XX PR 03-JUN-1997; 97US-0868452.
XX PA (HALL/) HALL F L.
XX PA (HANB/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX DR WPI: 1999-059875/05.
XX DR P-FSDB; AAW84208.
XX PT New bone morphogenetic fusion proteins - comprising a purification
XX tag and a bone morphogenetic active fragment, used for enhancing
XX wound healing or bone growth
XX
PS Disclosure; Page 42; 64pp; English.
XX The present sequence encodes a transforming growth factor beta active
XX fragment. The protein can be used in place of a bone morphogenetic
XX active fragment to create the fusion proteins of the invention. When a
XX bone morphogenetic active fragment is used, the fusion proteins are
XX designated bone morphogenetic fusion proteins. The bone morphogenetic
XX fusion protein may contain some or all of the following elements: a
XX purification tag, a proteinase site, an ECM/bone binding site, a second
XX proteinase site, and a bone morphogenetic protein active fragment.
XX The bone morphogenetic fusion proteins can be used for enhancing wound
XX healing or bone growth.
XX Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
XX
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x AAV99376 ..
Align seg 1/1 to: AAV99376 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
1 GCCTTGGATGCGCGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 50
17 lArgProLeuThrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAAATGCCAACTTCTGTCTGGAGCATGCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TATGGAGTTCAGACACTCAGCAGCAGAGGGTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAAAGCATCTGCTTCTCTTGTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACTATGTCACAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336
seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1999.DAT:AAV99376
seq_documentation_block:
ID AAV99376 standard; cDNA; 339 BP.
XX AC AAV99376;
XX DT 25-MAR-1999 (first entry)
DE cDNA encoding a transforming growth factor beta active fragment.
KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW bone morphogenetic protein; transforming growth factor beta;
KW active fragment; wound healing; bone growth; purification tag; ds.
XX OS Homo sapiens.
XX PN WO9855137-A1.
XX PD 10-DEC-1998.
XX PF 02-JUN-1998; 98WO-US11189.
XX PR 03-JUN-1997; 97US-0868452.
XX PA (HALL/) HALL F L.
XX PA (HANB/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX DR WPI: 1999-059875/05.
XX DR P-FSDB; AAW84208.
XX PT New bone morphogenetic fusion proteins - comprising a purification
XX tag and a bone morphogenetic active fragment, used for enhancing
XX wound healing or bone growth
XX
PS Disclosure; Page 42; 64pp; English.
XX The present sequence encodes a transforming growth factor beta active
XX fragment. The protein can be used in place of a bone morphogenetic
XX active fragment to create the fusion proteins of the invention. When a
XX bone morphogenetic active fragment is used, the fusion proteins are
XX designated bone morphogenetic fusion proteins. The bone morphogenetic
XX fusion protein may contain some or all of the following elements: a
XX purification tag, a proteinase site, an ECM/bone binding site, a second
XX proteinase site, and a bone morphogenetic protein active fragment.
XX The bone morphogenetic fusion proteins can be used for enhancing wound
XX healing or bone growth.
XX Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
XX
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x AAV99376 ..
Align seg 1/1 to: AAV99376 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
1 GCCTTGGATGCGCGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 50
17 lArgProLeuThrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAAATGCCAACTTCTGTCTGGAGCATGCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TATGGAGTTCAGACACTCAGCAGCAGAGGGTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAAAGCATCTGCTTCTCTTGTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACTATGTCACAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336
seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1999.DAT:AAV99376
seq_documentation_block:
ID AAV99376 standard; cDNA; 1695 BP.
XX AC AAT05877;
XX DT 25-JUN-1996 (first entry)
DE cDNA encoding transforming growth factor-beta 2.
XX KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
XX interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
XX nitric oxide production; hypotension; inflammation; septic shock;
XX treatment; ds.
XX OS Mammalian sp.
XX FH Mammalian sp.
XX Location/Qualifiers
XX Key
XX

```

```

FT CDS 182..1426
FT /*tag= a
FT /product= transforming growth factor-beta 2
XX
PN W09526745-A1.
XX
XX 12-OCT-1995.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX 05-APR-1994; 94WO-US03705.
XX (HARD ) HARVARD COLLEGE.
XX
XX Lee M, Perrella MA;
XX
XX WPI; 1995-358443/46.
XX P-PSDB; AAR83055.
XX
XX Treatment of hypotension, esp. in septic shock - by administering
XX transforming growth factor-beta e.g. to inhibit inducible nitric
XX oxide synthase gene transcription
XX
XX Disclosure; Fig 16; 52pp; English.
XX
XX The CDNA encodes transforming growth factor-beta 2 (TGF-beta 2) which
XX has been found to inhibit inducible nitric oxide synthase (iNOS) gene
XX transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
XX smooth muscle cells, and at a dose which does not inhibit constitutive
XX NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
XX in the treatment of hypotension, such as that associated with severe
XX inflammation or septic shock.
XX
XX Sequence 1695 BP; 523 A; 386 C; 354 G; 432 T; 0 other;
SQ

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x AAY05877 ..
Align seg 1/1 to: AAT05877 from: 1 to: 1695
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1088 GCTTGGATCGGCCCTATTGCTTTAGAATGTGCAGATAATGTGCTGCT 1137
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1138 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1188 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCGTAT 1237
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 57
1238 TTATGGAGTTCAGACACTCAGCAGCAGGAGGTCCTGAGCTTATATAATAC 1287
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1288 CATAATCCAGAGCATCTGCTTCTCCTGTGCTGCTGCCAAGATTAG 1337
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1338 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCAAGATTGAACAG 1387
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1388 CTTTCTAATATGATTGTAAGTCTTGGCAATGCAGC 1423
```

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20291
seq_documentation_block:
ID AAQ20291 standard; cDNA; 2208 BP.
XX
XX AC AAQ20291;
XX
XX DT 16-APR-1992 (first entry)
XX
XX DE Sequence encoding hybrid transforming growth factor (TGF)-
XX beta-1/beta-2.
XX
XX KW Hypertension therapy; hypotensive agent; blood pressure modulator;
XX ss.
XX
XX OS Homo sapiens and monkey.
XX
XX FH Key Location/Qualifiers
XX CDS 262..282
XX FT /*tag= a
XX FT sig_peptide 283..324
XX FT /*tag= b
XX FT CDS 325..1095
XX FT /*tag= c
XX FT mat_peptide 1096..1434
XX FT /*tag= d
XX FT polyA_site 2208
XX FT /*tag= e
XX
XX PN W09119513-A.
XX
XX PD 26-DEC-1991.
XX
XX PF 20-JUN-1991; 91WO-US04449.
XX
XX PR 20-JUN-1990; 90US-0541221.
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX PI Oleson FB, Comereski CR;
XX
XX DR WPI; 1992-024199/03.
XX
XX DR P-PSDB; AAR20126.
XX
XX PT Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX PS Disclosure; Fig 3; 42pp; English.
XX
XX CC A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX complex.
XX
XX SQ Sequence 2208 BP; 599 A; 576 C; 534 G; 499 T; 0 other;

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x AAQ20291 ..
Align seg 1/1 to: AAQ20291 from: 1 to: 2208
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
```

```
|||||: 1096 GCTTTGGATGCGGCTATTGCTTTAGAATGTCAGGATAATGCTGCT 1145
17 largProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
:|||||: 1146 AGCTCCACTTTACATGATTCAAGAGGATCTAGGTTGAATGGATAC 1195
34 IsGluProLysGlyTyriTyriAlaAsnPheCysSerGlyProCysProTyri 50
|||||: 1196 AGCAACCCAAAGGGTACAATGCCAACTTCTGCTGGAGCATGCCGTAT 1245
51 LeuArgSerAlaAspThrThriHisSerThrValLeuGlyLeuTyriAsnTh 67
|||||: 1246 TTATGGAGTTACAGACCTACAGACAGCAGGTCCTGAGCTTATATAATAC 1295
67 rleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
:|||||: 1296 CATAATCCAGAGCATCTGCTTCCTTCCTGCTGCTGCCAAGATTAG 1345
84 luProLeuThrIleLeuTyriValGlyArgThrProLysValGluGln 100
|||||: 1346 AACCTCTAACCATCTCTACTACATTGGCAAAACACCAAGATTGAACAG 1395
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||: 1396 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1431
seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1989.DAT: AAN90767

seq_documentation_block:
ID AAN90767 standard; cDNA; 2568 BP.
XX AC AAN90767;
XX PD 23-DEC-1990 (first entry)
XX DE Sequence of human transforming growth factor (TGF) beta-2 precursor
XX DE 442 cDNA in pPC-21.
XX KW Cell differentiation; cell proliferation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT misc_feature 466..1791 /*tag= a
FT CDS 466..1794 /*note="Claimed"
FT sig_peptide 475..522 /*tag= b
FT mat_peptide 1456..1794 /*tag= c
FT misc_feature 811..897 /*tag= d
FT /*tag= e
FT /*note="This entire SQ is replaced with AAT in simian
FT TGF-beta-2-414 cDNA"
FT misc_difference 493 /*tag= f
FT /*label=T
FT /*note="Possible sequencing error"
FT misc_difference 942 /*tag= g
FT /*label=G
FT /*note="Possible sequencing error"
FT misc_difference 1053 /*tag= h
FT /*label=G
FT /*note="Possible sequencing error"
FT misc_difference 1077 /*tag= i
FT /*label=C
FT /*note="Possible sequencing error"
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FT misc_difference 1143 /*tag= j
FT /*label=T
FT /*note="Possible sequencing error"
FT misc_difference 1282 /*tag= k
FT /*label=T
FT /*note="Possible sequencing error"
FT misc_difference 1509 /*tag= l
FT /*label=G
FT /*note="Possible sequencing error"
FT misc_difference 1566 /*tag= m
FT /*label=A
FT /*note="Possible sequencing error"
FT misc_difference 1698 /*tag= n
FT /*label=C
FT /*note="Possible sequencing error"
FT misc_difference 1017 /*tag= o
FT /*label=T
FT /*note="Possible sequencing error"
FT polyA_site 2568 /*tag= p
FT misc_feature 1456..1791 /*tag= q
FT /*note="Claimed"
XX DE3833897-A.
PN 03-MAY-1989.
XX PD 05-OCT-1988; 88DE-3833897.
XX PF 18-AUG-1988; 88US-0234065.
XX PR (ONCO-) ONCOGEN.
XX PA Purchio AF, Madisen L, Webb N;
XX PI WPI; 1989-138796/19.
XX DR P-PSDB; AAP91889.
XX PT New DNA sequence encoding transforming growth factor beta 2 -
XX used for large scale expression in eucaryotic cells
XX PS Disclosure; Fig 1a; 27pp; German.
XX CC PolyA-RNA was isolated from the tamoxifen-treated, human prostatic
XX adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is used
XX for control of the SV40 promoter and expressed in CHO cells. The simian
XX SQ is also claimed.
XX SQ Sequence 2568 BP; 772 A; 597 C; 513 G; 686 T; 0 other;

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x AAN90767 ..
Align seg 1/1 to: AAN90767 from: 1 to: 2568
1 AlaLeuAspThrAsnTyriCysPheArgAsnLeuGluAsnCysCysVa 17
|||||: 1456 GCTTTGGATGCGGCTATTGCTTTAGAATGTCAGGATAATGCTGCT 1505
17 largProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1506 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGTTGGAATGGATAC 1555
34  lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1556 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 1605
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1606 TTATGGAGTTTCAGACACTCAGACAGCAGGAGGTCCTGAGCTTATATAATAC 1655
67  rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
1656 CATAAATCCAGAACATCTGCTTCTCTGCTGCTGCCAAGATTAG 1705
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1706 AACCTCTAACCATCTCTACTACTATGGCAAAACACCCCAAGATTGAACAG 1755
101 LeuSerAsnMetValLysSerCysLysCysSer 112
1756 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1791
seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05126
seq_documentation_block:
ID  AAQ05126 standard; DNA; 2569 BP.
AC  AAQ05126;
XX
DT  02-NOV-1990 (first entry)
XX
DE  Human TGF-Beta2-442 precursor cDNA.
XX
KW  Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  CDS 467..1792
FT  /*tag= a
FT  mat_peptide 1457..1792
FT  /*tag= b
XX
PN  EP376785-A.
XX
PD  04-JUL-1990.
XX
PF  14-DEC-1989; 89EP-0403480.
XX
PR  16-DEC-1988; 88US-0285140.
PR  05-DEC-1989; 89US-0446020.
XX
PA  (ONCO-) ONCOGEN LTD PARTNER.
XX
PI  Purchio AF, Madisen L, Webb N;
XX
DR  WPI: 1990-203127/27.
DR  P-PSDB; AAR05748.
XX
PT  Cloning and expression of transforming growth factor beta 2 -
PT  used for treatment of tumors or for augmenting wound healing.
XX
PS  Claim 1; Fig 1a; 58pp; English.
XX
CC  TGF-Beta2 may be used in treatment of tumors at effective doses,
CC  and may also be useful in augmenting wound healing by stimulating
CC  cell proliferation. The growth factor can be produced at high
CC  levels from a CHO expression system.
XX
SQ  Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0 other;
XX
```

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alignment_scores:
  Quality: 535.00 Length: 112
  Ratio: 5.095 Gaps: 0
  Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
  TGF3P x AAQ05126 ..
  Align seg 1/1 to: AAQ05126 from: 1 to: 2569
1  AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
1457 GCTTTGGATGCGGCCCTATTGCTTTAGAAATGTCAGGATAATTGCGCCT 1506
17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTyrValH 34
1507 AGCTCCACTTTACATTGATTTCAAGAGGATCTAGGTTGGAATGGATAC 1556
34  lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1557 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 1606
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1607 TTATGGAGTTTCAGACACTCAGACAGCAGGAGGTCCTGAGCTTATATAATAC 1656
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1657 CATAAATCCAGAACATCTGCTTCTCTGCTGCTGCCAAGATTAG 1706
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1707 AACCTCTAACCATCTCTATTATATGGCAAAACACCCCAAGATTGAACAG 1756
101 LeuSerAsnMetValLysSerCysLysCysSer 112
1757 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1792
seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20290
seq_documentation_block:
ID  AAQ20290 standard; cDNA; 2569 BP.
XX
AC  AAQ20290;
XX
DT  16-APR-1992 (first entry)
XX
DE  Sequence encoding human transforming growth factor (TGF)-
DE  beta-2-442.
XX
KW  Hypertension therapy; hypotensive agent; blood pressure modulator;
KW  ss.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  CDS 467..475
FT  /*tag= a
FT  sig_peptide 478..525
FT  /*tag= b
FT  CDS 526..1456
FT  /*tag= c
FT  mat_peptide 1457..1792
FT  /*tag= d
FT  polyA_site 2569
FT  /*tag= e
XX
PN  WO9119513-A.
XX
PD  26-DEC-1991.
XX
PF  20-JUN-1991; 91WO-US04449.
XX
```

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PR 20-JUN-1990; 90US-0541221.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comerreski CR;
XX
XX WPI; 1992-024199/03.
XX P-PSDB; AAR20125.
XX
XX Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX Disclosure; Fig 2; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX beta2 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX complex.
XX
XX Sequence 2569 BP; 772 A; 598 C; 513 G; 686 T; 0 other;

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGF3P x AAQ20290 ..

Align seg 1/1 to: AAQ20290 from: 1 to: 2569

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnGluAsnCysCysVa 17
1457 GCTTTGGATCGCGCTATTGCTTTAGAAATGTGAGGATAATTGCTGCCT 1506
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1507 AGCTCCACTTTACATTGATTTTCAAGAGGGATCTAGGGTGGAAATGGATAC 1556
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1557 AGGAACCCAAAGGGTACAATGCCAACTTCTGTGGAGCATGCCCGTAT 1606
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1607 TTATGGAGTTCAGACACTCAGCAGCAGAGGGTCTTGAGCTTATATATAC 1656
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1657 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCTGCCAAGATTAG 1706
84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1707 AACCTCTAACCACTTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 1756
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1757 CTTTCTATATATGTTAAAGTCTTGGAAATGCAGC 1792

seq_name: /SIDSI/gcgdata/geneseq/geneseq/NA1995.DAT:AA04116
seq_documentation_block:
ID AA04116 standard; cDNA; 2592 BP.
XX
XX AA04116;
XX
XX 28-MAY-1996 (first entry)
XX

```

```

DE Human transforming growth factor-2 cDNA.
XX
XX TGF-beta1; TGF-beta2; transforming growth factor; protein;
XX cell differentiation; cell proliferation; CHO; Chinese hamster;
XX ovary; COS; monkey kidney; animal; mammal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX sig_peptide 503..550
XX /tag= a
XX mat_peptide 1484..1819
XX /tag= b
XX misc_feature 553
XX /tag= c
XX /note= "putative signal sequence cleavage site"
XX
XX EP676474-A1.
XX
XX 11-OCT-1995.
XX
XX 14-DEC-1989; 89EP-0104223.
XX
XX 05-DEC-1989; 89US-0445020.
XX 16-DEC-1988; 88US-0285140.
XX
XX (ONCO ) ONCOGEN LP.
XX
XX Madisen L, Purchio AF, Webb N;
XX
XX WPI; 1995-346094/45.
XX P-PSDB; AAR79922.
XX
XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
XX to produce biologically active, mature TGF-beta-2
XX
XX Disclosure; Fig.1a; 52pp; English.
XX
XX This DNA sequence is expressed in a host cell, preferably a
XX COS or CHO cell, containing a recombinant vector encoding this
XX sequence under the control of a 2nd nucleotide sequence that
XX regulates gene expression, preferably the SV40 promoter, so the host
XX cell produces active TGF-beta2. The produced TGF-beta2 protein can
XX be used to regulate cellular differentiation and proliferation.
XX
XX Sequence 2592 BP; 772 A; 613 C; 516 G; 691 T; 0 other;

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGF3P x AAT04116 ..

Align seg 1/1 to: AAT04116 from: 1 to: 2592

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnGluAsnCysCysVa 17
1484 GCTTTGGATCGCGCTATTGCTTTAGAAATGTGAGGATAATTGCTGCCT 1533
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1534 ACCTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 1583
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1584 ACGAACCCAAAGGGTACAATGCCAACTTCTGCTGGAGCATGCCCGTAT 1633
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1634 TTATGGAGTTCAGACACTCAGCAGCAGAGGGTCTGAGCTTATATATAC 1683

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alignment_scores:
  Quality: 532.00      Length: 112
  Ratio: 5.115        Gaps: 0
  Percent Similarity: 92.857  Percent Identity: 79.464

alignment_block:
  TGFb3P x AAQ03511  ..

Align seg 1/1 to: AAQ03511 from: 1 to: 2207

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1095 GCCTTGATCCGGCCCTATGCTTTAGAAATGTCAGCATATTCGCTCCT 1144

17 lArgProLeuThrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 ACCTCCACTTTACATTTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 1194

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1195 AGCAACCCAAAGGGTACAATGCCAATCTCTGCTGGAGCATGCCCGTAT 1244

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
1245 TTATGGAGTTTCAGACACTCAGCACAGCGGTCCTGAGCTTATATAATAC 1294

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1295 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1344

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1345 AACCTCTAACCATTTCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 1394

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1395 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 1430

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT:AAQ05127
seq_documentation_block:
ID AAQ05127 standard; DNA; 2207 BP.
XX
AC AAQ05127;
XX
XX
DT 02-NOV-1990 (first entry)
XX
DE Human TGF-Betal/TGF-Beta2 hybrid precursor cDNA expressing
DE TGF-Beta2.
XX
XX Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 261..1430
XX FT /*tag= a
XX mat_peptide 1092..1430
XX FT /*tag= b
XX
XX EP376785-A.
XX
XX 04-JUL-1990.
XX
XX 14-DEC-1989; 89EP-0403480.
XX
XX 16-DEC-1988; 88US-0285140.
XX
XX 05-DEC-1989; 89US-0446020.
XX
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX
```

```
DR WPI: 1990-203127/27.
DR P-PSDB; AAR05749.
XX
PT Cloning and expression of transforming growth factor beta 2 -
PT used for treatment of tumors or for augmenting wound healing.
XX
XX Claim 15; Fig 1b; 58pp; English.
XX
CC TGF-Beta2 may be used in treatment of tumors at effective doses,
CC and may also be useful in augmenting wound healing by stimulating
CC cell proliferation. The growth factor can be produced at high
CC levels from a CHO expression system.
XX
XX Sequence 2207 BP; 600 A; 577 C; 532 G; 498 T; 0 other;
SQ

alignment_scores:
  Quality: 532.00      Length: 112
  Ratio: 5.115        Gaps: 0
  Percent Similarity: 92.857  Percent Identity: 79.464

alignment_block:
  TGFb3P x AAQ05127  ..

Align seg 1/1 to: AAQ05127 from: 1 to: 2207

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1095 GCCTTGATCCGGCCCTATGCTTTAGAAATGTCAGCATATTCGCTCCT 1144

17 lArgProLeuThrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 ACCTCCACTTTACATTTGATTTCAAGAGGGATCTAGGTTGGAATGGATAC 1194

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1195 AGCAACCCAAAGGGTACAATGCCAATCTCTGCTGGAGCATGCCCGTAT 1244

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
1245 TTATGGAGTTTCAGACACTCAGCACAGCGGTCCTGAGCTTATATAATAC 1294

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1295 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1344

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1345 AACCTCTAACCATTTCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 1394

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1395 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 1430

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1989.DAT:AAAN90768
seq_documentation_block:
ID AAAN90768 standard; DNA; 2217 BP.
XX
XX
AC AAAN90768;
XX
XX
DT 23-DEC-1990 (first entry)
XX
DE Sequence of human transforming growth factor (TGF) beta-1/TGF-beta-2
DE precursor DNA.
XX
XX Cell differentiation; cell proliferation; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 198..2025
XX misc_feature /*tag= a
XX
XX
```


DR WPT: 1990-187401/25.
 DR P-PSDB: AAR05492.
 XX
 PT New chimeric transforming growth factor -
 PT with TGF-beta biological activity and increased secretion
 PT efficiency.
 XX
 FS Claim 2; Fig 1; 18pp; English.
 XX
 CC Chimeric gene has TGF activity and may be more desirable than its
 CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
 CC from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive
 CC than normal. The product is useful in treatment of cancer and wound
 CC healing.
 CC See also EP-373994.
 XX
 SQ Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 other;

alignment_scores:
 Quality: 503.00 Length: 112
 Ratio: 5.030 Gaps: 0
 Percent Similarity: 89.286 Percent Identity: 75.893

alignment_block:
 TGFβ3P x AAQ04908 ..

Align seg 1/1 to: AAQ04908 from: 1 to: 1561

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
 |||||
 1096 GCCTCGGACCAACTACTGCTTCAGAAATGTGCAGATAAATTGCTGCCT 1145
 |||||
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleAspValH 34
 :|||
 1146 AGCTCGCTTTACATTGCACTTCAAGAGGACCTCGGCTGGAAGTGGATCC 1195
 |||||
 34 lSclupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 |||||
 1196 ACGAGCCCAAGGGCTACCATGCGCAACTTCTGCCTGGGGCCCTGTCCCTAC 1245
 |||||
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 :|||
 1246 ATTTGGAGCTGGACGCGAGTACACCAAGGCTCGTGCCTGTACACCA 1295
 |||||
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |||||
 1296 GCATACCCGGGGCGCTCGGGGGCGGCTCGGTCGCGCCGACGGCGGTG 1345
 |||||
 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 |||||
 1346 AGCCACTGCCATCGTGACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1395
 |||||
 101 LeuSerAsnMetValLysSerCysLysCysSer 112
 |||||
 1396 CTGTCCACATGATCGTGGCTCCGTCAAATGCAGC 1431
 |||||

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ29177

seq_documentation_block:
 ID AAQ29177 standard; DNA; 1561 BP.
 XX
 CC AAQ29177;
 XX
 DT 10-MAR-1993 (first entry)
 XX
 DE TGF-beta 1/beta 2 chimeric gene.
 XX
 KW Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
 KW Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO
 KW vascular endothelial cell; ss.
 XX
 OS Synthetic.

```

XX FH Location/Qualifiers
FT CDS 262..1434
FT     /*tag= a
FT mat_peptide 1096..1431
FT     /*tag= b
FT     /note= "Mature TGF-5 beta"
FT sig_peptide 262..348
FT     /*tag= c
FT precursor_RNA 349..1095
FT     /note= "TGF-5 beta pre-pro-protein"
FT mutation 1120..1122
FT     /tag= d
FT     /note= "TGF-5 beta pro-protein"
FT     /*tag= e
FT mutation 1123..1125
FT     /label= S9R
FT     /*tag= f
FT mutation 1126..1128
FT     /label= S10N
FT     /*tag= g
FT mutation 1129..1131
FT     /label= T11V
FT     /*tag= h
FT mutation 1132..1134
FT     /label= E12Q
FT     /*tag= i
FT mutation 1144..1146
FT     /label= K13D
FT     /*tag= j
FT mutation 1150..1152
FT     /label= V17L
FT     /*tag= k
FT mutation 1188..1170
FT     /label= Q19P
FT     /*tag= l
FT mutation 1171..1173
FT     /label= R25K
FT     /*tag= m
FT old_sequence 1120..1155
FT     /*tag= n
FT     /note= "Mutagenic linker"
FT misc_feature 179..200
FT     /*tag= o
FT     /note= "Feature not labelled in the specification"
XX PN WO9216228-A.
XX XX
XX PD 01-OCT-1992.
XX PF 13-MAR-1992; 92WO-US01993.
XX PR 14-MAR-1991; 91US-0669171.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Madisen L, Merwin J, Purchio AF;
XX DR WPI; 1992-348938/42.
XX DR P-PSDB; AAR27522.
XX XX
XX PT Compn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
XX PT inhibits proliferation of vascular endothelial cells, useful for
XX PT treating cancer and to promote wound healing
XX PS Disclosure; Fig 1; 45pp; English.
XX XX
XX CC The sequence given encodes a hybrid transforming growth factor
XX CC (TGF)-beta termed TGF-beta 1/beta 2 (or TGF-5 beta). The mutations
XX CC indicated in the features table represent replacements of TGF-beta 1
XX CC bases with those from the corresponding positions of TGF-beta 2.
XX CC Simian codon usage was maintained. This DNA sequence could be placed

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CC under the control of Simian virus 40 (SV40) expression regulatory
CC region within an expression vector and used to transfect Chinese
CC Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
CC and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
CC effects on the proliferation of mature TGF-5 beta. TGF-5 beta induces
CC to those produced by TGF-beta 1.
XX SQ Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other;

alignment_scores:
    Quality: 503.00      Length: 112
    Ratio: 5.030        Gaps: 0
    Percent Similarity: 89.286    Percent Identity: 75.893

alignment_block:
TGF3p x AAQ29177 ..
Align seg 1/1 to: AAQ29177 from: 1 to: 1561
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1096 GCCTCGACACCAACTACTGCTTCAGAAATGTCAGGATTAATGCTGCCT 1145
|||||
17 laArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
1146 ACGTCGCTTTACATTGACTTCAAGAGGACCTCGGCTGGAAGTGGATCC 1195
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1196 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTGGGGCCCTGTCCCTAC 1245
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1246 ATTTGGAGCTGGACACGACGAGTACGCAAGTCTCTGCTGCTGTACACCA 1295
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1296 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1345
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1346 AGCCACTGCCCACATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1395
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1396 CTGTCCAACATGATCGTGGCTCCGTCATCAATGCAGC 1431

seq_name: /SIDS1/gcgdata/geneseq/NA1996.DAT:AA17235
seq_documentation_block:
ID AA17235 standard; cDNA to mRNA; 339 BP.
XX AC
XX AA17235;
XX DT 17-JUL-1996 (first entry)
XX XX
XX DE Human TGF-beta 1 cDNA.
XX KW Transforming growth factor type beta; TGF-beta 1;
XX KW protein renaturation; protein folding; ds.
XX OS Homo sapiens.
XX PN WO9603433-Al.
XX PD 08-FEB-1996.
XX PF 12-JUL-1995; 95WO-EP02719.
XX PR 25-JUL-1994; 94EP-0810439.
XX PA (CIBA ) CIBA GEIGY AG.

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|||||
101 ACGAGCCCAAGGCTACCATGCACTTCTGCTGGGCCCTGCCCTAC 150
XX
DT
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
XX
DT
151 ATTTGGAGCGTGGACACGACGATACAGCAAGGTCCTGGCCCTGTACACCA 200
XX
DT
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
XX
DT
201 GCATAACCCGGCGCGCTGGCGGCGCGTCTGCTGCGCGCAGGCGCTGG 250
XX
DT
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
XX
DT
251 AGCCCTGCCCATCGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAG 300
XX
DT
101 LeuSerAsnMetValLysSerCysLysCysSer 112
XX
DT
301 CTGTCCACATGATCGTGGCTCTTGCAGTGCACT 336
XX

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT42771

seq_documentation_block:

ID AAT42771 standard; cDNA; 339 BP.

AC AAT42771;

XX 26-AUG-1997 (first entry)

XX TGF-beta1 active fragment of a TGF-beta fusion protein encoding cDNA.

XX Transforming growth factor-beta fusion protein; wound healing;

KW artificial skin; surgery recovery time; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..339

FT /*tag= a

FT /function= TGF active fragment

XX W09639430-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 96WO-US08973.

XX 06-JUN-1995; 95US-0470837.

XX (CHEU/) CHEUNG D T.

XX (HALL/) HALL F L.

XX (NIMN/) NIMNI M E.

XX (TUAN/) TUAN T.

XX (WULL/) WU L.

XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX WPI: 1997-043065/04.

XX P-PSDB; AAW08173.

XX Prepn. of transforming growth factor-beta fusion protein - useful to

PT reduce surgery recovery time and to prepare artificial skin

XX Disclosure; Page 44-45; 59pp; English.

XX A novel transforming growth factor-beta (TGF-beta) fusion protein

CC comprises a purification tag and a TGF active fragment. The present

CC sequence encodes a specifically claimed TGF active fragment, TGF-beta1.

CC Additionally, the fusion protein may comprise proteinase-sensitive

CC linker sites and binding domain so the protein sequence may contain

CC some or all of the following elements: purification tag; proteinase

CC site; ECM binding site; proteinase site; TGF-beta. TGF-beta promotes

CC wound healing, and the fusion protein can be used to reduce surgery

CC recovery time and in the preparation of artificial skin. The inclusion

CC of a purification tag facilitates purification of the fusion protein.

CC The proteinase site is included to permit cleavage and release of the

CC purification tag after purification if desired. The extracellular

CC matrix binding site facilitates delivery of the fusion protein to the

CC desired site of action. Delivery of the TGF-beta to the site to be

CC treated reduces the amount of TGF-beta required to be administered to

CC be effective and reduces the concentration of circulating TGF-beta

CC which may result in undesirable effects.

XX

SQ Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

alignment_scores:

Quality: 500.00 Length: 112

Ratio: 5.102 Gaps: 0

Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAT42771 ..

Align seg 1/1 to: AAT42771 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

|||||

1 GCCCTGGACACCAACATATTGCTTTCAGCTCCACGGAGAACTGCTGCGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34

|||||

51 GCGGACAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

|||||

101 ATGAGCCCAAGGCGTACCATGCCAATCTTGCCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

|||||

151 ATTTGGAGCGCTGGACACGACGATACAGCAAGTCTGCGCTGCGCAGGCGTGG 250

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

|||||

201 GCATAACCCGGCGCGCTGGCGGCGCGTCTGCTGCGCGCAGGCGCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

|||||

251 AGCGCGTGGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300

101 LeuSerAsnMetValLysSerCysLysCysSer 112

|||||

301 CTGTCCACATGATCGTGGCTCTTGCAGTGCACT 336

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX15245

seq_documentation_block:

ID AAX15245 standard; cDNA; 339 BP.

XX AAX15245;

XX 28-APR-1999 (first entry)

XX cDNA encoding the mature form of transforming growth factor-beta-1.

XX Transforming growth factor-beta-1; TGF-beta-like protein;

KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

KW bone repair; tissue repair; bone marrow protective agent;

KW cardioprotection; anti-inflammatory; immunosuppressive;

XX ulcer; bed sore; ds.

XX Homo sapiens.

XX EP891985-A1.

XX 20-JAN-1999.

XX

PF 27-NOV-1990; 90EP-0810922.
XX
PR 06-DEC-1989; 89CB-0027546.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX
DR WPI; 1999-083520/08.
DR P-PSDB; AAW97091.
XX
PT Producing biologically active dimeric Transforming Growth
PT Factor-beta - by refolding new monomeric Transforming Growth
PT Factor-beta, useful for treatment of wounds and cancer
XX
XX
PS Example 1; Page 28; 32pp; English.
XX
CC The present sequence encodes the mature form of transforming growth
CC factor-beta-1. Dimeric, biologically active TGF-beta-like protein
CC can be produced by subjecting the denatured monomeric form to refolding
CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
CC useful for the production of the dimeric, biologically active
CC TGF-beta-like protein, which is useful for the treatment of wounds
CC (surface or internal) and cancer in a mammal, in bone and tissue
CC repair, as a bone marrow protective agent, a mediator of
CC cardioprotection, for the production of an anti-inflammatory or
CC immunosuppressive preparation. Treatment is useful for animals,
CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
CC particularly useful for the elderly.
XX
SQ Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;

alignment_scores:

Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAX15245 ..

Align seg 1/1 to: AAX15245 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAACTGCTCGGT 50
|||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCAAAGGCTACCATGCCAACTCTCGCTCGGCGCTGCCCTAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :|||
151 ATTTGGAGCCTGCACAGCGATACAGCAAGGTCCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATACCCGGGCGCTCGGCGCGCGCTGCTGCTGCGCGCGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTGTCCAACATGATCGTGCCTCTGCAAGTGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT-AAV99375

seq_documentation_block:

ID AAV99375 standard; cDNA; 339 BP.
XX
AC AAV99375;
XX
DT 25-MAR-1999 (first entry)
XX
DE cDNA encoding a transforming growth factor beta active fragment.
XX
KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW bone morphogenetic protein; transforming growth factor beta;
KW active fragment; wound healing; bone growth; purification tag; ds.
XX
OS Homo sapiens.
XX
PN WO9855137-A1.
XX
PD 10-DEC-1998.
XX
PF 02-JUN-1998; 98WO-US11189.
XX
PR 03-JUN-1997; 97US-0868452.
XX
PA (HALL/) HALL F L.
PA (HANB/) HAN B.
PA (NIMN/) NIMNI M E.
PA (SHOR/) SHORS E C.
PA (WULL/) WU L.
XX
PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX
XX WPI; 1999-059875/05.
DR P-PSDB; AAW84207.
XX
PT New bone morphogenetic fusion proteins - comprising a purification
PT tag and a bone morphogenetic active fragment, used for enhancing
PT wound healing or bone growth
XX
XX Example 1; Page 41; 64pp; English.
XX
CC The present sequence encodes a transforming growth factor beta active
CC fragment. The protein can be used in place of a bone morphogenetic
CC active fragment to create the fusion proteins of the invention. When a
CC bone morphogenetic active fragment is used, the fusion proteins are
CC designated bone morphogenetic fusion proteins. The bone morphogenetic
CC fusion protein may contain some or all of the following elements: a
CC purification tag, a proteinase site, an ECM/bone binding site, a second
CC proteinase site, and a bone morphogenetic protein active fragment.
CC The bone morphogenetic fusion proteins can be used for enhancing wound
CC healing or bone growth.
XX
SQ Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

alignment_scores:

Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAV99375 ..

Align seg 1/1 to: AAV99375 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAACTGCTCGGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

```
|||||
101 ATGAGCCCAAGGCTACCACTTCTGCTCGGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||::|||
151 APTTGGAGCGCTGACACGACGAGTACAGCAAGTCTCGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCGCGCGCTCGCGCGCGCTGCTGCGTGCAGCGCGCTGG 250
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
||||| ||::||| ||||| ||||| ||||| |||||
251 AGCCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ::||| ::||| ||||| |||||
301 CTGTCCAACATGATGCTGCGCTCCTGCAAGTGCAGC 336
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ09317
seq_documentation_block:
ID AAQ09317 standard; cDNA; 1303 BP.
XX
AC AAQ09317;
XX
DT 12-AUG-1990 (first entry)
XX
DE Monkey transforming growth factor-beta cDNA.
XX
KW Transforming growth factor-beta; simian; psoriasis;
KW TGF-beta.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT sig_peptide 22..63 /*tag= a
FT mat_peptide 836..1170 /*tag= b
FT /*product=monkey transforming growth factor-beta
XX
PN EP353772-A.
XX
PD 07-FEB-1990.
XX
XX 04-AUG-1989; 89EP-0114458.
XX
PR 05-AUG-1988; 88US-0229133.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR WPI; 1990-038499/06.
DR P-PSDB; AAR03743.
XX
PT Inhibition of proliferation of epidermal cells -
PT used to treat psoriasis by contacting cells with compositions
PT containing transforming growth factor-beta.
XX
XX 'disclosure; fig 1; 20pp; English.
XX
CC TGF-beta may be used in the treatment of hyperplasia
CC associated with acanthosis-categorised skin diseases, and
CC in alleviating psoriatic symptoms associated with cytokine-
CC induced phenomena. See also AAQ03268 and AAR03750.
XX
SQ Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;
```

```
alignment_scores:
Quality: 500.00 Length: 112
```

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Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGF3P x AAQ09317 ..
Align seg 1/1 to: AAQ09317 from: 1 to: 1303
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
838 GCCTGGACACCACTACTGCTTCTAGCTCCACGAGAAAGAACTGCTCGCT 887
17 laqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
888 CGGCGAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 937
34 isgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
938 ACAGGCCCAAGGCTACCATGCCAATCTTCTGCTGGGGCCCTGTCCCTAC 987
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||::|||
988 ATTTGGAGCGCTGACACGACGAGTACAGCAAGTCTGCGCTGTACAACCA 1037
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1038 GCATAACCGCGCGCTCGCGCGCGCTGCTGCGTGCAGCGCGCTGG 1087
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1088 AGCCACTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 1137
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ::||| ::||| ||||| |||||
1138 CTGTCCAACATGATGCTGCGCTCCTGCAATGCAGC 1173
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20289
seq_documentation_block:
ID AAQ20289 standard; cDNA; 1559 BP.
XX
AC AAQ20289;
XX
DT 16-APR-1992 (first entry)
XX
DE Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT CDS 262..282
FT /*tag= a
FT sig_peptide 283..324 /*tag= b
FT CDS 325..1098 /*tag= c
FT mat_peptide 1099..1436 /*tag= d
XX
PN W09119513-A.
XX
PD 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
PR 20-JUN-1990; 90US-0541221.
XX
PA (BRIM ) BRISTOL-MYERS SQUIB.
XX
PI Oleson FB, Comereski CR;
```



```
1396 CTGTCCACATGATGGTGGCTCTCTGCAAAATGCAGC 1431
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03269
seq_documentation_block:
ID   AAQ03269 standard; DNA; 1571 BP.
XX
AC   AAQ03269;
XX
DT   12-AUG-1990 (first entry)
XX
DE   Human transforming growth factor-beta cDNA.
XX
KW   Transforming growth factor-beta; psoriasis;
KW   TGF-beta.
XX
OS   Homo sapiens.
XX
FH   Key
FT   sig_peptide 22..63
FT   mat_peptide 836..1170
FT   /tag= a
FT   /tag= b
FT   /product=human transforming growth factor-beta
XX
PN   EP353772-A.
XX
PD   07-FEB-1990.
XX
PF   04-AUG-1989; 89EP-0114458.
XX
PR   05-AUG-1988; 88US-0229133.
XX
PA   (ONCO-) ONCOGEN LTD PARTNER.
XX
PI   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
DR   WPI; 1990-038499/06.
DR   P-PSDB; AAR03750.
XX
PT   Inhibition of proliferation of epidermal cells -
PT   used to treat psoriasis by contacting cells with compositions
PT   containing transforming growth factor-beta.
XX
PS   Disclosure; fig 1; 20pp; English.
XX
CC   TGF-beta may be used in the treatment of hyperplasia
CC   associated with acanthosis-categorised skin diseases, and
CC   in alleviating psoriatic symptoms associated with cytokine-
CC   induced phenomena. See also AAQ03268 and AAR03743.
XX
SQ   Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ03269 ..
Align seg 1/1 to: AAQ03269 from: 1 to: 1571
1 AlalaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1106 GCCCTGGACACCACTACTGCTTACGCTCCACGGAGAAAGTGTGGGT 1155
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1156 CGGCAGCTGATATTGACTTCCGCAAGACGCTGGCTGGAAGTGGATCC 1205
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
```

```
|||||
1206 ACAGGCCCAAGGCTACCATGCCCAACTTCTGCTGGGGCCCTGTCCCTAC 1255
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::| |||||:|||||
1256 ATTTGGAGCTGGACAGCAGTACAGCAAGTCTGCTGCCCTGTACAACCA 1305
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||:|||||:|||||:||||| |||
1306 GCATAACCGGGCGCTCGGCGCGCGTCTGCTGCGCGCAGCGCTGG 1355
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||:|||||:|||||:||||| |||
1356 AGCCACTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1405
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||:|||||:|||||:||||| |||
1406 CTGTCCACATGATGCTGCGCTCTGCAAAATGCAGC 1441
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ13392
seq_documentation_block:
ID   AAQ13392 standard; DNA; 1821 BP.
XX
AC   AAQ13392;
XX
DT   20-NOV-1991 (first entry)
XX
DE   Human pro-TGF-beta 1 gene.
XX
KW   Osteogenetic; tumoricidal; ss.
XX
OS   Homo sapiens.
XX
FH   Key
FT   CDS 512..1684
FT   /tag= a
FT   sig_peptide 512..598
FT   /tag= b
FT   misc_RNA 599..1684
FT   /tag= c
FT   /note= "pro-TGF-beta 1"
FT   mat_peptide 1346..1684
FT   /tag= e
FT   /note= "TGF-beta 1"
XX
PN   JP03180192-A.
XX
PD   06-AUG-1991.
XX
PF   07-DEC-1989; 89JP-0318243.
XX
PR   07-DEC-1989; 89JP-0318243.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
WPI; 1991-271579/37.
DR   P-PSDB; AAR13813.
XX
Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
preparing DNA chain contg. base sequence coding for human
pre:pro-TGF-beta 1, forming expression vector etc.
XX
PS   Claim 1; Fig 1; 16pp; Japanese.
XX
CC   The DNA sequence encodes human prepro-TGF-beta 1 which can be
CC   produced by recombinant methods, it has osteogenetic and
CC   tumoricidal activity.
XX
SQ   Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;

alignment_scores:
```



```
FT CDS 842..2014
FT /*tag= a
FT mat_peptide 1676..2011
FT /*tag= b
FT misc_difference 37..113
FT /*tag= c
FT /*note="stable hairpin loops"
FT misc_feature 2015..2100
FT /*tag= d
FT /*note="G-C rich sequence
FT and a downstream TATA-like sequence"
FT
FT
XX US4886747-A.
XX
XX 12-DEC-1989.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1990-051338/07.
XX P-PSDB; AAR05258.
XX
XX Nucleic acid encoding transforming growth factor-beta
XX cloned into expression vectors for expression in eukaryotic host
XX cells for therapeutic use
XX
XX Disclosure; Flg 1b; 28pp; English.
XX
XX It was obtained by an analysis of several overlapping cDNAs and gene
XX fragments, leading to the detn. of a continuous sequence corres. to the
XX TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
XX encode biologically active transforming growth factor (TGF-beta),
XX operably linked to DNA that encodes a secretory leader (SL). It, or a
XX nucleic acid capable of hybridising with it, can also be labelled and
XX used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
XX proteins.
XX
XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

alignment_scores:
    Quality: 500.00 Length: 112
    Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ03301 ..
Align seg 1/1 to: AAQ03301 from: 1 to: 2537
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1676 GCCCTGGACACCACTATTGCTTACGTCCTCCAGGAGAGAACTGCTGCT 1725
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGAGCTGTACATTGACTTCCGCAAGGACCTCGCTCGGAAGTGGATCC 1775
|||||
34 lSgLeuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACGAGCCCAAGGGCTACCACTTCTGCTCGGCCCTCGGCCCTAC 1825
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1826 ATTTGGAGCCTGGACACCGAGTACAGCAAGGTCCTGGCCCTGTACAACA 1875
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
```

```
1876 GCATAACCGGGCGCTCGGGCGCGCTGCTGCTGCGCGCAGCGCTGG 1925
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1926 AGCCGCTGCGCATCGTGTACTAGTGGCGCAAGCCCAAGGTGGAGCAG 1975
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAACATGATCGTGGCTGCTCTGCAAGTGCAGC 2011
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT.AAQ02814
seq_documentation_block:
ID AAQ02814 standard; cDNA; 2537 BP.
XX
XX AAQ02814;
XX
XX 31-MAY-1989 (first entry)
XX
XX Sequence of pre-TGF-beta1 cDNA.
XX
XX Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX inhibition.
XX
XX Key Location/Qualifiers
XX CDS 842..2011
XX /*tag= a
XX /label=pre-TGF beta 1
XX 1677..2011
XX /*tag= b
XX /label=mature TGF-beta 1
XX 2015..2092
XX /*tag= c
XX misc_feature 2093..2099
XX /*tag= d
XX /label=TATA-like sequence
XX 37..113
XX stem_loop
XX /*tag= e
XX 863..911
XX misc_feature
XX /*tag= f
XX /label=hydrophobic domain
XX
XX WO8912101-A.
XX
XX 14-DEC-1989.
XX
XX 08-JUN-1988; 88WO-US01945.
XX
XX 08-JUN-1988; 88WO-UO01945.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RM, Goeddel DV;
XX
XX WPI; 1990-007474/01.
XX P-PSDB; AAR04034.
XX
XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
XX probe, or to produce TGF beta 3, for growth inhibition of certain normal
XX and neoplastic cells, eg A549.
XX
XX Disclosure; Fig. 1b; 61pp; English.
XX
XX Sequence encodes the 390 amino acid (AA) precursor transforming growth
XX factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
XX the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
XX potential secondary structure. The TATA-like sequence in the 3' untrans-
XX lated region of the gene is presumably a polyadenylation signal. Mature
XX TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
XX cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
XX acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a
XX probe or to produce TGF-beta 3 for inhibition of growth of normal and
XX neoplastic cells.
```

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XX SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

alignment_scores:
  Quality: 500.00 Length: 112
  Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
  TGFB3P x AAQ02814 ..

Align seg 1/1 to: AAQ02814 from: 1 to: 2537

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1676 GCCCTGGACACCAACTATTGCTTCAGCTCCACGAGAGAAGAACTGCTGGT 1725

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1726 GCGGCAGCTGTACATTGACTTCGCGCAAGGACCTCGGCTGGAAGTGGATCC 1775

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1776 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1825

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| |||||| |||||| |||||| |||||| |||||| ||||||
1826 ATTTGGAGCTGGACACGACGAGTACAGCAAGCTCTGGCCCTGTACAACCA 1875

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1876 GCATAACCCGGCGCCTCGCGCGCGCGTCTGCTGCCGCGAGCGCTGG 1925

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1926 AGCCGCTGCCCATCGTGTACTAGCTGGGCGCGCAAGCCCAAGGTGGAGCAG 1975

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1976 CTGTCCAACATGATGTGGCCTCTCTGCAAGTGCAGC 2011

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56923
seq_documentation_block:
ID AAQ56923 standard; cDNA; 2537 BP.
XX AC AAQ56923;
XX DT 09-JUL-1994 (first entry)
XX DE Human pre-TGF-beta-1.
XX KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnerary; SS.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT misc_structure 47..113 /*tag= a
FT /note= "possible hairpin loop region"
FT CDS 842..2014 /*tag= b
FT FT 1676..2011 /*tag= c
FT mat_peptide 2515..2521 /*tag= d
FT polyA_signal
XX US5284763-A.
XX PN 08-FEB-1994.
XX PD

```

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XX PF 22-MAR-1985; 85US-0715142.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PA (GETH ) GENENTECH INC.
XX PI Derynk RMA, Goeddel DV;
XX DR WPI; 1994-056343/07.
XX DR P-PSDB; AAR46227.
XX PT Nucleic acid sequences encoding transforming growth factor-beta -
XX PT diagnostic probes, and for use in therapeutics
XX PS Disclosure; Fig 1b; 25pp; English.
XX CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC plg TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX SQ Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;

alignment_scores:
  Quality: 500.00 Length: 112
  Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
  TGFB3P x AAQ56923 ..

Align seg 1/1 to: AAQ56923 from: 1 to: 2537

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1676 GCCCTGGACACCAACTATTGCTTCAGCTCCACGAGAGAAGAACTGCTGGT 1725

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1726 GCGGCAGCTGTACATTGACTTCGCGCAAGGACCTCGGCTGGAAGTGGATCC 1775

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1776 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1825

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| |||||| |||||| |||||| |||||| |||||| ||||||
1826 ATTTGGAGCTGGACACGACGAGTACAGCAAGCTCTGGCCCTGTACAACCA 1875

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1876 GCATAACCCGGCGCCTCGCGCGCGCGTCTGCTGCCGCGAGCGCTGG 1925

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1926 AGCCGCTGCCCATCGTGTACTAGCTGGGCGCGCAAGCCCAAGGTGGAGCAG 1975

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||| |||||| |||||| |||||| |||||| ||||||
1976 CTGTCCAACATGATGTGGCCTCTCTGCAAGTGCAGC 2011

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1996.DAT:AA15720
seq_documentation_block:

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ID XX AAT15720 standard; cDNA; 2537 BP.
AC AAT15720;
XX 24-JUL-1997 (revised)
DT 25-JAN-1980 (first entry)
XX Pre-transforming growth factor beta 1 cDNA.
DE transforming growth factor beta 1; wound healing;
KW recombinant production; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..841
FT 5'UTR
FT /*tag= a
FT 37..113
FT misc_feature
FT /*tag= b
FT /*note= "GC-rich region forms stable hairpin loops;
FT similar to structural organisation of c-myc RNA,
FT could play role in mRNA stability or in
FT regulation of transcription"
FT CDS 842..2014
FT /*tag= c
FT /product= pre-TGF_beta_1
FT mat_peptide 1676..2011
FT /*tag= d
FT /product= mature_TGF_beta_1
FT repeat_region 2015..2100
FT /*tag= e
FT /note= "GC-rich region; possibly responsible for the
FT fact 3'UTR of mRNA could not be cloned as cDNA;
FT may be important for transcription efficiency"
FT repeat_unit 2019..2023
FT /*tag= f
FT TATA_signal 2094..2100
FT /*tag= g
FT /note= "TATA-like sequence; no evidence that this
FT functions a promoter"
FT polyA_signal 2514..2520
FT /*tag= h
FT misc_signal 2529..2536
FT /*tag= i
FT /note= "consensus sequence immediately precedes
FT polyA-tail (Benoist et al)"
XX US5482851-A.
XX 09-JAN-1996.
XX 22-MAR-1985; 85US-0715142.
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX (GETH) GENENTECH INC.
XX Derynck RMA, Goeddel DV;
XX WPI; 1996-076891/08.
XX P-PSDB; AAR90827.
XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications
XX or in therapy
XX Example 3; Fig 1; 26pp; English.
XX The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC

CC The nucleotide sequence was obtbd. by an analysis of several overlapping
CC cDNAs and gene fragments. The DNA is useful for the recombinant
CC production of TGF beta 1, which can be used in, e.g. wound healing.
CC (Revised entry submitted to correct sequence analysis breakdown.)
XX
XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
SQ
alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGFb3p x AAT15720 ..
Align seg 1/1 to: AAT15720 from: 1 to: 2537
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
1676 GCCTGGACACCAACTATTCTTCAGCTCCACGGAGAGAAGAACTGCTGGT 1725
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGCTGGAAGTGGATCC 1775
34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACGAGCCCAAGGGCTACCATGCCAATCTCGCTCGGGCCCTGCCCTAC 1825
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1826 ATTTGGAGCCTGCAGCAGCAGTACAGCAAGTCTCGCCCTGTACAACCA 1875
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1876 GCATAACCCGGCGCCTCGCGCGCGCTGCTGCTGCCGAGCGCTGG 1925
84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1926 AGCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAACATGATCGTGGCTCTCTCAAGTGGCAGC 2011
seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52933
seq_documentation_block:
ID AAV52933 standard; cDNA; 2537 BP.
XX
XX AC AAV52933;
XX
XX DT 21-DEC-1998 (first entry)
XX DE Human pre-transforming growth factor-beta 1 cDNA.
XX
XX KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 842..2014
FT /*tag= a
FT mat_peptide 1676..2011
FT /*tag= b
FT stem_loop 37..113
FT /*tag= b
FT /note= "putative stable hairpin loop"
FT misc_feature 2015..2100
FT /*tag= c
FT /note= "GC-rich sequence"
FT polyA_signal 2514..2520

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FT XX /*tag= d
PN US5801231-A.
XX
PD 01-SEP-1998.
XX
XX 22-MAR-1985; 85US-0715142.
XX
PR 13-MAR-1987; 87US-0025423.
PR 22-MAR-1985; 85US-0715142.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
PR 05-NOV-1993; 93US-0147364.
PR 30-MAY-1995; 95US-0454466.
XX
PA (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
DR WPI; 1998-494840/42.
DR P-PSDB; AAW78785.
XX
XX DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein
XX
PS Example 3; Fig 1B 1-3; 26pp; English.
XX
CC This nucleotide sequence codes for the human transforming growth
CC factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC composite of overlapping cDNA clones isolated from different cDNA
CC libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC TGF-beta exon (see AAV52936) restriction fragments as probes.
CC The 3' region of the sequence was determined using cloned genomic
CC DNA. The invention relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiated anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
XX
SQ Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
  TGF3P x AAV52933 ..
Align seg 1/1 to: AAV52933 from: 1 to: 2537

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1676 GCCTGCACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTCGT 1725

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGCAGCTGTACATTGACTTCGCGAAGACCTCGGCTGGAGTGGATCC 1775

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACAGGCCCAAGGCTACCAAGGCACTTCGCTCGGCGCTGCCCTAC 1825

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||
1826 ATTTGGAGCTTGACACGACGACGTACACGAAGTCTCTGGCCCTGTACACCA 1875

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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1876 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1925

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1926 AGCCGCTGCCATCGTGTACTACGTGGCGCCCAAGCCCAAGGTGGAGCAG 1975

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAACATGATGCTGCGCTCCTGCAAGTGCAGC 2011

seq_name: /STDs1/gcgdata/geneseq/geneseqn/NA1995.DAT: AAT05876

seq_documentation_block:
ID AAT05876 standard; cDNA; 2745 BP.
XX
AC AAT05876;
XX
XX 25-JUN-1996 (first entry)
XX
DE CDNA encoding transforming growth factor-beta 1.
XX
KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW nitric oxide production; hypotension; inflammation; septic shock;
KW treatment; ds.
XX
XX Mammalian sp.
XX
XX Key Location/Qualifiers
FH 842..2017
CDS /*tag= a
FT /product= transforming growth factor-beta 1
FT
XX
PN W09526745-A1.
XX
XX 12-OCT-1995.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Lee M, Perrella MA;
XX
XX WPI; 1995-358443/46.
XX P-PSDB; AAR83054.
XX
XX Treatment of hypotension, esp. in septic shock - by administering
XX transforming growth factor-beta e.g. to inhibit inducible nitric
XX oxide synthase gene transcription
XX
XX Disclosure; Fig 15; 52pp; English.
XX
XX The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which
XX has been found to inhibit inducible nitric oxide synthase (iNOS) gene
XX transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
XX smooth muscle cells, and at a dose which does not inhibit constitutive
XX NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
XX in the treatment of hypotension, such as that associated with severe
XX inflammation or septic shock.
XX
XX Sequence 2745 BP; 527 A; 938 C; 801 G; 479 T; 0 other;

```

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alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

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TGFB3P x AAT05876 ..
Align seg 1/1 to: AAT05876 from: 1 to: 2745

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
||||| 1679 GCCTGGACACCACTATTGCTTACGTCACGAGGAGAACTGCTGCGT 1728

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValh 34
||||| 1729 GCGGAGCTGTACATTGACTCCGCAAGGACCTCGCTGGAAGTGGATCC 1778

34 lSgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| 1779 ACAGGCCCAAGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCCCTAC 1828

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| 1829 ATTTGGAGCGCTGGACACGACAGTACAGCAAGGTCTCTGGCCCTGTACAACCA 1878

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
||||| 1879 GCATACCCGGCGGCTCGGCGCGCGCTGCTGCGTCCGCGAGGCGCTGG 1928

84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| 1929 AGCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1978

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| 1979 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 2014

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NAL196.DAT: AAT16516
seq_documentation_block:
ID AAT16516 standard; DNA; 3541 BP.
XX
AC AAT16516;
XX
DT 01-OCT-1996 (first entry)
XX
DE Collagen A1/TGF-beta-1 chimeric gene.
XX
KW Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
KW bone formation; tissue repair; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 20..3535
FT /*tag= a
FT /*product= collagen IA/TGF-beta-1 fusion protein
FT misc_difference 2679
FT /*tag= b
FT /*note= "base 2679 is not identified in the
FT specification"
FT misc_difference 2688
FT /*tag= c
FT /*note= "base 2688 is not identified in the
FT specification"
XX
PN CA2151547-A.
XX
PD 11-DEC-1995.
XX
PF 12-JUN-1995; 95CA-2151547.
XX
PR 10-JUN-1994; 94US-0259263.
XX
PA (USSU ) US SURGICAL CORP.
XX
PI Espino P, Gruskin EA;
XX

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```

DR WPI; 1996-140144/15.
DR P-PSDB; AAR89470.
XX
PT Chimaeric DNA encoding protein contg. extracellular matrix protein
PT domain - and cellular regulatory factor domain, partic. useful as
PT osteogenic agents, also related vectors, transformed cells and
PT chimaeric proteins.
XX
PS Disclosure; Fig 2; 59pp; English.
XX
CC A chimeric gene (AAT16516) codes for a fusion protein (AAR89470) between
CC the helical region of human collagen I(a) and human transforming
CC growth factor beta-1 (TGF-beta-1). The collagen moiety was cloned
CC from human fibroblast AG02261A cells by PCR amplification. The
CC construct was inserted into a pMal vector for expression in E. coli.
CC The fusion protein provides sustained release and delivery of
CC TGF-beta-1 to a target tissue. The TGF increases efficacy of
CC the body's normal soft tissue repair response and also induces
CC osteogenesis.
XX
SQ Sequence 3541 BP; 504 A; 1143 C; 1188 G; 704 T; 2 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAT16516 ..
Align seg 1/1 to: AAT16516 from: 1 to: 3541

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
||||| 3197 GCCTGGACACCACTATTGCTTACGTCACGAGGAGAACTGCTGCGT 3246

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValh 34
||||| 3247 GCGGAGCTGTACATTGACTCCGCAAGGACCTCGCTGGAAGTGGATCC 3296

34 lSgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| 3297 ACAGGCCCAAGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCCCTAC 3346

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| 3347 ATTTGGAGCGCTGGACACGACAGTACAGCAAGGTCTCTGGCCCTGTACAACCA 3396

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
||||| 3397 GCATACCCGGCGGCTCGGCGCGCGCTGCTGCGTCCGCGAGGCGCTGG 3446

84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| 3447 AGCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 3496

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| 3497 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 3532

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT: AAL12498
seq_documentation_block:
ID AAL12498 standard; cDNA; 3541 BP.
XX
AC AAL12498;
XX
DT 25-JUL-2000 (first entry)
XX
DE cDNA encoding a chimeric collagen I (alpha1)/TGF-beta1 protein.
XX
KW Extracellular matrix protein; self aggregation; hydroxylated proline;

```


KW trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;
KW collagen; fibronectin; fibronectin; post translational hydroxylation; ss.
KW transforming growth factor-beta1; TGF-beta1; chimera; ss.

OS Chimeric - Homo sapiens.
OS Chimeric - Unidentified.

Key Location/Qualifiers
CDS 20..3535
FT /*tag= a
FT /product= "chimeric collagen 1 (alpha1)/TGF-beta1
FT protein"
FT /transl_except= (pos: 2591..2593, aa: Gly)

PN Ep992586-A2.

PD 12-APR-2000.

XX 07-OCT-1999; 99EP-0119184.

XX 09-OCT-1998; 98US-0169768.

XX (USSU) US SURGICAL CORP.

XX Gruskin EA, Buechter DD, Zhang G, Connolly K;

XX WPI; 2000-259138/23.

XX P-PSDB; AAY84538.

XX Production of extracellular matrix proteins containing

PT 4-trans-hydroxyproline results in native self aggregating proteins,

PT useful on medical implants -

PS Disclosure; Fig 16A-C; 260pp; English.

XX The specification describes a method for producing an extracellular
CC matrix protein or its fragment. The extracellular matrix protein is
CC capable of self aggregating in a cell which does not ordinarily
CC hydroxylated prolines. The method comprises optimising a nucleic acid
CC sequence for expression in the cell by substitution of codons preferred
CC by that cell for naturally occurring codons not preferred by the cell;
CC incorporating the nucleic acid sequence into the cell; and contacting
CC the cell with a hypertonic growth medium containing at least one amino
CC acid, selected from the group consisting of trans-4-hydroxyproline and
CC 3-hydroxyproline to allow at least one of the amino acids to be
CC assimilated into the cell and incorporated into the extracellular matrix
CC protein. The method may be used to make host cells assimilate and
CC incorporate trans-4-hydroxyproline into proteins. This is especially
CC useful in the recombinant production of proteins such as collagen,
CC fibronectin and fibronectin whose ability to self aggregate and produce
CC functional proteins depends on the post translational hydroxylation of
CC proline. The method is also useful in studying the structure and function
CC of polypeptides which do not normally contain trans-4-hydroxyproline.
CC The present sequence encodes a chimeric collagen 1 (alpha1)/transforming
CC growth factor-beta1 (TGF-beta1) protein, which may be produced using the
CC method of the invention.

XX Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAAL2498 ..

Align seg 1/1 to: AAAL2498 from: 1 to: 3541

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
3197 GCCTGGACCAACCACTATTCTTCAGCTCCACGGAGAAGAACTCTCGCT 3246

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
|||||
3247 GCGGAGCTGTATACATTGACTTCGCAAGACCTCGCTGGAGTGGATCC 3296
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
3297 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 3346
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::|||
3347 ATTTGGAGCTGGACACGACGACGACGACGACGACGACGACGACGAC 3396
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeu 84
|||||
3397 GCATAACCGCGCGCTCGGGCGCGCGCTGCTGCTGCGCGACGCGCTGG 3446
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
3447 AGCCGCTGCCATCGTACTACTGCTGGGCGCAAGCCCAAGGTGGAGCAG 3496
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
3497 CTGTCCAAATGATGCTGCGCTCCTGCAAGTGCAGC 3532

seq_name: /SIBS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ55624

seq_documentation_block:

ID AAQ55624 standard; DNA; 4105 BP.

XX AAQ55624;

XX 12-JUL-1994 (first entry)

XX TGFbeta1 5'-UTR-CDS-3'-UTR.

XX Transforming Growth Factor beta 1; TGF; non-coding region;
KW coding region; resonance; interaction; optimisation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mRNA

FT /*tag= a

FT /note= "the inventor has used T instead of U in
FT the TGFbeta1 full-length mRNA"

FT 5'UTR 1..2202

FT /*tag= b

FT enhancer 231..631

FT /*tag= c

FT misc_RNA 1..230

FT /*tag= d

FT /note= "N1 region"

FT misc_RNA 632..910

FT /*tag= e

FT /note= "N2 region"

FT misc_RNA 911..1039

FT /*tag= f

FT /note= "p region"

FT CDS 2203..3378

FT /*tag= g

FT /product= TGFbeta1

FT 3'UTR 3379..4105

FT /*tag= h

FT /note= "the N residues at positions 3464 and
FT 3465 each appear as the letter F in
FT the specification"

XX FR2692594-A.

XX 24-DEC-1993.

XX 22-JUN-1992;

XX 92FR-0007571.

```

XX PR 22-JUN-1992; 92FR-0007571.
XX PA (PERE/) PEREZ J.
XX PI Perez J;
XX XX WPI: 1994-028256/04.
XX DR Application of optimised gene expression - for scientific,
XX PT industrial and therapeutic purposes
XX PT Disclosure; Fig 1; 110pp; French.
XX PS
XX CC The TGFbeta1 mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and
XX CC 3'-UTR) for various "perturbation" experiments. The relative order
XX CC of the 3 regions was altered, e.g. the 3'-UTR was positioned
XX CC upstream of the CDS and the 5'-UTR was positioned downstream of the
XX CC CDS. The experiments showed that interactions between coding and non-
XX CC coding regions are destroyed by such perturbations.
XX CC
XX SQ Sequence 4105 BP; 744 A; 1407 C; 1201 G; 751 T; 2 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ55624 ..

Align seg 1/1 to: AAQ55624 from: 1 to: 4105
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
3040 GCGCTGGACCAACATATTGCTTACGCTCCACGAGAGAACTGCGCGT 3089
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
3090 GCGGACGCTGTACATTGACTTCCGCAAGACCTCGGCTGGAAGTGATCC 3139
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
3140 ACGAGCCCAAGGCTACCATGCCAATCTTGCTCGGCGCTGCCCTTAC 3189
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
3190 ATTTGGAGCGCTGCACACGACGATACAGCAAGGTCTGCGCTGTACAACCA 3239
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
3240 GCATACCCGCGCGCTGCGGCGCGCTGCTGCTGCGCGAGCGCTGG 3289
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
3290 AGCGCTGCCCTCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 3339
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
3340 CTGTCCAACATGATGTCGGCTCTCCTCAAGTGCAGC 3375

seq_name: /SIDS1/cgdata/geneseq/geneseq/NA1993.DAT:AAQ41604
seq_documentation_block:
ID_AAQ41604 standard; cDNA; 336 BP.
XX AC AAQ41604;
XX XX
XX DT 26-AUG-1993 (first entry)
XX XX Transforming Growth Factor-beta2(44/45)beta1 hybrid.
XX DE
XX XX

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```

KW hTGF-beta1; hTGF-beta2; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..336
XX FT /*tag= a
XX FT /note= "TGF-beta2=1-132, TGF-beta1=133-336"
XX PN EP542679-A.
XX PD 19-MAY-1993.
XX XX 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX XX (CIBA ) CIBA GEIGY AG.
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX DR WPI: 1993-161126/20.
XX DR P-PSDB; AAR39643.
XX PT New hybrid transforming growth factor-beta molecules - comprise
XX PT portions of mature TGF-beta isoforms; useful as wound healants,
XX PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 8; Page 28; 48pp; English.
XX CC The invention covers hybrid TGF-beta molecules consisting of parts
XX CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX CC derived from different parent isoforms are pref. between amino acids
XX CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
XX CC possible hybrids using these hinge points and one part each
XX CC from two of the isoforms, 6 are preferred including the hybrid
XX CC TGF-beta2(44/45)beta1. The hybrid molecules promote cell migration,
XX CC inhibit the growth of A375 melanoma cells, accelerate the healing of
XX CC partial-thickness burn wounds and full-thickness incisional wounds and
XX CC increase formation of fibrous granular tissue.
XX CC See AAQ41602-Q41607 for the most pref. hybrids.
XX XX
XX SQ Sequence 336 BP; 71 A; 99 C; 97 G; 69 T; 0 other;

alignment_scores:
    Quality: 496.00      Length: 112
    Ratio: 5.010        Gaps: 0
    Percent Similarity: 88.393      Percent Identity: 75.000

alignment_block:
TGFB3P x AAQ41604 ..

Align seg 1/1 to: AAQ41604 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCTTTGGATCGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAAATGCCAATCTTGCCTCGGCGCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTGCGCTGTACAACCA 200

```

```

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||||:::||||| ||||||| |||
201 GCATAACCCGGCGCGCTCGCGCGCGCTGCTGCTGCCGCGAGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||||| ||||||| ||||||| ||||||| |||
251 AGCCGCTGCCCATCGGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||||:::||||| ||||||| |||
301 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGC 336

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41599

seq_documentation_block:

ID_AAQ41599 standard; cDNA; 345 BP.

XX_AAQ41599;

XX_26-AUG-1993 (first entry)

XX_Mature human Transforming Growth Factor-beta1.

XX_hTGF-beta1; hybrid protein; wound healing; cancer treatment;
KW_bone repair; growth regulation; ss.

XX_Homo sapiens.

XX_Key Location/Qualifiers
FH_mat_peptide 1..336
FT /*tag= a

XX_EP542679-A.

XX_19-MAY-1993.

XX_03-NOV-1992; 92EP-0810845.

XX_11-NOV-1991; 91EP-0810870.

XX_(CIBA) CIBA GEIGY AG.

XX_McMaster GK, Cox D, Cerletti N, Kuhla J;

XX_WPI; 1993-161126/20.

XX_P-PSDB; AAR39638.

XX_New hybrid transforming growth factor-beta molecules - comprise
PT_portions of mature TGF-beta isoforms; useful as wound healants,
PT_cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX_Claim 4; Page 21-22; 48pp; English.

XX_The invention covers hybrid TGF-beta molecules consisting of parts
CC_of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC_AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC_derived from different parent isoforms are pref. between amino acids
CC_44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
CC_molecules promote cell migration, inhibit the growth of A375
CC_melanoma cells, accelerate the healing of partial-thickness burn
CC_wounds and full-thickness incisional wounds and increase formation
CC_of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.

XX_Sequence 345 BP; 68 A; 115 C; 102 G; 60 T; 0 other;

alignment_scores:

Quality: 496.00 Length: 111
Ratio: 5.113 Gaps: 0
Percent Similarity: 87.387 Percent Identity: 76.577

alignment_block:

TGFB3P x AAQ41599 ..

Align seg 1/1 to: AAQ41599 from: 1 to: 345

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1 AlaLeuAsnThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ||||||| ||||||| ||||||| ||||||| |||
1 GCCCTGGAGCACCACTATTGCTTCAGCTCCACGAGAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| ||||||| ||||||| ||||||| ||||||| |||
51 CGCGCAGCTGTACATTGACTTCCGCAAGACCTCGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||||| ||||||| ||||||| ||||||| |||
101 ACGAGCCCAAGGCTACCATGCCAACTTCTGCTCGGCGCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| |||||||:::||||| ||||||| |||
151 ATTTGGAGCCTGGACACGACGAGTACAGCAAGGTCTTGGCCCTGTACAACA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||||| ||||||| ||||||| ||||||| |||
201 GCATAACCCGGCGCGCTCGCGCGCGCTGCTGCTGCCGCGAGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||||| ||||||| ||||||| ||||||| |||
251 AGCGCTGCCCATCGGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCys 111
||||| |||||||:::||||| ||||||| |||
301 CTGTCCAACATGATCGTGGCTCCTGCAAGTGC 333

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11993

seq_documentation_block:

ID_AAQ11993 standard; cDNA; 339 BP.

XX_AAQ11993;

XX_29-AUG-1991 (first entry)

XX_Transforming Growth Factor beta 1.

XX_TGF-beta1; biologically active protein production; ss.

XX_Homo sapiens.

XX_EP433225-A.

XX_19-JUN-1991.

XX_27-NOV-1990; 90EP-0810922.

XX_06-DEC-1989; 89GB-0027546.

XX_(CIBA) CIBA GEIGY AG.

XX_Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

XX_WPI; 1991-180005/25.

XX_P-PSDB; AAR12402.

XX_Prodn. of Transforming Growth Factor type-beta-like proteins - by
PT_subjecting denatured monomeric form to refolding conditions

XX_Disclosure; Page 27; 35pp; English.

XX_TGF-beta1 is one example of a novel TGF-beta produced as a dimeric,
CC_biologically active protein using the method of the invention.
CC_This coding sequence was isolated from the CI-215 human glioma cell
CC_line. It was incorporated into an appropriate vector to transform
CC_Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
CC_denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M NaCl, 5mM EDTA,
CC_2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps.

CC After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
 CC conc. 10 times. The conc. soln was diluted to the original vol. with
 CC 10mM HCl and conc to a final vol of 10 ml. The supernatant from
 CC centrifugation at 5000g for 30 min contained disulphide-linked dimeric
 CC TGF-beta1.

XX
 SQ Sequence 339 BP; 66 A; 113 C; 101 G; 59 T; 0 other;

alignment_scores:
 Quality: 494.00 Length: 112
 Ratio: 5.041 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 75.893

alignment_block:
 TGF3P x AAQ11993 ..

Align seg 1/1 to: AAQ11993 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGAACTGCTGCT 50
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrPlyTyrValH 34
 51 GCGGAGCTGTACATGTACTTCGCAAGGACCTCGCTGGAAGTGGATCC 100
 34 lsgLupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 101 ACGAGCCCAAGGCTACCATGCCAATCTTGCTCGGGCCCTGCCCTAC 150
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 151 ATTTGGAGCTGGACACGACGATACAGCAAGGTCCTGGCCCTGTACAACCA 200
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 201 GCATAAGCGGGCGCTCGGGCGCGCTGCTGCTGCGCGAGCGCTGG 250
 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 251 AGCGCTGCCCATCGTGTACTAGCTGGGCGCGCAAGCCCAAGGTGGAGCAG 300
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 301 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGC 336

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1992.DAT:AAQ29178

seq_documentation_block:

XX ID AAQ29178 standard; DNA; 1565 BP.

AC AAQ29178;

XX (first entry)

DT 10-MAR-1993

DE TGF-beta 1.

XX Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;

DE Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;

KW vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.

XX Homo sapiens.

OS

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WO9216228-A.

01-OCT-1992.

13-MAR-1992; 92WO-US01993.

14-MAR-1991; 91US-0669171.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Madisen L, Merwin J, Purchio AF;

WPI; 1992-348938/42.

P-PSDB; AAR29657.

Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -

inhibits proliferation of vascular endothelial cells, useful for

treating cancer and to promote wound healing

Disclosure; Fig 1; 45pp; English.

The sequence given encodes the human transforming growth factor

(TGF) beta 1. This was used within the scope of the invention to

compare to a simian TGF hybrid termed TGF-beta 1/beta 2 (or TGF-5

beta) (see also AAQ29177). The chimeric DNA sequence could be placed

under the control of Simian virus 40 (SV40) expression regulatory

region within an expression vector and used to transfect Chinese

Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize

and secrete high levels of mature TGF-5 beta. TGF-5 beta induces

effects on the proliferation of vascular endothelial cells equivalent

to those produced by TGF-beta 1.

Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;

alignment_scores:

Quality: 489.00 Length: 112

Ratio: 4.990 Gaps: 1

Percent Similarity: 87.500 Percent Identity: 75.893

alignment_block:

TGF3P x AAQ29178 ..

Align seg 1/1 to: AAQ29178 from: 1 to: 1565

1 AlaLeuAspThrAsnTyrCysPheArgGlnAspLeuGluGluAsnCysCysVa 17

1106 GCCCTGGACACCAACTATTGCTTCAGAAATGTGCAAGATAATTGCTGCCT 1155

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrPlyTyrValH 34

1156 AGTCCGCTTTACATTGATTTC.....GATCTAGGGTGGAAATGGATCC 1199

34 lsgLupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

1200 ACGAGCCCAAGGCTACCATGCCAATCTTGCTCGGGCCCTGCCCTAC 1249

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

1250 ATTTGGAGCTGGACACGACGATACAGCAAGGTCCTGGCCCTGTACAACCA 1299

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

1300 GCATAACCCGGCGCTCGGGCGCGCTGCTGCTGCGCGAGCGCTGG 1349

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

1350 AGCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1399

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

1400 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGC 1435

```
seq_name: /SIDS1/gcgdata/geneseq/NA1988.DAT:AA81084
seq_documentation_block:
ID AA81084 standard; cDNA; 1560 BP.
XX
AC AA81084;
XX
DT 09-OCT-1990 (first entry)
XX
DE Coding sequence of simian transforming growth factor-beta 1.
XX
KW Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS Cercopithecus aethiops.
XX
FH Key Location/Qualifiers
FT CDS 261..1433
FT FT /*tag= a
FT sig_peptide 282..323
FT FT /*tag= b
FT mat_peptide 1095..1433
FT FT /*tag= c
XX
PN EP293785-A.
XX
PD 07-DEC-1988.
XX
PF 27-MAY-1988; 88EP-0108528.
XX
PR 29-MAY-1987; 87US-0055662.
PR 25-JAN-1988; 88US-0147842.
XX
PA (ONCO-) ONCOGEN.
XX
PI Purchio AF, Gentry L, Twardzik D;
XX
DR WPI; 1988-347488/49.
DR P-PSDB; AAP80647.
XX
PT Prodn. of simian transforming growth factor beta-1 - by culturing
PT transfectd eucaryotic cells, and new precursor proteins, useful for
PT treating tumours.
XX
PS Disclosure; ; pp; English.
XX
CC The cDNA is prepd. from African green monkey cell line BSC-40 and is
CC expressed in eukaryotic cells in plasmid psV2. There is 100% homology
CC between mature simian and human TGF-beta 1. The plasmid also contains
CC the SV40 promoter and a selection marker, esp. DHFR.
XX
SQ Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

alignment_scores:
Quality: 487.00 Length: 112
Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGFB3P x AA81084 ..
Align seg 1/1 to: AA81084 from: 1 to: 1560
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1095 GCCTGGACCACTACTGCTTCAGCTCCACGAGAAAGAACTGCTGCGT 1144
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 GCGGCAGCTGTATATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCC 1194
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
```

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|||||
1195 ACGAGCCCAAGGGTACCATGCAACTTCTGCCTGGGCCCTGTCCCTAC 1244
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
1245 ATTTGGAGCCTGGACGACGACGTACAGCAAGGTCCTGGCCCTGTACAACCA 1294
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||:::||||| ||||| |||||
1295 GCATAACCCGGCGCTCGGGCGCGCTGCTGCTGCGCAGGCGCTGG 1344
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||:::||||| ||||| |||||
1345 AGCCACTGCCATGCTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAG 1394
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||:::||||| |||||
1395 CTGTCCAAACATGATCGTGGCTCTCTGAAATGCAGC 1430
|||||
seq_name: /SIDS1/gcgdata/geneseq/NA1990.DAT:AAQ03508
seq_documentation_block:
ID AAQ03508 standard; DNA; 1560 BP.
XX
AC AAQ03508;
XX
DT 14-AUG-1990 (first entry)
XX
DE Simian Transforming growth factor - Beta1.
XX
KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW factors; ds.
XX
FH Key Location/Qualifiers
FT CDS 267..1437
FT FT /*tag= a
FT mat_peptide 1103..1437
FT FT /*tag= b
XX
PN EP356935-A.
XX
PD 07-MAR-1990.
XX
PF 25-AUG-1989; 89EP-0115719.
XX
PR 25-AUG-1988; 88US-0236698.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Brankovan V, Lioubin M, Purchio A;
XX
DR WPI; 1990-068723/10.
DR P-PSDB; AAR05663.
XX
CC Compens. contg. transforming growth factor beta -
CC used for inhibitions of HIV infection and replication in vivo.
XX
CC TGF-beta may be used in vivo to prevent formation of syncytia and
CC inhibit HIV infection. TGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
PS Disclosure; Fig 1; 20pp; English.
XX
SQ Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

alignment_scores:
Quality: 487.00 Length: 112
Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGFB3P x AAQ03508 ..
```

```
Align seg 1/1 to: AAQ03508 from: 1 to: 1560
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1095 GCCCTGGACACCACTACTGCTTACGCTCCACGGAGAAGAACTGCTGCGT 1144
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 GCGGAGCTGTATATGTACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1194
34 lsgLupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1195 AGGACCCCAAGGCGTACCATGCCAATCTCTGCGTGGGGCCCTGTCCCTAC 1244
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||||
1245 ATTGTGAGCGCTGGACACGACGATACAGCAAGTCTCTGGCCCTGTACAACCA 1294
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1295 GCATAACCGGGCGCGCTCGGGCGCGCGTGCCTGCGTGGCGAGGCGCTGG 1344
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1345 AGCCACTGCGCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1394
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1395 CTGTCCACATGATCGTGGCTCTCTGAAATGCAGC 1430
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT: AAN81085

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seq_documentation_block:
ID_AAN81085 standard; DNA; 1569 BP.
XX
AC_AAN81085;
DT
DT 09-OCT-1990 (first entry)
DE
DE Coding sequence of human transforming growth factor-beta 1.
XX
XX Transforming growth factor-beta 1; tumour treatment; ss cDNA.
KW
KW Homo sapiens.
OS
OS
FH
FH Key Location/Qualifiers
FT CDS 267..1442
FT /*tag= a
FT sig_peptide 288..329
FT /*tag= b
FT mat_peptide 1104..1442
FT /*tag= c
```

```
XX
XX EP293785-A.
XX
XX 07-DEC-1988.
XX
XX 27-MAY-1988; 88EP-0108528.
XX
XX 29-MAY-1987; 87US-0055662.
XX
XX 25-JAN-1988; 88US-0147842.
XX
XX (ONCO-) ONCOGEN.
XX
XX Purchio AF, Gentry L, Twardzik D;
PI
XX
XX WPI; 1988-347488/49.
XX
XX P-PSDB; AAP81362.
XX
XX Prodn. of stamian transforming growth factor beta-1 - by culturing
PT transfected eucaryotic cells, and new precursor proteins, useful for
PT treating tumours.
```

```
XX
XX Disclosure; ; pp; English.
XX
XX cDNA is human and mature human TGF-beta 1 has 100% homology with mature
XX simian TGF-beta 1.
XX
XX Sequence 1569 BP; 295 A; 563 C; 445 G; 266 T; 0 other;
SQ
alignment_scores:
Quality: 487.00 Length: 112
Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGPB3P x AAN81085 ..
Align seg 1/1 to: AAN81085 from: 1 to: 1569
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1104 GCCTGGACACCACTATTGCTTACGCTCCACGGAGAAGAACTGCTGCGT 1153
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1154 GCGGACGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1203
34 lsgLupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1204 ACGAGCCCAAGGCGTACCATGCCAATCTCTGCGTGGGGCCCTGTCCCTAC 1253
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||||
1254 ATTGTGAGCGCTGGACACGACGATACAGCAAGTCTCTGGCCCTGTACAACCA 1303
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1304 GCATAACCGGGCGCGCTCGGGCGCGCGTGCCTGCGTGGCGAGGCGCTGG 1353
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1354 AGCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1403
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1404 CTGTCCACATGATCGTGGCTCTCTGAAAGTGCAGC 1439
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT: AAQ03509
```

```
seq_documentation_block:
ID_AAQ03509 standard; DNA; 1569 BP.
XX
AC_AAQ03509;
XX
XX 14-AUG-1990 (first entry)
XX
XX Human Transforming growth factor - Betal.
XX
XX HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; transforming growth factor;
XX TGF-beta1; ds.
XX
XX Key Location/Qualifiers
XX CDS 267..1437
XX /*tag= a
XX mat_peptide 1103..1437
XX /*tag= b
XX
XX EP356935-A.
XX
XX 07-MAR-1990.
XX
XX 25-AUG-1989; 89EP-0115719.
XX
```

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PR 25-AUG-1988; 88US-0236698.
XX (ONCO-) ONCOGEN LTD PARTNER.
XX Brankovan V, Lioubin M, Purchio A;
XX WPI; 1990-068723/10.
XX P-PSDB; AAR05664.
XX Compsns. contg. transforming growth factor beta -
XX used for inhibitions of HIV infection and replication in vivo.
XX TGF-beta may be used in vivo to prevent formation of syncytia and
XX inhibit HIV infection. TGF may also be used with other HIV treatments
XX (AZT, soluble CD4 etc.).
XX Disclosure; Fig 1; 20pp; English.
XX Sequence 1569 BP; 295 A; 565 C; 444 G; 265 T; 0 other;

alignment_scores:
  Quality: 487.00 Length: 112
  Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893

alignment_block:
TGFB3P x AAQ03509 ..
Align seg 1/1 to: AAQ03509 from: 1 to: 1569

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1104 GCCTCGACACCAACTATTGCTTCAGCTCCACGAGAGAAGACTGCTCGT 1153

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1154 GCAGCAGCTGATACCTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCC 1203

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1204 ACAGGCCCAAGGCTACCATCTGCTGCGGCGCTGCTGCGGCGCTGCTAC 1253

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
  ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1254 ATTGGAGCTGACACGACGAGTACAGCAAGTCTGCGCTGTACACCA 1303

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1304 GCATAACCGCGCGCTCGCGCGCGCTGCTGCTGCTGCGCGCGCTGG 1353

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1354 AGCCGCTGCGCATCTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1403

101 LeuSerAsnMetValLysSerCysLysCysSer 112
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1404 CTGTCCAACATGATCGTGGCTCCTGAAAGTGCAGC 1439

seq_name: /SID51/gcgdata/geneseq/geneseq/NA2000.DAT:AAA63944

seq_documentation_block:
ID AAA63944 standard; cDNA; 2754 BP.
XX
AC AAA63944;
XX
XX 04-DEC-2000 (first entry)
XX
DE cDNA encoding a pancreatic ductal trophic factor (PDTF).
XX Pancreatic ductal trophic factor; PDTF; mesenchyme cell;
KW transforming growth factor-beta; TGF-beta; pancreatic tissue growth;
KW pancreatic duct tissue outgrowth; diabetes; ss.
```

```
XX OS
XX Unidentified.
XX Key Location/Qualifiers
XX CDS 504..1652
XX FT /*tag= a
XX FT /product= "a pancreatic ductal trophic factor (PDTF)"
XX FT sig_peptide
XX FT mat_peptide
XX FT /*tag= b
XX FT /*tag= c
XX
XX WO200047243-A1.
XX 17-AUG-2000.
XX
XX 10-FEB-2000; 2000WO-US03424.
XX
XX 10-FEB-1999; 99US-0119574.
XX
XX (ONTO-) ONTOGENY INC.
XX
XX Guicherit O, Pang K, Wang M;
XX
XX WPI; 2000-524488/47;
XX P-PSDB; AAB08338.
XX
XX Inducing outgrowths of pancreatic duct tissue, using pancreatic ductal
XX trophic factors expressed by el4.5 pancreatic mesenchyme cells, for the
XX treatment of diabetes -
XX
XX Disclosure; Page 73-75; 76pp; English.
XX
XX The present sequence encodes a pancreatic ductal trophic factor (PDTF)
XX polypeptide. The polypeptide is expressed by el4.5 pancreatic mesenchyme
XX cells (specially members of the TGF-beta (transforming growth
XX factor-beta) super family), and is capable of stimulating growth
XX and differentiation of pancreatic tissue. The polypeptides may be used
XX for inducing outgrowths of pancreatic duct tissue, e.g. for treating
XX diabetes.
XX
XX Sequence 2754 BP; 905 A; 525 C; 599 G; 725 T; 0 other;

alignment_scores:
  Quality: 439.00 Length: 107
  Ratio: 4.933 Gaps: 0
Percent Similarity: 83.178 Percent Identity: 71.963

alignment_block:
TGFB3P x AAA63944 ..
Align seg 1/1 to: AAA63944 from: 1 to: 2754

6 TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIle 22
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1329 TATTGCTTTGGGAACAATGGCCCAACCTGCTGTGAACACCTTTTACAT 1378

22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT 39
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1379 AAATTTTCGGAAGGATCTAGGCTGGAAGTGGATCCATGAGCCTAAGGAT 1428

39 yTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp 55
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1429 ATGAAGCAAAATATTGTTTAGGAAATTTGCTTACATCTGGAGCATGGAT 1478

56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl 72
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1479 ACTCAGTACAGCAAGGTGCTATCATTTTATAATCAGAACAAATCCCGGTGC 1528

72 aserAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL 89
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1529 ATCTATATCTCCCTGCTGTGTTCTCTGATGCTTGGAGCCACTGCCATCA 1578
```

89 euTyrTrpValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
1579 TTTATATGTTGGCCGCACTGTAAGTAGAGCAGCTCTTAATATGGTG 1628
106 ValLysSerCysLysCysSer 112
1629 GTAAGTCTTGCACTGCAGC 1649

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11774

seq_documentation_block:

ID_AAQ11774 standard; DNA; 852 BP.

AC_AAQ11774;

XX 23-JUL-1991 (first entry)

XX Encodes Fb-Fb-truncated (6 Cys)-TGF-beta.

XX Transforming Growth Factor beta; AIDS; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT sig_peptide 1..180

FT /*tag= a

FT /note= "modified trp-LE leader sequence"

FT misc_RNA 181..375

FT /*tag= b

FT /product= fragment B of Staphylococcal Protein A

FT /note= "directly linked to a second Fb fragment"

FT misc_RNA 376..552

FT /*tag= c

FT /product= Fragment B of Staphylococcal Protein A

FT misc_structure 553..564

FT /*tag= d

FT /product= hinge region

FT mat_peptide 565..843

FT /*tag= e

FT /product= truncated TGF-beta containing 6 x Cys

XX WO9105565-A.

XX 02-MAY-1991.

XX 18-OCT-1990; 90WO-US06006.

XX 18-OCT-1989; 89US-0422962.

XX (CREA-) CREATIVE BIOMOLECUL.

XX Cohen CM;

XX PI

XX XX

DR WPI; 1991-148530/20.

DR P-PSDB; AAR11956.

XX XX

PT Recombinant truncated transforming growth factor-beta analogues -
capable of inducing an anti-proliferative effect in mammalian
epithelial cells in vitro

XX XX

XX Claim 23; Fig 2; 42pp; English.

PS PS

CC This synthetic gene was designed based on reported sequence data,
codons inferred from known amino acid sequences and observations of
partial homology with known genes of the TGF-beta family. It was
assembled from chemically synthesised oligonucleotides and can be
expressed in prokaryotic host cells. The truncated 6 Cys TGF-beta
protein is cleaved from the Fb-Fb domain at the hinge region to give
the truncated product.

CC See also AAQ11775, AAR11942-7 and AAR11954.

XX XX

XX Sequence 852 BP; 216 A; 222 C; 225 G; 189 T; 0 other;

alignment_scores:
Quality: 412.00 Length: 93
Ratio: 5.024 Gaps: 0
Percent Similarity: 88.172 Percent Identity: 76.344
alignment_block:
TGFB3P x AAQ11774 ..

Align seg 1/1 to: AAQ11774 from: 1 to: 852

20 LeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluPr 36
|||||
565 CTGTACATCGATTCCGTTAAAGACCTGGTGGAGTGGATTGATGAACC 614

36 oLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgS 53
|||||
615 TAAGGGTTACCATGCCAACTCTGCGTGGGCCCTTGTCCTACATCTGGT 664

53 erAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsn 69
|||
665 CTCTGGATACCCAGTACTCCAAGTGCTGCTCTGTACAAATCAGCATAAC 714

70 ProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLe 86
|||
715 CCGGGGGCTAGCGCAGCTCGTGTGTTCCACAGGCCCTTGGAAACCGCT 764

86 uThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerA 103
|
765 GCCGATCGTCTATTAGCTGCGCGCTAAGCCTAAGTTGAACAGCTGTCTA 814

103 sMetValValLysSerCysLysCysSer 112
|||
815 ACGTGATTGGCCAGTTGCCAAGTGCTCT 843

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11775

seq_documentation_block:

ID_AAQ11775 standard; DNA; 817 BP.

XX AC_AAQ11775;

XX 23-JUL-1991 (first entry)

XX Encodes Fb-Fb-truncated " (8 Cys) "-TGF-beta.

XX Transforming Growth Factor beta; AIDS; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT sig_peptide 1..180

FT /*tag= a

FT /note= "modified trp-LE leader sequence"

FT misc_RNA 181..375

FT /*tag= b

FT /product= fragment B of Staphylococcal Protein A

FT /note= "directly linked to a second Fb fragment"

FT misc_RNA 376..552

FT /*tag= c

FT /product= Fragment B of Staphylococcal Protein A

FT misc_structure 553..564

FT /*tag= d

FT /product= hinge region

FT mat_peptide 565..843

FT /*tag= e

FT /product= truncated TGF-beta containing 8 x Cys

FT /note= "only contains 6 Cys residues; sequence
disclosed in specification omits 50 bases"

XX WO9105565-A.


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PD 02-MAY-1991.
XX
XX PF 18-OCT-1990; 90WO-US06006.
XX
XX PR 18-OCT-1989; 89US-0422962.
XX
XX PA (CREA-) CREATIVE BIOMOLECUL.
XX
XX PI Cohen CM;
XX
XX WPI; 1991-148530/20.
DR P-PSDB; AAR11957.
XX
XX Recombinant truncated transforming growth factor-beta analogues -
PT capable of inducing an anti-proliferative effect in mammalian
PT epithelial cells in vitro
XX
XX Claim 23; Fig 2B; 42pp; English.
XX
XX This synthetic gene was designed based on reported sequence data,
CC codons inferred from known amino acid sequences and observations of
CC partial homology with known genes of the TGF-beta family. It was
CC assembled from chemically synthesised oligonucleotides and can be
CC expressed in prokaryotic host cells. The sequence is that given in
CC the specification, however, 50 bases should be inserted between
CC nucleotides 600 and 601 of this sequence; the two "missing" Cys
CC codons are presumably contained in the omitted sequence. The
CC truncated TGF-beta protein is cleaved from the Fb-Fb domain at the
CC hinge region to give the truncated product.
CC See also AAQ11774, AAR11942-7 and AAR11954.
XX
XX Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0 other;
SQ

alignment_scores:
    Quality: 302.50      Length: 99
    Ratio: 4.321        Gaps: 2
    Percent Similarity: 70.707      Percent Identity: 60.606

alignment_block:
TGFB3P x AAQ11775  ..
Align seg 1/1 to: AAQ11775 from: 1 to: 817

15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrp.L 31
565 TGTCTGGTGGCTGAGTGTACATCGATTTCCTGTAAGACCTGGGTGGAA 614
31 ysrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPro 47
615 GT.....
48 CysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLe 64
617 ...CCGTACATCTGGTCTCTGGATACCCAGTACTCCAAAGTGTGGTCT 663
64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81
664 GTACAATCAGCATACCGCGGGGTAGCGAGCTCCGTGTGTGTTCAC 713
81 InAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97
714 AGGCCCTGGAACCGCTGCCGATCGTCTATTACGTCCGCCCTAAGCCTAAG 763
98 ValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
764 GTTGAACAGCTGTCTACGTCGATTGTGCGGAGTGTGAAGTGTCT 808

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1986.DAT: AAN60973
seq_documentation_block:
ID AAN60973 standard; DNA; 975 BP.
XX
```

```
AC AAN60973;
XX
XX DT 28-OCT-1991 (first entry)
XX
XX DE Genomic sequence encoding TGF-beta exon.
XX
XX KW Transforming growth factor beta; cancer; wound healing.
XX
XX FH Key Location/Qualifiers
XX Intron 1..347
XX FT /*tag= a
XX Exon 348..500
XX FT /*tag= b
XX Intron 501..975
XX FT /*tag= c
XX
XX PN EP200341-A.
XX
XX PD 10-DEC-1986.
XX
XX PF 21-MAR-1986; 86EP-0302112.
XX
XX PR 22-MAR-1985; 85US-0715142.
XX 13-MAR-1987; 87US-0025423.
XX (GETH ) GENENTECH INC.
XX
XX PI Derynck RMA;
XX
XX DR WPI; 1986-326875/50.
XX
XX PT TGF-beta prodn. from transformed hosts - useful esp. for treating
XX wounds (J6 2/9/86).
XX
XX PS Disclosure; Fig 2; 26pp; English.
XX
XX CC The gene product is known to stimulate cell proliferation and
XX inhibit anchorage-dependent growth of a variety of human cancer cell
XX lines, it is esp. useful in treatment of burns and the promotion of
XX surface and internal wound healing. TGF-beta may be expressed from a
XX transformed CHO cell line.
XX See also AAN60972.
XX
XX SQ Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

alignment_scores:
    Quality: 237.50      Length: 60
    Ratio: 4.847        Gaps: 1
    Percent Similarity: 81.667      Percent Identity: 68.333

alignment_block:
TGFB3P x AAN60973  ..
Align seg 1/1 to: AAN60973 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
124 GAGAGAACTGCTGGCTGGCAGCTGATGATTGATTCCTCCGAAGGACCT 403
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
124 GGGCTTGGAAAGTGGAATCCACGAGCCCAAGGGCTACCATTCCTGCC 453
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
454 TCGGGCCCTGCCCTTACATTTGGAGCCTGGACACGACAGTACACAGGTA 503
62 .....LeuGlyLeuTyrAsnThrLeu 68
504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1990.DAT: AAQ02815
```

```

seq_documentation_block:
ID  AAQ02815 standard; DNA; 975 BP.
XX  AC
XX  AAQ02815;
XX  31-MAY-1989 (first entry)
XX  DE
XX  Sequence of genomic fragment encoding a TGF-beta 1 exon.
XX  KW
XX  Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX  inhibition.
XX  FH
XX  Key Location/Qualifiers
XX  CDS 348..500
XX  FT /*tag= a
XX  FT
XX  WO8912101-A.
XX  PN
XX  PD 14-DEC-1989.
XX  PF
XX  08-JUN-1988; 88WO-US01945.
XX  PR
XX  08-JUN-1988; 88WO-U001945.
XX  PA (GETH ) GENENTECH INC.
XX  PI
XX  Derynck RM, Goeddel DV;
XX  DR
XX  WPI; 1990-007474/01.
XX  DR P-PSDB; AAR04075.
XX  XX
XX  Nucleotide sequence encoding transforming growth factor beta-3 -used as a
XX  PT probe, or to produce TGF beta 3, for inhibition of growth of normal
XX  PT and neoplastic cells, eg A549.
XX  PA
XX  PS Disclosure; Fig. 2; 61pp; English.
XX  CC
XX  This sequence encodes an exon of transforming growth factor-beta 1 (TGF-
XX  CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.
XX  CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
XX  CC beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
XX  CC neoplastic cell growth inhibition.
XX  CC
XX  SQ Sequence 975 BP; 274 A; 183 C; 339 G; 179 T; 0 other;

```

```

alignment_scores:
Quality: 237.50 Length: 60
Ratio: 4.847 Gaps: 1
Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:
TGFB3P x AAQ02815 ..
Align seg 1/1 to: AAQ02815 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
354 GAGAGAAGTGTGCTGCGCGAGCTGTACATTGACTTCCGCAAGGACCT 403

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
|||||
404 CGCTGGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCC 453

45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||
454 TCGGGCCCTGCCCTTACATTGGAGCCTGGACAGCAGTACAGCAAGGTA 503

62 .....LeuGlyLeuTyrAsnThrLeu 68
|||||
504 CGCTGCGCACCGGGCTACGAGATCGGCTT 533

```

```

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT:AA15721
seq_documentation_block:
ID  AAT15721 standard; DNA; 975 BP.
XX  AC
XX  AAT15721;
XX  XX
XX  24-JUL-1997 (revised)
XX  DT 25-JAN-1980 (first entry)
XX  DE
XX  Partial pre-transforming growth factor beta 1 DNA.
XX  KW
XX  transforming growth factor beta 1; wound healing;
XX  recombinant production; ss.
XX  OS Homo sapiens.
XX  FH
XX  Key Location/Qualifiers
XX  exon 347..500
XX  FT /*tag= a
XX  FT /note= "encodes TGF beta 1 residues 252 to 302"
XX  XX
XX  PN US5482851-A.
XX  PD 09-JAN-1996.
XX  PF
XX  22-MAR-1985; 85US-0715142.
XX  PR
XX  13-MAR-1987; 87US-0025423.
XX  PR 22-MAR-1985; 85US-0715142.
XX  PR 04-AUG-1989; 89US-0389929.
XX  PR 04-MAR-1992; 92US-0845893.
XX  PR 05-NOV-1993; 93US-0147364.
XX  PA (GETH ) GENENTECH INC.
XX  PI
XX  Derynck RMA, Goeddel DV;
XX  DR
XX  WPI; 1996-076891/08.
XX  DR P-PSDB; AAR90828.
XX  PT
XX  New recombinant human transforming growth factor-beta prods. - produced
XX  PT using Chinese hamster ovary cells, for use in diagnostic applications
XX  PT or in therapy
XX  PS
XX  Example 2; Fig 2; 26pp; English.
XX  CC
XX  The transforming growth factor (TGF) beta 1 exon was identified using
XX  CC the "long probe" strategy used previously for TGF-alpha. Long
XX  CC oligonucleotides (T1572-23) designed on the basis of the partial protein
XX  CC sequence were used as hybridisation probes for the exon in a human
XX  CC genomic DNA library. The TGF beta 1 exon was then used as a probe for
XX  CC the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding TGF beta
XX  CC 1 is useful for the recombinant production of the protein, which is
XX  CC useful in, e.g. wound healing.
XX  CC (Revised entry submitted to correct sequence analysis breakdown.)
XX  SQ Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

alignment_scores:
Quality: 237.50 Length: 60
Ratio: 4.847 Gaps: 1
Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:
TGFB3P x AAT15721 ..
Align seg 1/1 to: AAT15721 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
354 GAGAGAAGTGTGCTGCGCGAGCTGTACATTGACTTCCGCAAGGACCT 403

```

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
 |||||
 404 CGGCTGGAAGTGGATCCACGAGCCAAAGGCTACCATGCAACTTCTGCC 453
 45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
 |||||
 454 TCGGGCCCTGCCCTACATTTGGAGCTGGACACGCGAGTACAGCAAGGTA 503
 62LeuGlyLeuTyrAsnThrLeu 68
 |||||
 504 CGTCTGGCCACCGGCTACGAGATGCGCTT 533

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52936

seq_documentation_block:
 ID AAV52936 standard; DNA; 975 BP.

XX AC AAV52936;

XX DT 21-DEC-1998 (first entry)

XX DE Human transforming growth factor-beta gene exon fragment.

XX KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT intron 1..346

FT exon /*tag= a

FT exon 347..500

FT intron /*tag= b

FT exon 501..976

FT intron /*tag= c

XX PN US5801231-A.

XX PD 01-SEP-1998.

XX PF 22-MAR-1985; 85US-0715142.

XX PR 13-MAR-1987; 87US-0025423.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PR 05-NOV-1993; 93US-0147364.

XX PR 30-MAY-1995; 95US-0454468.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX DR WPI; 1998-494840/42.

XX DR P-PSDB; AAW78788.

XX PT DNA encoding transforming growth factor-beta precursor sequence -
 useful for analysis to perform manipulations to increase yield of
 recombinant production of the protein

XX PS Example 2; Fig 2; 26pp; English.

XX CC This nucleotide sequence comprises a fragment of the human
 transforming growth factor-beta 1 (TGF-beta 1) gene incorporating
 an exon and flanking intron sequences. It was isolated from a
 human genomic library using probes based on a partial protein
 sequence of TGF-beta 1. The exon encodes amino acids 288-338
 (see AAW78788) of TGF-beta 1. Restriction fragments of the isolated
 exon were used as probes for the isolation of TGF-beta 1 cDNAs
 (see AAV52933). The invention relates to the recombinant production
 of TGF-beta. Nucleic acids encoding TGF-beta have been isolated
 and cloned into vectors which are replicated in bacteria and
 expressed in eukaryotic cells. TGF-beta recovered from transformed

CC cells is used in known therapeutic applications. TGF-beta nucleic
 acids are also useful in diagnosis and identification of TGF-beta
 clones.

XX SQ Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

alignment_scores:

Quality: 237.50 Length: 60

Ratio: 4.847 Gaps: 1

Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:

TGFB3P x AAV52936 ..

Align seg 1/1 to: AAV52936 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
 |||||
 354 GAGAAGAACTGCTGGCTGGCGAGCTGTACATTGACTTCGCAAGGACCT 403

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
 |||||
 404 CGGCTGGAAGTGGATCCACGAGCCAAAGGCTACCATGCAACTTCTGCC 453

45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
 |||||
 454 TCGGGCCCTGCCCTACATTTGGAGCTGGACACGCGAGTACAGCAAGGTA 503

62LeuGlyLeuTyrAsnThrLeu 68

|||||

504 CGTCTGGCCACCGGCTACGAGATGCGCTT 533

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56924

seq_documentation_block:

ID AAQ56924 standard; DNA; 975 BP.

XX AC AAQ56924;

XX DT 09-JUL-1994 (first entry)

XX DE Human pre-TGF-beta-1.

XX KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
 transforming growth factor beta-3; recombinant; wound healing;
 vulnerable.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT exon 1..975

FT exon /*tag= a

FT exon /*codon_start= 348..350

XX PN US5284763-A.

XX PD 08-FEB-1994.

XX PF 22-MAR-1985; 85US-0715142.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 13-MAR-1987; 87US-0025423.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX DR WPI; 1994-056343/07.

XX DR P-PSDB; AAQ56924.


```

DT 11-MAY-2001 (first entry)
DE Salmon GDF-8 allele 2 coding sequence.
XX
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musclogenative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease; ss.
XX
OS Oncorhynchus sp.
XX
XX WO200112777-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22884.
XX
XX 19-AUG-1999; 99US-0378238.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;
XX
XX WPI; 2001-211209/21.
XX
XX P-PSDB; AAB73198.
XX
XX New substantially purified growth differentiation factor-8 polypeptide,
XX useful for treating muscle wasting disease, obesity, muscular
XX dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
XX and cachexia -
XX
XX Claim 39; Fig 2; 124pp; English.
XX
XX The present invention relates to growth differentiation factor-8 (GDF-8)
XX coding sequences and proteins. The present sequence is a coding sequence
XX for GDF-8, which was isolated in the present invention. GDF-8 is useful
XX for treating neurodegenerative diseases (e.g. amyotrophic lateral
XX sclerosis and muscular dystrophy), musclogenative diseases or in
XX tissue repair due to trauma, obesity and disorders related to abnormal
XX proliferation of adipocytes. GDF-8 is also useful for treating
XX or adipose tissues and in gene therapy for the treatment of cell
XX GDF-8 is also useful for treating muscle wasting disease, neuromuscular
XX disorder, spinal cord injury, traumatic injury, congestive obstructive
XX pulmonary disease (COPD), AIDS or cachexia.
XX
XX Sequence 412 BP; 91 A; 134 C; 112 G; 75 T; 0 other;

alignment_scores:
  Quality: 216.50      Length: 108
  Ratio: 3.331         Gaps: 4
  Percent Similarity: 60.185      Percent Identity: 38.889

alignment_block:
TGFB3P x AAF63558 ..
Align seg 1/1 to: AAF63558 from: 1 to: 412

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
116 GAGTCCGGTGTGCGCGGTACCCCGCTCACGCGTGGACTTT...GAAGACTT 162
28 uGlyTyrLysTrpValHisGluProLysGlyTyrTyrAlaAspPheCys 45
163 TGCTGGAGTGGATTATTCGCCCAAGCCGCTACAGGCCCAACTACTGCT 212
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
213 CTGCTGAGTGGAGTACATGCACCTGCAGAGTACCCCAACACC..... 256

```

```

62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
257 ...CACCTGGTGAACAGGCTAACCCCTGCGGCACCGGGGGCCCTGCTG 303
78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyr..... 91
304 CACCCCAACCAAGATGTCCTCCCATCATCATGCTCTACTTCAACCGCAAG 353
92 .....ValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
354 AGCAGATCATCTACGGCAAGATCCCC.....TCCATG 385
105 ValValLysSerCysLysCysSer 112
386 GTGGTGACCGCTGCGGTGCTCG 409

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA2001.DAT:AAF63557
seq_documentation_block:
ID AAF63557 standard; cDNA; 476 BP.
XX
XX AAF63557;
XX
XX 11-MAY-2001 (first entry)
XX
XX Salmon GDF-8 allele 1 coding sequence.
XX
XX Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
XX neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
XX muscular dystrophy; musclogenative disease; tissue repair;
XX muscle wasting disease; neuromuscular disorder; spinal cord injury;
XX traumatic injury; congestive obstructive pulmonary disease; ss.
XX
XX Oncorhynchus sp.
XX
XX WO200112777-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22884.
XX
XX 19-AUG-1999; 99US-0378238.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;
XX
XX WPI; 2001-211209/21.
XX
XX P-PSDB; AAB73197.
XX
XX New substantially purified growth differentiation factor-8 polypeptide,
XX useful for treating muscle wasting disease, obesity, muscular
XX dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
XX and cachexia -
XX
XX Claim 39; Fig 2; 124pp; English.
XX
XX The present invention relates to growth differentiation factor-8 (GDF-8)
XX coding sequences and proteins. The present sequence is a coding sequence
XX for GDF-8, which was isolated in the present invention. GDF-8 is useful
XX for treating neurodegenerative diseases (e.g. amyotrophic lateral
XX sclerosis and muscular dystrophy), musclogenative diseases or in
XX tissue repair due to trauma, obesity and disorders related to abnormal
XX proliferation of adipocytes. GDF-8 is also useful for treating
XX or adipose tissues and in gene therapy for the treatment of cell
XX GDF-8 is also useful for treating muscle wasting disease, neuromuscular
XX disorder, spinal cord injury, traumatic injury, congestive obstructive
XX pulmonary disease (COPD), AIDS or cachexia.
XX
XX Sequence 476 BP; 111 A; 145 C; 133 G; 87 T; 0 other;

```


109 CysLysCysSer 112
1114 TCGGGTGTCTCA 1125

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ06453

seq_documentation_block:
ID AAZ06453 standard; cDNA; 1128 BP.

XX AAZ06453;

DT 08-DEC-1999 (first entry)

DE cDNA of Baboon Growth Differentiation Factor-8.

XX growth differentiation factor; tissue growth; muscle growth;
KW cell differentiation; animal feed; muscle disorder;
KW bone degeneration; nerve degeneration; GDF-8; development;
KW transforming growth factor beta; TGF-beta; ds.

XX Papio anubis.

PN WO9940181-A1.

PD 12-AUG-1999.

PF 05-FEB-1999; 99WO-US02511.

XX 28-JUL-1998; 98US-0124180.

PR 05-FEB-1998; 98US-0019070.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

XX WPI; 1999-494289/41.

DR P-PSDB; AAY33843.

XX New differentiation factor useful for treating neurodegenerative diseases

XX Example 9; Fig 14a; 138pp; English.

XX This is the cDNA nucleotide sequence of the Baboon Growth Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from this species were screened with the murine GDF-8 probe, in order to isolate the GDF-8. The absolute conservation of the C-terminal region between species as evolutionarily far apart as humans and chickens, baboons and turkeys, suggests that this region will be highly conserved in many other species as well.
CC GDF-8 has been shown to result in increased bone and muscle mass (such as ribs) when expressed in reduced amounts. GDF-8 minus transgenic animals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.
CC GDF-8 expression may also have a role in the therapy of abnormal growth of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient suffering from a disorder such as muscle wasting disease, neuro muscular disorder, muscle atrophy, osteoporosis, bone degenerative diseases, obesity or other adipocyte cell disorders, and aging for example.
XX Sequence 1128 BP; 371 A; 225 C; 238 G; 294 T; 0 other;

alignment_scores:
Quality: 208.50 Length: 104
Ratio: 3.159 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 40.385

alignment_block:
TGFB3P x AAZ06453 ..

Align seg 1/1 to: AAZ06453 from: 1 to: 1128

12 GluGluAsnCysCysValargProLeuTyrlleAspPheArgGlnAspLe 28
||||:||||| ||||| :||||| :||
832 GAATCGCGATGCTGCTGTACCTCTAAGTGGATTTT...GAAGCTCT 878

28 uGlyTrpLysTrpValHisGluProLysGlyTyTyTyAlaAsnPhCysS 45
||||| :||||| ||| :||||| :||
879 TGGATGGGATTGGATTATCGCTCCTAAAAGATATAAGGCCAATTACTGCT 928

45 erGlyProCysPro.....TyrlLeuArgSerAlaAspThrThrHisSer 59
||||| ||| :||||| :||||| :||
929 CTGGAGAGTGTGAATTGTATTTTACAAAAATATCCTCATCTCAT... 975

60 ThrValLeuGlyLeuTyTyAsnThrLeuAsnProGluAlaSerAlaSerPr 76
||| :||| :||||| :||||| :||
976CTGGTACACCAACCAACCCAGAGGTTTCAGCAGGCC 1013

76 oCysCysValProGlnAspLeuGluProLeuThrleLeuTyTyTyValG 93
||||| :||||| :||||| :||||| :||
1014 TTGCTGTACTCCCAAGATGCTCCCAATTAATATGCTATATATTTAATG 1063

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
||||| :||| :||||| :||||| :||
1064 GCAAGAACAAATAATATATGGGNAATTCAGCCATGCTAGTAGACGC 1113

109 CysLysCysSer 112
||| |||||

1114 TCGGGTGTCTCA 1125

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ09366

seq_documentation_block:
ID AAZ09366 standard; cDNA; 1128 BP.

XX AAZ09366;

XX 29-OCT-1999 (first entry)

XX Baboon GDF-8 cDNA.

XX GDF-8; growth differentiation factor receptor; GDF-11; therapy; human;
KW veterinary; medicine; treatment; muscle tissue disease; wasting disease;
KW neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat;
KW traumatic injury; acquired immune deficiency syndrome; cachexia; baboon;
KW congenital obstructive pulmonary disease; transgenic animal; transgene;
KW food animal; cholesterol; muscle mass; diagnostic; ds.

OS Papio sp.

XX Key Location/Qualifiers

FT CDS 1..1128

FT /*tag= a

FT /product= "GDF-8"

XX WO9906559-A1.

XX 11-FEB-1999.

XX 28-JUL-1998; 98WO-US15598.

XX 01-AUG-1997; 97US-0054461.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron A;

XX WPI; 1999-153789/13.

XX P-PSDB; AAY31190.

XX Recombinant cells that express growth-differentiation factor receptors - and related antibodies, nucleic acids, vector,

```

; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; US-08-486-057B-3

alignment_scores:
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    Ratio: 5.652         Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCTTTGGACACCAATTAAGTCTCCGCACTTGGAGGAACTGCTGTGT 50

17 largProLeuTyrIleAspPheArgGlnAspLeuglyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATGTGACTTCGACAGGATCTGGGCTGGAAGTGGTCC 100

34 lsGluProLysGlyTyrTyrIleAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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201 TCTGAACCTTGAAGCATCTGCCTCGCCTTGTGCTGCCCGCCAGGACCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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301 CTCTCCAACAATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-33

seq_documentation_block:
; Sequence 33, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Ian
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
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; NAME/KEY: mat_peptide
; LOCATION: 1
; US-08-470-837-33

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000
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1 GCTTTGGACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTTACATGACTCCACAGGATCTGGCTGGAGTGGGTCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACCAACCCAGCAGCGTCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCCTTGCCTGCGCTGGTGGAGTGGGTCC 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCTGCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-789-588-3

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; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...339
US-08-789-588-3

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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1 GCTTTGGACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTTACATGACTCCGACAGGATCTGGGCTGGAAAGTGGGTCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACCAACCCAGCAGCGTCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCCTTGCCTGCGCTGGTGGAGTGGGTCC 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCTGCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-5

seq_documentation_block:
; Sequence 5, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430e1 process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.htGF-beta3 (DSM 5658)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta3"
US-09-123-233-5

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: US-09-123-233-5 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCTTTGGACACCAATTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATGACTCTCCGACAGGATCTGGGCTGGAGTGGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGGCCATAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCCGCGAGTGCAGACACACACCCAGCAGCGTGTGGGACTGTACAACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCGCTGCTGCGCTGCGCCAGGACCTGG 250

84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
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301 CTCTCCAACATGGTGTGAAGTCTTTGTAATGTAGC 336

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: PCT-US91-04541-1

seq_documentation_block:
Sequence 1, Application PC/TUS9104541
GENERAL INFORMATION:
APPLICANT: Oncogene Science Inc.
TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/04541
FILING DATE: 19910625
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Transforming Growth Factor-Beta 3
IMMEDIATE SOURCE:
CLONE: TGF-B3
FEATURE:
NAME/KEY: CDS
LOCATION: 263..1498
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 263..1498
OTHER INFORMATION:
PCT-US91-04541-1

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1213 GCGCCCCCTCTACATGACTCTCCGACAGGATCTGGGCTGGAGTGGGTCC 1262

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1263 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGGCCATAC 1312

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1313 CTCCGCGAGTGCAGACACACCCAGCAGCGTGTGGGACTGTACAACAC 1362

METHODS OF PR

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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1413 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1462

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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5262319-1
seq_documentation_block:
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO:1
; LENGTH: 2529
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Ratio: 5.652 Gaps: 0
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1213 GCSCCCCTCTACATTCGACATCCGACAGGATCTGGGCTGGAGTGGTCC 1262

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1263 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 1312

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block:
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:9
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Percent Similarity: 99.107 Percent Identity: 98.214

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1209 GCGCCCTCTACATTCGACATCCGACAGGATCTGGGCTGGAGTGGTCC 1258

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCGTAC 1308

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCCGAGTCACACACACACACACACACACACACACACACACACAC 1358

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CTTGAACCCCGAAGCTCGGCTCTCCGCTGCTGCGTGGCCCGAGGACCTGG 1408

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block:
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
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  |||
  328 GGGCCCCCTCTACATGACTTCGCACAGGATCTGGGCTGGAGTGGGTCC 377

  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
  |||
  427 CTCGCCAGTGCAGACACACACCCAGCAGCGTGTGGGACTGTACAACAC 476

  67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
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  477 TCTGAACCTTGAAGCATCTGCCTCGCTTGTCTGCAATGCCCGGAGCTGG 526

  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
  |||
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  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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  577 CTCTCCACATGGTGGTGAAGTCTTGTAATGTAGC 612

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seq_documentation_block:
; Sequence 7, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123.233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "recombinant hybrid DNA of
; TGF-beta1 and TGF-beta3 DNA"
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLmu.TGF-beta1(44/45)beta3
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..132
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seq_documentation_block:
; Sequence 2, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-486-057B-2

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
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Align seq 1/1 to: US-08-486-057B-2 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCITTTGGATCGCGCCTATTGCTTTAGAAATGTCAGGATAAATTGCTGCCT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:
51 ACGTCCACTTTTACATTGATTTCAGAGAGGATCTAGGTGGAAATGGATAC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ACGAACCCAAAGGGTACAATGCCCAACTTCTGCTGGAGCATGCCCGTAT 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 TTATGGAGTTCACACTCAGCACGAGGCTCTGAGCTTATATAATAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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201 CATAAATCCAGAGCATCTGCTTCTCCTGCTGCTGCCAAGATTAG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:
251 AACCTCTAACCATTTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300

101 LeuSerAsnMetValVallYsserCysLysCysSer 112
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301 CTTTCTAATGATTGAAGCTTGCAGGATGCGC 336

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-470-837-31
seq_documentation_block:
; Sequence 31, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
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251 AACCTCTAACCAATCTCTACTACTATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValVallySerCysLysCysSer 112
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301 CTTTCTAAATGATTGTAAGTCTTGCAAAATGCAGC 336

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-3

seq_documentation_block:
; Sequence 3, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.htGF-beta2 (DSM5657)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta2"
US-09-123-233-3

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
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Align seg 1/1 to: US-09-123-233-3 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCTTTGGATGCGCCCTATTGCTTTAGAAATGTGAGGATAATGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
:|||||
51 ACCTCCACTTTACATGATTTCAGAGGGATCTAGGTGGAATGGATAC 100
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAACCCAAAGGGTACAATGCCAATCTCTGTCTGGAGCATGCCGCTAT 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGTTACAGACTACAGACAGAGGGTCCCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
:|||||
201 CATAAATCCAGAGGATCTGCTTCCTTCCTGCTGCTGCTGCTGCTGCT 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AACCTCTAACCAATCTCTACTACTATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValVallySerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-03705-4

seq_documentation_block:
; Sequence 4, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; TITLE OF INVENTION: TRANSFORMING GROWTH
; INHIBITORS
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; TITLE OF INVENTION: TRANSCRIPTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US94-03705-4

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
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Align seg 1/1 to: PCT-US94-03705-4 from: 1 to: 1695
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1088 GCTTTGGATGCGCCCTATTGCTTTAGAAATGTGAGGATAATGCTGCCT 1137
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1138 ACCTCCACTTTACATGATTTCAGAGGGATCTAGGTGGAATGGATAC 1187

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alignment_scores:      Length: 112
                        Quality: 532.00
                        Ratio: 5.115
                        Gaps: 0
                        Percent Similarity: 92.857
                        Percent Identity: 79.464

alignment_block:
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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
1145 AGCTCCACCTTACATGATTTCGAAGGAGGTCTAGGGTGGAAATGGATAC 1194

34 isGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyr 50
1195 AGCAACCCAAAGGGTACATGCCAACTCTGTGCTGGAGCATGCCCGTAT 1244

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1245 TTATGGAGTTCAGACACTCAGCAGCAGCGGTCTTGAGCTTATATAATAC 1294

67 rleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1295 CATAATCCGAAGCATCTGCTCTCCTGCTCGGTGCCAAGATTATG 1344

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1345 AACCTCTACCATTCTCTACTACATTGGCAAAACACCCAGAGATTGACAG 1394

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1395 CTTTCTAAATGATTGTTAAAGTCTTGCAATGCAGC 1430

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-669-171-3
seq_documentation_block:
; Sequence 3, Application US/07669171
; Patent No. 530451
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/D2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-669-171-3

alignment_scores:
Quality: 513.00 Length: 112
Ratio: 5.079 Gaps: 0
Percent Similarity: 90.179 Percent Identity: 76.786

alignment_block:
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1104 GCGCTGGACCAACCACTATTGCTTCAGAAATGTGCAGGATAATTGCTGCCT 1153
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrIleValH 34
1154 AGTCGCGCTTTACATTCATTTCAGAGGATCTAGGCTGGAAGTGGATCC 1203
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1204 ACGAGCCCAAGGCTACCATGCCAACTTCGCTCGGCGCTGCCCTAC 1253
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1254 ATTTGGAGCGCTGGACACAGCAGTACAGCAAGGTCTGGCCCTGTACAACCA 1303
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1354 AGCGCTGCGCCATCGTGTACTACTGTCGCGCGCAGCCCAAGTGGAGCAG 1403
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-486-057B-1
seq_documentation_block:
; Sequence 1, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
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US-08-486-057B-1

alignment_scores:
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Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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201 GCATAACCGGGCGCTCGGCGCGCGCTGCTGCTGCGCGCGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-29

seq_documentation_block:
; Sequence 29, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/470,837
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30630-1US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1
US-08-470-837-29

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
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Align seg 1/1 to: US-08-470-837-29 from: 1 to: 339
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1 GCCCTGGACACCAACTATTCTTCAGCTCCACGAGGAAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ATGAGCCCAAGGCTACCATGCTCCCAACTTCTGCTCGGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACAGCGACGAGTACAGCAAGGCTCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCGGGCGCTCGGCGCGCGCTGCTGCTGCGCGAGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTGTCCAACATGATCGTGGCTCTGCAAGTGGCAGC 336

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-789-588-1

seq_documentation_block:
; Sequence 1, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert

APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-789-588-1

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

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Align seg 1/1 to: US-08-789-588-1 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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1 GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACTGCTGCT 50
1 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerglyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACAGCGAGTACAGCAAGGTCTCTGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGGCGCTCGGGCGCGCTGCTGCGTCCGCGAGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTCTACTAGTGGCCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCAACATGATCGTGGCTCTCTCAAGTGCAGC 336
seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-1
seq_documentation_block:
; Sequence 1, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.htGF-beta1 (DSM 5656)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human tGF-beta1"
US-09-123-233-1

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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1 GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACTGCTGCGT 50
1 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1826 ATTGGAGCGTGGACACGAGTACAGCAAGTCTGGCGCTGTACAACCA 1875
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1876 GCATAACCCGGCGCGCTCGCGCGCGTGTGCTGCGCGCAGCGCTGG 1925
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1926 AGCGCGTCCCATCGGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1976 CTGTCCAACATGATCGTGGCTCTCAAGTGCAGC 2011

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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: PCT-US94-03705-3

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seq_documentation_block:
; Sequence 3, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; APPLICANT: Mark A. Perrella
; TITLE OF INVENTION: TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; TITLE OF INVENTION: TRANSCRIPTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2745
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US94-03705-3

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alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500      Percent Identity: 76.786
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1679 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTCGT 1728
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1729 GCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1778
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1779 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1828
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1829 ATTGGAGCGCTGGACACGACGACGCAAGGTCTGCGCTGTACAACCA 1878
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67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
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1879 GCATAACCCGGCGCGCTCGCGCGCGTGTGCTGCGCGCAGCGCTGG 1928
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1929 AGCGCGTCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1978
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1979 CTGTCCAACATGATCGTGGCTCTCAAGTGCAGC 2014

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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq: 5168051-3

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seq_documentation_block:
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:3:
; LENGTH: 975
5168051-3

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alignment_scores:
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  Ratio: 4.724        Gaps: 1
  Percent Similarity: 81.667      Percent Identity: 66.667
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Align seg 1/1 to: 5168051-3 from: 1 to: 975

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12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
354 GAGAAGAACTGCTCGCGCGCAGCTGTACATTGACTTCCGCAAGGACCT 403
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
404 CGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCATGCCACCTTCGCC 453
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
454 TCGGGCCCTGCCCTACATTGGAGCGCTGGACACGACGACGACGAGTA 503
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 .....LeuGlyLeuTyrAsnThrLeu 68
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504 CGTGTGCCACCGGGCTACGAGATGCGCTT 533

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq: US-08-274-215A-11

[illegible]

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TGFB3P x US-08-765-662-11  ..
Align seg 1/1 to: US-08-765-662-11 from: 1 to: 360

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46 TGTTCAGCGAGACCATACGTAGACTTC...CAGGAACCTGGGATGGCG 92

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
: |||:|||||:|||||:|||||:|||||
93 GGACTGGATACGACCGCGAGGGGTACCAGCTGATTTACTGCAGTGGCG 142

47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
||| |||:|||||: ||| |||:|||||
143 AGTGCCTCCACCTGGTGGCAGCCAGCATTTGCTCTTTCCAT 192

59 SerThrValLeuGlyLeuAsnThrLeuAsnProGluAlaSerAlaSe 75
||||| |||:|||||: ||| |||:|||||
193 TCTGCGCTCTTCCAGCTCTCTCAAGCCACATCTTGGCCTGCCAGTAC 242

75 rProCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
: |||:|||||: |||:|||||: |||:|||||
243 CTCCTGTTGTCTCTACTGCGCGAGGGCCCTCTCTCTCTCTCTCTCT 292

91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
: |||:|||||: |||:|||||: |||:|||||
293 ATCATATGGCAATGGTCAAGACGGAT...GTGCCAGATATGGTGGTG 339

107 LysSerCysLysCysSer 112
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340 GAGGCGCTGGCTGCAGC 357

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-184-933-11

seq_documentation_block:
; Sequence 11, Application US/09184933
; Patent No. 6130050
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Esqueda, Aurora F.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,933
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/274,215
; FILING DATE: 13-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-68-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...357
; US-09-184-933-11

alignment_scores:
Quality: 206.00 Length: 106
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Percent Similarity: 69.811 Percent Identity: 41.509

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Align seg 1/1 to: US-09-184-933-11 from: 1 to: 360

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46 TGTTCAGCGAGACCATACGTAGACTTC...CAGGAACCTGGGATGGCG 92

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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93 GGACTGGATACGACCGCGAGGGGTACCAGCTGATTTACTGCAGTGGCG 142

47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
||| |||:|||||: ||| |||:|||||
143 AGTGCCTCCACCTGGTGGCAGCCAGCATTTGCTCTTTCCAT 192

59 SerThrValLeuGlyLeuAsnThrLeuAsnProGluAlaSerAlaSe 75
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193 TCTGCGCTCTTCCAGCTCTCTCAAGCCACATCTTGGCCTGCCAGTAC 242

75 rProCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
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243 CTCCTGTTGTCTCTACTGCGCGAGGGCCCTCTCTCTCTCTCTCTCT 292

91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
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107 LysSerCysLysCysSer 112
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340 GAGGCGCTGGCTGCAGC 357

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-184-933-11

seq_documentation_block:
; Sequence 11, Application PC/TUS9508745
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
;
; seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-08745-11

seq_documentation_block:
; Sequence 11, Application PC/TUS9508745
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
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; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/764,731B  
; FILING DATE: 19910924  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kapinos, Ellen J.  
; REGISTRATION NUMBER: 32,245  
; REFERENCE/DOCKET NUMBER: G15159B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-876-1170  
; TELEFAX: 617-876-5851  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 400 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: C-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; CELL LINE: U2-OS Osteosarcoma  
; IMMEDIATE SOURCE:  
; LIBRARY: U2-OS human osteosarcoma cDNA library  
; CLONE: U2-7  
; POSITION IN GENOME:  
; UNITS: bp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..399  
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; NAME/KEY: mat_peptide  
; LOCATION: 1..400  
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US-07-764-731B-5
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20 utvrtleAaspPheArgGlnAspLeuGlyTrpLys...TriValHisGluP 36  
|||||.....| | | | | | | | | | | | : | | | | | | | | | |  
108 GTATGTGGATTTC....CAAGACCTGGGATGCCAGGACTGGATCATTGCCAC 154  
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36 roLYSGLyTYrTYrAlaAsnPHeCysSerGlyProCysProTYrLeuArg 52  
|||||.....| | | | | | | | | | | | : | | | | | | | | | |  
155 CCAGAGGCTATGCTGCCAATTACTGTGATGAGAATACTCTCTCCACTC 204  
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; ORGANISM: bmp-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..396
US-08-360-914B-7

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  Quality: 206.00      Length: 113
  Ratio: 2.822        Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: US-08-360-914B-7 from: 1 to: 406

4 ThrAsnTyrCysPheArgGlnAsnLeuGluGlnAsnCysCysValArgProLe 20
58 TCAGATTACACACAGCAGTGAATTGAAACAGCCTGCAGGAAGCATGAGCT 107
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGACTGGATCATTCGCAC 154
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
155 CCAAGGCGTATGCTGCCAATTACTGTGATGGAGAATGCTCCTTCCCACTC 204
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
205 AACGCACACATGAATGCAACCAACCGCGATTGTGCAGACCTTGGTTCA 254
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
255 CCTTATGAACCCGAGTATCTCCCAACCGTGTGTGCGCCAACTAAGC 304
83 euGluProLeuThrIleLeuGlyValGlyArgThrProLysVal... 98
305 TAAATGCCATCTCGGTTCTTACTTTGATGACACAACTCCCATGTCTCTG 354
99 GluGlnLeuSerAsnMetValLysSerCysLysCys 111
355 AAAAAATACAGGAATATGGTTGTAAGACTTGTGGATGC 393

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seq_documentation_block:
; Sequence 7, Application US/08741589A
; Patent No. 5804416
; GENERAL INFORMATION:
; APPLICANT: Neil M. WOLFMAN and John MCCOY
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,589A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
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; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-6
; NAME/KEY: CDS
; LOCATION: 1..396
US-08-741-589A-7

alignment_scores:
  Quality: 206.00      Length: 113
  Ratio: 2.822        Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: US-08-741-589A-7 from: 1 to: 406

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58 TCAGATTACACAGCAGTGAATTGAAACAGCCTGCAGGAAGCATGAGCT 107
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGACTGGATCATTCGCAC 154
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
155 CCAAGGCGTATGCTGCCAATTACTGTGATGGAGAATGCTCCTTCCCACTC 204
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
205 AACGCACACATGAATGCAACCAACCGCGATTGTGCAGACCTTGGTTCA 254
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
255 CCTTATGAACCCGAGTATCTCCCAACCGTGTGTGCGCCAACTAAGC 304
83 euGluProLeuThrIleLeuGlyValGlyArgThrProLysVal... 98
305 TAAATGCCATCTCGGTTCTTACTTTGATGACACAACTCCCATGTCTCTG 354
99 GluGlnLeuSerAsnMetValLysSerCysLysCys 111
355 AAAAAATACAGGAATATGGTTGTAAGACTTGTGGATGC 393

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seq_documentation_block:
; Sequence 7, Application PC/TUS9413181
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
```

```
;
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13181
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..396
;
PCT-US94-13181-7

alignment_scores:
    Quality: 206.00    Length: 113
    Ratio: 2.822      Gaps: 4
    Percent Similarity: 64.602    Percent Identity: 37.168

alignment_block:
TGFB3P x PCT-US94-13181-7 ..
Align seg 1/1 to: PCT-US94-13181-7 from: 1 to: 406

4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
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58 TCAGATTACACAGCAGTGAATTGAAACAGCGCTGCAGGAAGCATGAGCT 107
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGlu 36
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGGACTGGATCATTCAC 154
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
155 CCAAGGGCTATGCTGCCAATTACTGTGATGGAGAAATGCTCTCCCACTC 204
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
   :::::|::| |||:::|::| |||:::|::| |||:::|::|
205 ACGGCACACATGAATGCACACCAACCGGATGTGCAGACATTTGGTTCA 254
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
   : :::::|::| :::::|::| :::::|::| :::::|::|
255 CCTTATGAACCCCGAGTATGTCCCAACCGTGTGTGGCCCACTAAGC 304
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
305 TAAATGCCATCTCGTTCCTTTACTTTTGATGACAACCTCAATGTCATTCG 354
   |||:::|::| |||:::|::| |||:::|::| |||:::|::|
99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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355 AAAAAATACAGGAATATGTTGTAAGAGCTTGTGGATGC 393
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seq_documentation_block:
; Sequence 3, Application US/07764731B
; Patent No. 5366875
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/764,731B
; FILING DATE: 19910924
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: G15159B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; TISSUE TYPE: Fetal long bone
; IMMEDIATE SOURCE:
; LIBRARY: Bovine bone cDNA library
; CLONE: HELI6
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..669
; NAME/KEY: mat_peptide
; LOCATION: 250..666
; NAME/KEY: mRNA
; LOCATION: 1..894
;
US-07-764-731B-3

alignment_scores:
    Quality: 206.00    Length: 113
    Ratio: 2.822      Gaps: 4
    Percent Similarity: 64.602    Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: US-07-764-731B-3 from: 1 to: 894
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Align seg 1/1 to: 5187076-3 from: 1 to: 894

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328 TCAGACTACACGACGACGAGCTGAACAGCGCCTGCGGAGCATGAGCT 377
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
20 uTyrtleAspPheArgGluAspLeuGlyTyrLys...TyrValHisGluUp 36
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
378 CTACGTGAGCTTC...CAGGACCTGGGGTGCGAGGACTGGATCATTGCCC 424
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
36 roLysGlyTyrTyrrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
425 CCAAGGGGTACGCTGCCCACTACTGTGACGGAGAAATGTTCTGTTCCCTCTC 474
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrrAs 66
   :::::: :::::: :::::: :::::: :::::: ::::::
475 AACGCACACATGAACCGCTACCAACCATGCCATCGTCGACAGCCCTGGTCA 524
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
525 CCTCATGAACCCCGGAGTAGCTGCCCAACCGTGCTGGCGGCCACGAAAC 574
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
83 euGluProLeuThrIleLeuTyrrTyrValGlyArgThrProLysVal... 98
   :::::: :::::: :::::: :::::: :::::: ::::::
575 TGAACGCCATCTCGGTGCTCTACTTTCGACGACAACCTCCAATGTCTACCTG 624
   :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
99 GluGluLeuSerAsnMetValValLysSerCysLysCys 111
   :::::: :::::: :::::: :::::: :::::: ::::::
625 AAGAAGTACCGGAACATGTTGCTGACGAGCGTTGGGTGC 663
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-765-662-13
seq_documentation_block:
; Sequence 13, Application US/08765662
; Patent No. 5929213
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,662
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
; TELECOMMUNICATION INFORMATION:

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,
, TELEFAX: 619-678-5099
,
, TELEX:
,
, INFORMATION FOR SEQ ID NO: 13:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 2419 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
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; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 218..1267
; OTHER INFORMATION:
US-08-765-662-13

alignment_scores
  Quality: 206.00      Length: 106
  Ratio: 2.784        Gaps: 6
Percent Similarity: 69.811 Percent Identity: 41.509

alignment_block
TGFB3P x US-08-765-662-13

Align seg 1/1 to: US-08-765-662-13 from: 1 to: 2419

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956 TGTTCAGCGGAGACCATACGTAGACTTC...CAGGAACGGGATGGCG 1002

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyP 47
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1003 GGACTGGTACTGCAGCCCGAGGGGTACCAGCTGAATTACTGCAGTGGCG 1052

47 rOCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
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1053 AGTGCCTCCCTCCACCTGGCTGGCAGCCAGCATTTGCTCTCTTCCAT 1102

59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
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1103 TCTGCGCTTCAGCTCTCTCAAGCCCAACATCTTGGCCTGCCAGTAC 1152

75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
||||| ||| |||:||||| |||:||||| |||:|||||
1153 CTCTGTTGTGTCTCTACTGCCGAGGCCCTCTCTCTCTCTCTCTCTCT 1202

91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
||| |||:||||| |||:||||| |||:||||| |||:|||||
1203 ATCATATGGCAATGTGTCAAGACGGAT...GTGCCAGATATGTGTGTG 1249

107 LysSerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-08745-13

seq_documentation_block:
; Sequence 13, Application PC/TUS9508745
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 218..1267
; OTHER INFORMATION:
PCT-US95-08745-13

alignment_scores
  Quality: 206.00      Length: 106
  Ratio: 2.784        Gaps: 6
Percent Similarity: 69.811 Percent Identity: 41.509

alignment_block
TGFB3P x PCT-US95-08745-13

Align seg 1/1 to: PCT-US95-08745-13 from: 1 to: 2419

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956 TGTTCAGCGGAGACCATACGTAGACTTC...CAGGAACGGGATGGCG 1002

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyP 47
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47 rOCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
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59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
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1103 TCTGCGCTTCAGCTCTCTCAAGCCCAACATCTTGGCCTGCCAGTAC 1152

75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
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91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
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1203 ATCATATGGCAATGTGTCAAGACGGAT...GTGCCAGATATGTGTGTG 1249

107 LysSerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-377-292-6

seq_documentation_block:
; Sequence 6, Application US/08377292
; Patent No. 5693615
; GENERAL INFORMATION:
; APPLICANT: STONE, ROGER L.
; TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
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; FILING DATE: 23-JUN-1989
; APPLICATION NUMBER: 347,559
; FILING DATE: 04-MAY-1989
; APPLICATION NUMBER: 329,610
; FILING DATE: 28-MAR-1989
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 179,101
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 179,197
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 31,346
; FILING DATE: 26-MAR-1987
; APPLICATION NUMBER: 943,322
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO:5
; LENGTH: 2923
5187076-5

alignment_scores:
    Quality: 206.00      Length: 113
    Ratio: 2.822         Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: 5187076-5 from: 1 to: 2923

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20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TyrValHisGluP 36
1410 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGGACTGATCATGTCAC 1456

36 rOlySGlyTyrTrpAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
1457 CCAAGGCGTATGCTGCCAATCTACTGTGATGAGAGTCTCTCTCCCACTC 1506

53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
1507 AAGGCACACATGAATGCAACCAACACGCGGATGTGCGAGACCTTGGTTCA 1556

66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGluAspL 83
1557 CCTATGAACCCGGATGATGTCCTCCCAACCGTCTGTGCGCCCACTAAGC 1606

83 euGluProLeuThrIleLeuTyrTrpValGlyArgThrProLysVal... 98
1607 TAAATCCCATCTCGGTCTTACTTTGATGACACCACTCCAATGTCATCTG 1656

99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
1657 AAAAAATACAGGAATATGTTGTGAAGAGCTGTGTGGATGC 1695

seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-525-596B-5

seq_documentation_block:
; Sequence 5, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mouse GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59...436
; US-08-525-596B-5

alignment_scores:
    Quality: 204.50      Length: 104
    Ratio: 3.098         Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
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Align seg 1/1 to: US-08-525-596B-5 from: 1 to: 550

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28 uGlyTrpLysTrpValHisGluProLysGlyTyrTrpAlaAsnPheCys 45
190 TGGATGGGACTGGATTATCGCACCCCAAGATATAAGGCCAATTACTGCT 239

45 eRglyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
240 CAGGAGAGTGTGAATTTGTGTTTACAAAAATATCCGCATCTCAT... 286

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
287 .....CTGTGCACCAACCAACCCAGAGGCTCAGCAGGCC 324

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrValG 93
325 TTGCTGCACCTCGACAAAAATGCTCTCCCAATTAATATGATATTTAATG 374

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValLysSer 108
375 GCAAGAACAAATAATATATATGGGAAATTCAGCCCATGCTAGACCC 424
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109 CysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-177-860A-5

seq_documentation_block:
; Sequence 5, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D. Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mouse GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59...436
US-09-177-860A-5

alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
TGFB3P x US-09-177-860A-5 ..
Align seg 1/1 to: US-09-177-860A-5 from: 1 to: 550

12 GluGluAsnCysCysValArgProLeuThrIleAspPheArgGlnAspLe 28
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143 GAATCCCGGTGTCTGCGGTACCCCTCCAGCGTCGATTTT...GAAGCCCT 189

28 ucGlyTrpLysTrpValHisGlyProLysGlyTyrTyrAlaAsnPheCys 45
|||||
190 TGGATGGGACTGGATATCGCACCAAGATATAGGCCAATTAATCTGCT 239

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
|||||
240 CAGGAGAGTGTGAATTGTTTACAAAATATCCGCATCAT... 286
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||
287 .....CTGTGACCAACCAACCCAGAGGCTCAGCAGGCC 324
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||
325 TTGCTGCACTCCGACAAAAATGTCTCCATTAAATATGCTATATTTAATG 374
93 lyArgThrProLysVal...GluClnLeuSerAsnMetValValLysSer 108
|||||
375 GCAAGAACAAATAATATATGGGAAATTCAGCCATGGTAGTAGACCGC 424
109 CysLysCysSer 112
|||
425 TGTGGTGTCTCA 436

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-525-596B-11

seq_documentation_block:
; Sequence 11, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D. John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: Murine GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104...1231
US-08-525-596B-11

alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
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Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
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Align seg 1/1 to: US-08-525-596B-11 from: 1 to: 2676

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938 GAATCCCGGTGCTGCGCTACCCCTCAGCGTCGATTTT...GAAGCCTT 984

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
985 TGGATGGGACTGGATATCCGACCAAGATATAAGGCCAATTACTGCT 1034

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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1035 CAGAGAGTGTGAATTTGTTTACAAAAATATCCGCATCAT... 1081

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1082 .....CTGTGCACCAAGCAAAACCCAGAGGCTCAGCAGGCC 1119

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1120 TTGCTGCACCTCCGACAAAAATGCTCCCATTAATATGCTATATTTAATG 1169

93 lVArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1170 GCAAGAACAAATATATATGGGAAAATTCAGCCATGGTAGTAGACCGC 1219

109 CysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-177-860A-11

seq_documentation_block:
; Sequence 11, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: Murine GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104...1231
US-09-177-860A-11

alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
TGFB3P x US-09-177-860A-11 ..
Align seg 1/1 to: US-09-177-860A-11 from: 1 to: 2676

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
938 GAATCCCGGTGCTGCGCTACCCCTCAGCGTCGATTTT...GAAGCCTT 984

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
985 TGGATGGGACTGGATATCGCACCAAGATATAAGGCCAATTACTGCT 1034

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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1035 CAGAGAGTGTGAATTTGTTTACAAAAATATCCGCATCAT... 1081

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1082 .....CTGTGCACCAAGCAAAACCCAGAGGCTCAGCAGGCC 1119

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1120 TTGCTGCACCTCCGACAAAAATGCTCCCATTAATATGCTATATTTAATG 1169

93 lVArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1170 GCAAGAACAAATATATATGGGAAAATTCAGCCATGGTAGTAGACCGC 1219

109 CysLysCysSer 112
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1220 TGTGGGTGCTCA 1231

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-177-860A-11

seq_documentation_block:
; Sequence 5, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-891-789B-5

alignment_scores:
    Quality: 204.50      Length: 104
    Ratio: 3.098         Gaps: 4
    Percent Similarity: 63.462      Percent Identity: 39.423

alignment_block:
TGFB3P x US-08-891-789B-5 ..
Align seg 1/1 to: US-08-891-789B-5 from: 1 to: 2676

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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938 GAATCCCGGTGCTGCGCTACCCCTACCGTGGATTTT...GAAGCCTT 984

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
985 TGGATGGGACTGGATTATCGCACCAAAAGATATAGGCCAATTACTGCT 1034

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1035 CAGGAGAGTGAATTTGTGTTTTACAAAAATATCCGCATCTCAT... 1081

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1082 .....CTGTGCACCAAGCAACCCAGAGGCTCAGCAGGCC 1119

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1120 TTGCTGCTACTCCGACAAAATCTCTCCCATTAATATGCTATATTTAATG 1169

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1170 GCAAGAACAATAATATATATGCAAAATTCACGCGATGGTAGACCGC 1219

109 CysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-525-596B-13

seq_documentation_block:
; Sequence 13, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
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1034 .....CTGTACCAACCAACCCAGAGGTTTCACAGGCC 107
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrValG 93
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93 lYargThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
1122 GCAAAGAACAAATAATATATATGGGAAATTCACGCGATGTTAGTAGACCGC 1171
109 CysLysCysSer 112
1172 TGTGGGTGCTCA 1183
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-765-875-3
seq_documentation_block:
; Sequence 3, Application US/08765875
; Patent No. 5914234
; GENERAL INFORMATION:
; APPLICANT: LEE SE-JIN
; APPLICANT: MCPHERRON, ALEXANDRA C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,875
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,958
; FILING DATE:
; APPLICATION NUMBER: US/08/272,763
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: MOUSE GDF-11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 198..575
US-08-765-875-3
alignment_scores:
Quality: 203.00 Length: 120
Ratio: 3.076 Gaps: 5
Percent Similarity: 55.000 Percent Identity: 36.667
seq_documentation_block:
; Sequence 13, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: Human GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59...1183
US-09-177-860A-13
alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423
alignment_block:
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Align seg 1/1 to: US-09-177-860A-13 from: 1 to: 2743
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. |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
890 GAATCAGCATGCTCGTACCTCTAACTGTGGATTTT...GAAGCTTT 936
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
937 TGGATGGGATTGGATTATCGTCTCTAAAGATATTAAGGCCAATTACTGCT 986
45 eRGlyProCysPro.....TyrIleuArgSerAlaAspThrThrHisSer 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
987 CTGGAGAGTGGAATTGTTGATTTTACAAAAATATCCTCACTACTCAT... 1033
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76

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alignment block:


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9 ArgAsnLeu.....GluGluAsnCysCy 16
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372 CGGAACCTGGCGCTGGACTCGGATGACATTCAAAGTGAGTCCGCTGTG 421
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16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
422 CCGCTACCCCTCCTGCTGGACTTT...GAGGCTTTTGGCTGGGACTGGA 468
|||||

33 aHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
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469 TCATCGCTCTCTAAACGCTACAAAGCCAACTACTGCTCGGCCAGTGGAG 518
|||||

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
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519 TACATGTTTATGCAAAAGTATCCGCACACC.....CACTTGGTGCA 559
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66 nThrLeuAsnProGluAlaSerAlaSerProCysValProGlnAspL 83
:::
560 ACAGGCTAACCCCAAGAGGCTCTCGGGGGCCCTGCTGCACACCCACCAAGA 609
|||||

83 euGluProLeuThrIleLeuTyrTyr.....Val 92
|||||
610 TGTCTCCCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTAC 659
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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660 GGCAAGATCCCT.....GGCATGGTGGTGGATCGCTG 691
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109 sLysCysSer 112
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692 TGGCTGCTCC 701
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-05288-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9405288
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05288
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bos Taurus
; STRAIN: Bovine Activin WC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 324..704
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 322..323
; OTHER INFORMATION: /note= "putative 3' end of intron"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 375..701
; PCT-US94-05288-1

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alignment_scores:
  Quality: 203.00      Length: 120
  Ratio: 3.076        Gaps: 5
  Percent similarity: 55.000  Percent Identity: 36.667

alignment_block:
TGFB3P x PCT-US94-05288-1 ..

Align seg 1/1 to: PCT-US94-05288-1 from: 1 to: 789

9 ArgAsnLeu.....GluGluAsnCysCy 16
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16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
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33 aHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
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469 TCATCGCTCTCTAAACGCTACAAAGCCAACTACTGCTCGGCCAGTGGAG 518
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50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
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519 TACATGTTTATGCAAAAGTATCCGCACACC.....CACTTGGTGCA 559
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66 nThrLeuAsnProGluAlaSerAlaSerProCysValProGlnAspL 83
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560 ACAGGCTAACCCCAAGAGGCTCTCGGGGGCCCTGCTGCACACCCACCAAGA 609
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83 euGluProLeuThrIleLeuTyrTyr.....Val 92
|||||
610 TGTCTCCCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTAC 659
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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660 GGCAAGATCCCT.....GGCATGGTGGTGGATCGCTG 691
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109 sLysCysSer 112
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692 TGGCTGCTCC 701
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seq_documentation_block:
; Sequence 10, Application US/08247907A
; Patent No. 5639638
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,907A
; FILING DATE: May 20, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI5205-A
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human BMP-11
; IMMEDIATE SOURCE:
; CLONE: FB30.5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1086
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 760..1086
US-08-247-907A-10
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alignment_scores:
    Quality: 203.00      Length: 120
    Ratio: 3.076        Gaps: 5
    Percent Similarity: 55.000    Percent Identity: 36.667

alignment_block:
TGFB3P x US-08-247-907A-10 ..

Align seg 1/1 to: US-08-247-907A-10 from: 1 to: 1270

9 ArgAsnLeu.....GluGluAsnCysCy 16
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16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
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807 CCGATATCCCTCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 853

33 alHisGluProLysGlyTyrTyraAlaAsnPheCysSerGlyProCysPro 49
: : ||||| :||| :||| :||| :||| :||| :||| :||| :|||
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50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
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66 nThrLeuAsnProGluAlaSerProCysCysValProGlnAspL 83
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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1077 TGGCTGCTCT 1086

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-452-772-10
seq_documentation_block:
; Sequence 10: Application US/08452772
; Patent No. 5700911
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; TITLE OF INVENTION: BMP-11 COMPOSITIONS

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; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/452.772
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,907
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: G15205-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human BMP-11
; IMMEDIATE SOURCE:
; CLONE: FB30.5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1086
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 760..1086
US-08-452-772-10
..

alignment_scores:
    Quality: 203.00      Length: 120
    Ratio: 3.076        Gaps: 5
    Percent Similarity: 55.000    Percent Identity: 36.667

alignment_block:
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Align seg 1/1 to: US-08-452-772-10 from: 1 to: 1270

9 ArgAsnLeu.....GluGluAsnCysCy 16
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757 CGGAACCTGGGCTGGACTCGGAGCAGCACTCAAGCGAGTCCCGCTGCTG 806

16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
807 CCGATATCCCTCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 853

33 alHisGluProLysGlyTyrTyraAlaAsnPheCysSerGlyProCysPro 49
: : ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
854 TCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCCGCCAGTGGCGAG 903

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
904 TACATGTCATGCAAAATATCCGCATACC.....CATTTGGTGCA 944

```



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66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
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945 GCAGGCCAATCAAGAGGCTCTGCTGGCCCTGTGTGTACCCCAAGA 994
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 euGluProLeuThrIleLeuTyTyTyr.....Val 92
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995 TGTCCTCCCAATCAACATGCTCTACTTCAATGACAGCAGCATTTATCTAC 1044
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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1045 GGCAAGATCCCT.....GGCATGGTGGTGATCGCTG 1076
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109 sLysCysSer 112
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1077 TGGCTGCTCT 1086
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: PCT-US94-05288-10

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seq_documentation_block:
; Sequence 10, Application PC/TUS9405288
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05288
; FILING DATE:
; CLASSIFICATION:

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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human BMP-11
; IMMEDIATE SOURCE:
; CLONE: FB30.5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1086
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 760..1086
;
PCT-US94-05288-10

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alignment_scores:
Quality: 203.00      Length: 120
Ratio: 3.076        Gaps: 5
Percent Similarity: 55.000      Percent Identity: 36.667

alignment_block:
TGFB3P x PCT-US94-05288-10 ..
Align seg 1/1 to: PCT-US94-05288-10 from: 1 to: 1270

9 ArgAsnLeu.....GluGluAsnCysCy 16
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757 CGGACCTGGGTCTGGACTGCCAGCAGCACTCAGCGAGTCCCGTGGCTG 806
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 sValArgProLeuTyTrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
807 CGGATATCCCTCCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 853
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 alHisGluProLysGlyTyTrIleAspPheCysSerClyProCysPro 49
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```

854 TCATCGCACCTAAGCGCTACAGGCCAACTACTGCTCGGCCAGTGCCGAG 903
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50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyTrAs 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
904 TACATGTTTCATGCAAAAATATCCGCATACC.....CATTTGGTGCA 944
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
945 GCAGGCCAATCAAGAGGCTCTGCTGGCCCTGTGTGTACCCCAAGA 994
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83 euGluProLeuThrIleLeuTyTyTyr.....Val 92
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
995 TGTCCTCCCAATCAACATGCTCTACTTCAATGACAGCAGCATTTATCTAC 1044
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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109 sLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq: US-08-765-875-1

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seq_documentation_block:
; Sequence 1, Application US/08765875
; Patent No. 5914234
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,875
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,958
; FILING DATE:
; APPLICATION NUMBER: US/08/272,763
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: HUMAN GDF-11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1274
;
US-08-765-875-1

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alignment_scores:
  Quality: 203.00      Length: 120
  Ratio: 3.076         Gaps: 5
  Percent Similarity: 55.000  Percent Identity: 36.667

alignment_block:
  TGF3P x US-08-765-875-1 ..

Align seg 1/1 to: US-08-765-875-1 from: 1 to: 1393

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|||||
945 CGGAACCTGGCTCGACTGCGACGAGCAGCTCAAGCGAGTCCCGCTGCTG 994

16 sValArgProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
995 CCGATATCCCTCAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 1041

33 alHisGluProLysGlyTyriTyriAlaAsnPheCysSerGlyProCysPro 49
|||||
1042 TCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCGGCCAGTGGCGAG 1091

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyriAs 66
|||||
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66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
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83 euGluProLeuThrIleLeuTyriTyri.....Val 92
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-795-671-1

seq_documentation_block:
; Sequence 1, Application US/08795671
; Patent No. 6008434
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: HUMAN GDF-11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1274
; US-08-795-671-1

alignment_scores:
  Quality: 203.00      Length: 120
  Ratio: 3.076         Gaps: 5
  Percent Similarity: 55.000  Percent Identity: 36.667

alignment_block:
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Align seg 1/1 to: US-08-795-671-1 from: 1 to: 1393

9 ArgAsnLeu.....GluGluAsnCysCy 16
|||||
945 CGGAACCTGGCTCGACTGCGACGAGCAGCTCAAGCGAGTCCCGCTGCTG 994

16 sValArgProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
995 CCGATATCCCTCAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 1041

33 alHisGluProLysGlyTyriTyriAlaAsnPheCysSerGlyProCysPro 49
|||||
1042 TCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCGGCCAGTGGCGAG 1091

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyriAs 66
|||||
1092 TACATGTTTCATGCAAAAATATCCGCATACC.....CATTTGGTGCA 1132

66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
|||||
1133 GCAGGCCAATCAAGAGGCTCTGCTGGGCCCTGTGTACCCCAACCAAGA 1182

83 euGluProLeuThrIleLeuTyriTyri.....Val 92
|||||
1183 TGTCCCAATCAACATGCTCTACTTCAATGACAGCAGCAGATATCTAC 1232

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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1233 GGCAAGATCCCT.....GGCATGGTGGTGGATCGCTG 1264

109 sLysCysSer 112
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seq_documentation_block:
; Sequence 1, Application US/08795671
; Patent No. 6008434
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
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; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-3

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  Quality: 202.50      Length: 104
  Ratio: 3.022        Gaps: 4
Percent Similarity: 64.423 Percent Identity: 39.423

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12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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867 GAATCTCGATGCTGCTTACCTCTAAGTGGATTT...GAAGCTTT 913

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
914 TGGATGGGATGGATTTATTCACCTAAAGATATAAGGCCAATTACTGCT 963

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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964 CTGGAGAATGTGAATTTGTTATTTTGCACCAAGTATCCTCATACCCAT... 1010

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1011 .....CTGTGCACCAAGCAACCCAGAGGTTACGCCGCC 1048

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1049 CTGCTACTCTACAAAGATGTCCTCAATTAATATGCTATATTTAATG 1098

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1099 GCGAGGACAAATAATATACGGGAAGATCCAGCCATGGTAGTAAATCGC 1148

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; Sequence 1, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals

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; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-1

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alignment_block:
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878 GAATCTCGATGCTGCTTACCTCTAAGTGGATTT...GAAGCTTT 924

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
925 TGGATGGGATGGATTTATTCACCTAAAGATATAAGGCCAATTACTGCT 974

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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975 CTGGAGAATGTGAATTTGTTATTTTGCACCAAGTATCCTCATACCCAT... 1021

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1060 CTGCTACTCTACAAAGATGTCCTCAATTAATATGCTATATTTAATG 1109

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1110 GCGAGGACAAATAATATACGGGAAGATCCAGCCATGGTAGTAGTCGC 1159

109 CysLysCysSer 112
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1160 TGTGGGTGTTC 1171

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; TOPOLOGY: linear
; US-08-197-792-42

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  Percent Similarity: 69.159  Percent Identity: 37.383

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1197 TGCTGTGAAGAACAGTCTTTGTCAGTTTCAAG...GACATCGGCTGGAA 1243

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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1244 TGACTGGATCATGTCCTCCCTGCTGCTATCATGCCAACTACTGCGAGGGTG 1293

47 roCysPro.....TyrLeuArgSerAlaAspThrHis 58
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAla 73
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1344 TCAACAGTCATCAACCACTACCGCATGCGGGGCCATAGCCCTTCCCAA 1393

73 rLaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeu 90
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1394 CCTCAATCGTGTGTCGCCCAACCAAGCTGAGACCCATGTCATGTTGT 1443

90 yTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
1444 ACTATGATGATGTCGTCACCAATCATCAAAAGGACATTCAGAACATGATC 1493

106 ValLysSerCysLysCysSer 112
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1494 GTGGAGGAGTGTGGGTGCTCA 1514

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-850-42

seq_documentation_block:
; Sequence 42, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-850-42

alignment_scores:
  Quality: 200.00      Length: 107
  Ratio: 2.703         Gaps: 5
  Percent Similarity: 69.159  Percent Identity: 37.383

alignment_block:
  TGFB3P x US-08-459-850-42      ..

  Align seg 1/1 to: US-08-459-850-42 from: 1 to: 1633

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1197 TGCTGTGAAGAACAGTCTTTGTCAGTTTCAAG...GACATCGGCTGGAA 1243

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
1244 TGACTGGATCATGTCCTCCCTGCTGCTATCATGCCAACTACTGCGAGGGTG 1293

47 roCysPro.....TyrLeuArgSerAlaAspThrHis 58
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1294 AGTCCCGAGCCATATAGCAGGACGTCGCGGTCTCTCACTGCTCTCCAC 1343

59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAla 73
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1344 TCAACAGTCATCAACCACTACCGCATGCGGGGCCATAGCCCTTCCCAA 1393

73 rLaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeu 90
: : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
1394 CCTCAATCGTGTGTCGCCCAACCAAGCTGAGACCCATGTCATGTTGT 1443

90 yTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
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1444 ACTATGATGATGTCGTCACCAATCATCAAAAGGACATTCAGAACATGATC 1493

106 ValLysSerCysLysCysSer 112
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1494 GTGGAGGAGTGTGGGTGCTCA 1514
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-42

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seq_documentation_block:
; Sequence 42, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,214
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-459-214-42
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alignment_scores: Quality: 200.00 Length: 107
Ratio: 2.703 Gaps: 5
Percent Similarity: 69.159 Percent Identity: 37.383
alignment_block: TGFB3P x US-08-459-214-42 ..

Align seg 1/1 to: US-08-459-214-42 from: 1 to: 1633

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1197 TGCTGTAGAAACAGTTCTTTGTCAAGTTCAG...GACATCGCGTGGAA 1243

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
: ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
1244 TGACTGGATCATTTGCTCCCTCTGGCTATCATGCAACTACTGCGAGGGTG 1293

47 roCysPro.....TyrLeuArgSerAlaAspThrThrHis 58
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1294 AGTGCCCGAGCATATAGCAGGCACGTCGGGTCTCACTGTCTCTCCAC 1343

59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlase 73
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1344 TCAACAGTCATCAACCACTACCGCATCGCGGGGCCATAGCCCCCTTGC 1393

73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeu 90
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1394 CCTCAATCGTCTGTGTGCCCAACCAAGCTGAGACCCATGTCCATGTGT 1443

90 yzTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
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1444 ACTATGATGATGTCAAAACATCATCAAAAGGACATTCAGAACATGATC 1493

106 ValLysSerCysLysCysSer 112
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1494 GTGGAGAGTGTGGTGTCA 1514
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-197-792-32

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seq_documentation_block:
; Sequence 32, Application US/08197792
; Patent No. 5525488
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin a
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,792
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297PD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3588 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-197-792-32

alignment_scores:
    Quality: 200.00      Length: 107
    Ratio: 2.703        Gaps: 5
Percent Similarity: 69.159 Percent Identity: 37.383

alignment_block:
TGFB3P x US-08-197-792-32 ..
Align seg 1/1 to: US-08-197-792-32 from: 1 to: 3588

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988 TGCTGTAGAACGACAGTTCTTGTCAAGTTTCGAAG...GACATCGGTGGAA 1034

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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47 roCysPro.....TyrLeuArgSerAlaAspThrHrHis 58
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1085 AGTGCCCGCCGCACATAGCGGCGCACGTGCGGTCTCTCGTCTCTGCCAC 1134

59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73
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: : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1185 CCTAAGTCGTGTCGTCGCCCAACCAAGCTGAGGCCCATGTCATGCTGT 1234

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seq_documentation_block:
; Sequence 32, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/056,564
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/577,892
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1667 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-455-550-1
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; alignment_scores:
;      Quality: 199.00      Length: 108
;      Ratio: 2.689        Gaps: 6
; Percent Similarity: 68.519 Percent Identity: 38.889
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; alignment_block:
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; Align seg 1/1 to: US-08-455-550-1 from: 1 to: 1667
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; 58 HisSerThrValLeuGlyLeuTyrAsnThr.....LeuAsnProGluAl 72
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; seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-278-729A-24
;
; seq_documentation_block:
; Sequence 24, Application US/08278729A
; Patent No. 5650276
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMANN, HERMAN
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;
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,729A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-058CPEW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-278-729A-24
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; alignment_scores:
;      Quality: 195.00      Length: 103
;      Ratio: 2.868        Gaps: 4
; Percent Similarity: 66.019 Percent Identity: 39.806
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; alignment_block:
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; 46 LysProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
; : : : : : : : : : : : : : : : : : : : : : : : :
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;
; 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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; 1204 ATGCTCCAGACCCCTGTGCCACCTGCTGGAGCCCAAGAGGTGCCAAGCC 1253
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; 76 ocCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1204 ATCGTCCAGACCCCTGGTCCACTGCTGGAGGCCAAGAAGGTGCCCAAGCC 1253
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      ||| :::|||||:::
      93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108.
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      109 CysLysCys 111
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seq_documentation_block:
; Sequence 24, Application US/08406672
; Patent No. 5674484
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
; TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,672
; FILING DATE: 20-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 752,857

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, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 667,274
, FILING DATE: 11-MAR-1991
, ATTORNEY/AGENT INFORMATION:
, NAME: FENTON ESQ., GILLIAN M.
, REGISTRATION NUMBER: 36,508
, REFERENCE/DOCKET NUMBER: CRP-0600CN
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (617) 248-7560
, TELEFAX: (617) 248-7100
, INFORMATION FOR SEQ ID NO: 24:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 1368 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear

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, REGISTRATION NUMBER: 36,508
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, REFERENCE/DOCKET NUMBER: CRP-0600CN
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, TELECOMMUNICATION INFORMATION:
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, TELEPHONE: (617) 248-7560
,
, TELEFAX: (617) 248-7100
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, INFORMATION FOR SEQ ID NO: 24:
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, LENGTH: 1368 base pairs
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, TYPE: nucleic acid
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, STRANDEDNESS: single
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, TOPOLOGY: linear
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; FEATURE:
; NAME/KEY:  CDS
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US-08-406-672-24

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  Ratio: 2.868        Gaps: 4
Percent Similarity: 66.019  Percent Identity: 39.806

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; Sequence 24, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER:  US/08/643,563A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY ESQ., MICHAEL J.
; REGISTRATION NUMBER: 38,349
; REFERENCE/DOCKET NUMBER:  CRP-058CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:  CDS
; FEATURE:
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; LOCATION:  1..1365
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  Ratio: 2.868        Gaps: 4
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; Sequence 24, Application US/08643763A
; Patent No. 5733878
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
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; TITLE OF INVENTION: REGENERATION.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,763A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
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; NAME/KEY: CDS
; LOCATION: 1..1365
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seq_documentation_block:
; Sequence 24, Application US/08462623
; Patent No. 5739107
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; TITLE OF INVENTION: ULCERS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/445,882
; FILING DATE: 22-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-074CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
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seq_documentation_block:
; Sequence 24, Application US/08445468A
; Patent No. 5849686
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,468A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-072FW2

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
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; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H. L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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; LOCATION: 1..1365
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; Patent No. 5994131
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/912.088
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,729
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-058CPFW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 433-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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    Percent Similarity: 66.019    Percent Identity: 39.806

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1104 GCATGACTGGATCATCGCACCGAGGGGTATGGCGCTTCTACTCGAGG 1153

46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGG 1203
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1204 ATCTCCAGACCCCTGGTCCACTGCTGGAGCCCAAGAGGTGCCCAAGCC 1253
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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93 Ly...ArgThrProLysValGlnLeuSerAsnMetValValLysSer 108
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1304 ACGACGAGAATGTGAACCTGAAAGATAGAAACATGATGTGAAATCC 1353
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seq_name: /cqn2_6/ptodata/2/ina/6A_COMB.seq:US-08-278-730A-24
seq_documentation_block:
; Sequence 24, Application US/08278730A
; Patent No. 6022853
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,730A
; FILING DATE: 20-JULY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-071FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-278-730A-24
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    Quality: 195.00      Length: 103
    Ratio: 2.868        Gaps: 4
    Percent Similarity: 66.019    Percent Identity: 39.806

alignment_block:
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1057 AGCTGCCAGATGCAGACCCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103

30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
1104 GCATGACTGGATCATCCACAGAGGCTATGGCGCTTCTACTGCACGC 1153

46 LysProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCATTTCCGCTCAATGCCACATGACGCCACGACCATGCG 1203

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerPr 76
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seq_documentation_block:
; Sequence 24, Application US/08445467
; Patent No. 6077823
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: PANG, ROY HL
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: RUEGER, DAVID C
; APPLICANT: COHEN, CHARLES M
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF
; TITLE OF INVENTION: INFLAMMATORY RESPONSE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,467
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,511
; FILING DATE:
; APPLICATION NUMBER: US/07/938,336
; FILING DATE:
; APPLICATION NUMBER: US 07/667,274
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,059
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  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019  Percent Identity: 39.806

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  Align seg 1/1 to: US-08-271-556A-1 from: 1 to: 1368

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1057 AGCTGCAGATGCAGACCCCTGATAGACTTCAAG...GATCTGGGCTG 1103
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30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
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1104 GCATGACTGGATCATCCACAGAGGCTATGGCGCTTCTACTGCAGCG 1153
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46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1204 ATGCTCAGACCCCTGGTCCACCTGCTGGAGCCTATGCCGCTTCTACTGCAGCG 1253
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93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValVallySer 108
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109 CysLysCys 111
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seq_documentation_block:
; Sequence 24, Application PC/TUS9307190
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN-ENRICHED DIETARY COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07190
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-071
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
PCT-US93-07190-24

alignment_scores:
  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019  Percent Identity: 39.806

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  TGFB3P x PCT-US93-07190-24 ..
  Align seg 1/1 to: PCT-US93-07190-24 from: 1 to: 1368

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30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
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1104 GCATGACTGGATCATCCACAGAGGCTATGGCGCTTCTACTGCAGCG 1153
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46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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; Sequence 24, Application PC/TUS9307231
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07231
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08742
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY ESQ, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7477
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
PCT-US93-08742-24

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Percent Similarity: 66.019 Percent Identity: 39.806

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1104 GCATGACTGGATCATCGCACAGAGGGGTATGGCGCTTCTACTCAGCG 1153

46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCAATTTCCCGCTCAATGCGCATGAACGCCACGAACCATGCG 1203

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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; Sequence 24, Application PC/TUS9308742
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN-INDUCED PERIODONTAL TISSUE REGENERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; seq_documentation_block:
; Sequence 24, Application PC/TUS9308808
; GENERAL INFORMATION:

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;; APPLICANT:
;; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
;; STREET: 45 SOUTH STREET
;; CITY: HOPKINTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 01748
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/08808
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KELLEY ESQ, ROBIN D.
;; REGISTRATION NUMBER: 34,637
;; REFERENCE/DOCKET NUMBER: CRP-072
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7477
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1368 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1368
PCT-US93-08808-24

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  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019  Percent Identity: 39.806

alignment_block:
TGFB3P x PCT-US93-08808-24  ..

Align seg 1/1 to: PCT-US93-08808-24 from: 1 to: 1368

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30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerg 46
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1104 GCATGACTGATCATCGCACAGAGGCTATGGCGCTTCTACTGCAGCG 1153

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1204 ATGCTCCAGACCTGGTCCACCTGCTGGAGCCCAAGAAAGTGCCCAAGCC 1253

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1304 ACGACGAGAATCTGAACCTGAAARAAAGTAGAAACATGATTGTGAATCC 1353

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seq_documentation_block:
; Sequence 24, Application PC/TUS9308885
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08885
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY ESQ, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7477
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
PCT-US93-08885-24

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  Percent Similarity: 66.019  Percent Identity: 39.806

alignment_block:
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Align seg 1/1 to: PCT-US93-08885-24 from: 1 to: 1368

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1057 AGCTGCCAGATGCAGACCCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103

30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerg 46
   |||:::  |||:::  |||:::  |||:::  |||:::  |||:::  |||:::  |||:::
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; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
US-08-741-589A-9

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    Ratio: 2.662        Gaps: 5
Percent Similarity: 61.739 Percent Identity: 34.783

alignment_block:
TGFB3P x US-08-741-589A-9 ..
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18 gProLeuTyrlleAspPheargGlnaspLeuGlyTrplys...TrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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34 IsgluProLysGlyTyTyTyAlaAsnPheCysSerGlyProCysProTyr 50
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170 TCGCGCTGAAGCTACGCCGCTACTACTGTGAGGGGAGTGTGCCCTTC 219

51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe 64
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220 CCTCTGAACCTCTATACTAAGCGCACCAACGCCATCGTGACAGCGCT 269

64 uTyraSnThrLeuasnProgluAlaSerAlaSerProCysCysValProg 81
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
270 GTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGTGTGGCGCCA 319

81 InAspLeuGluproLeuThrIleLeuTyTyTyValGlyArgThrProlys 97
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98 Val...GluGlnLeuSerAsnMetValVallysserCystLysCys 111
::: ::::: |||||:|||||:|||||:|||||
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seq_name: /cgm2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-13181-9

seq_documentation_block:
; Sequence 9, Application PC/TUS9413181
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13181
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
; PCT-US94-13181-9

alignment_scores:
    Quality: 189.00      Length: 115
    Ratio: 2.662        Gaps: 5
    Percent Similarity: 61.739      Percent Identity: 34.783

alignment_block:
TGFB3P x PCT-US94-13181-9 ..

Align seg 1/1 to: PCT-US94-13181-9 from: 1 to: 417

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18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34
: |||||:|||||: |||||:|||||: |||||:
123 CGAGCTGTATGTCAGCTCCGA...GACCTGGGCTGGCAGGACTGGATCA 169

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe 64
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64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81
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81 InAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97
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320 CCGACTCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCCAACGC 369

98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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; Sequence 248, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..548
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label= EcoRI
; OTHER INFORMATION: /note="residues 1-65 comprise EcoRI site to beginning of pe
; OTHER INFORMATION: B."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 1-22
; OTHER INFORMATION: /label= pel B
; OTHER INFORMATION: /note="pel B is the leader sequence from the pectate lyase
; OTHER INFORMATION: gene of Erwinia carotovora."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 23-161
; OTHER INFORMATION: /label= "Bone D"
; OTHER INFORMATION: /note="Bone D is the subunit of human osteogenic protein (
; OTHER INFORMATION: U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9,
; OTHER INFORMATION: ID Nos: 1 and 2."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 549-557
; OTHER INFORMATION: /label= XhoI
; OTHER INFORMATION: /note="residues 549-557 comprise stop codon and XhoI site.
; US-08-621-803-248

alignment_scores:
    Quality: 189.00      Length: 115
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 30, 2001, 08:49:56 ; Search time 16.82 Seconds
(without alignments)
511.755 Million cell updates/sec

Title: TGFB3P
Perfect score: 634
Sequence: 1 ALDNYCFRNLNCCVRPL.....RTPKVEQLSNMVKSCSX 113

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	99.8	410	2 A41397	transforming growt
2	633	99.8	412	2 A36169	transforming growt
3	630	99.4	410	2 A55706	transforming growt
4	629	99.2	412	2 A34939	transforming growt
5	621	97.9	409	2 S01825	transforming growt
6	539	85.0	412	2 A39489	transforming growt
7	535	84.4	412	2 A61439	transforming growt
8	535	84.4	414	1 WFMKB2	transforming growt
9	535	84.4	414	2 A31249	transforming growt
10	535	84.4	442	2 B31249	transforming growt
11	530	83.6	414	1 WFXSB2	transforming growt
12	516	81.4	413	1 WFXLB2	transforming growt
13	503	79.3	390	1 WFM52	transforming growt
14	503	79.3	390	2 S10219	transforming growt
15	500	78.9	315	2 A40057	transforming growt
16	500	78.9	390	1 WFXH2	transforming growt
17	500	78.9	390	2 JC4023	transforming growt
18	500	78.9	390	2 A26960	transforming growt
19	500	78.9	390	2 A27512	transforming growt
20	500	78.9	390	2 I46463	transforming growt
21	500	78.9	391	2 S01413	transforming growt
22	488	77.0	130	2 I48196	transforming growt
23	461	72.7	373	2 A41918	transforming growt
24	439	69.2	382	2 B61036	transforming growt
25	208	32.8	350	2 JC5241	transforming growt
26	206	32.5	207	2 S37618	activin beta E cha
27	206	32.5	513	1 BMHU6	vgr protein - rat
28	205	32.3	510	2 A54798	bone morphogenetic
29	204	32.2	425	2 I47072	Vg-1-related prote
					inhibin beta-A cha

30	200	31.5	424	1 WFPGBA	inhibin beta-A cha
31	200	31.5	424	1 S31440	inhibin beta-A cha
32	200	31.5	425	1 S50898	inhibin beta-A cha
33	200	31.5	426	1 B24248	inhibin beta-A cha
34	197.5	31.2	367	2 JC4151	activin beta D cha
35	195	30.8	455	2 A43918	TGF-beta-related p
36	193	30.4	413	2 JC4862	activin beta-A cha
37	191.5	30.2	365	2 T43286	act-1 protein - Ca
38	191	30.1	424	1 B40905	inhibin beta-A cha
39	190	30.0	313	2 I51284	bone morphogenetic
40	190	30.0	360	2 A29619	Vg1 embryonic grow
41	189	29.8	43	2 B26356	transforming growt
42	189	29.8	431	1 BMHU7	bone morphogenetic
43	188.5	29.7	370	2 I51199	activin beta B sub
44	187	29.5	426	2 JH0690	bone morphogenetic
45	186.5	29.4	349	1 WFPGBB	inhibin beta-B cha
46	186.5	29.4	407	1 A40150	inhibin beta-B cha
47	186.5	29.4	408	2 S50899	betaB inhibin prec
48	184.5	29.1	255	2 I48235	inhibin beta-B cha
49	184.5	29.1	393	2 I50103	activin beta B - z
50	184.5	29.1	411	2 B41398	inhibin beta-B cha
51	183.5	28.9	115	2 PN0505	activin beta B-1 c
52	183	28.9	115	2 PN0504	activin beta A cha
53	183	28.9	430	2 JQ1184	osteogenic protein
54	182.5	28.8	393	2 S37073	bone morphogenetic
55	182.5	28.8	394	2 S45355	bone morphogenetic
56	182.5	28.8	396	1 BMHU2	bone morphogenetic
57	182.5	28.8	398	2 JH0688	bone morphogenetic
58	182.5	28.8	398	2 JH0687	bone morphogenetic
59	182	28.7	495	2 S43294	bone morphogenetic
60	182	28.7	501	2 A55452	cartilage-derived
61	182	28.7	501	2 JC2347	growth/differentia
62	181.5	28.6	115	2 PN0506	activin beta B-2 c
63	181	28.5	461	2 S52408	SPDV1 protein - s
64	180	28.4	352	2 JC2466	inhibin beta-C cha
65	180	28.4	352	2 JC5366	activin beta C - m
66	180	28.4	352	2 S70580	activin beta C pre
67	179	28.2	125	2 S43295	bone morphogenetic
68	179	28.2	452	2 I49542	bone morphogenetic
69	179	28.2	454	1 BMHU5	bone morphogenetic
70	176	27.8	151	2 S43296	bone morphogenetic
71	175	27.6	436	2 B55452	cartilage-derived
72	174	27.4	372	2 C39364	GDF-1 embryonic gr
73	172	27.1	588	2 A26158	decapentaplegic pr
74	171.5	27.1	102	2 A36192	inhibin beta-A cha
75	171.5	27.1	353	2 I50607	bone morphogenetic
76	171	27.0	34	2 C42320	transforming growt
77	170.5	26.9	405	2 I50608	bone morphogenetic
78	170.5	26.9	408	1 BMHU4	bone morphogenetic
79	170.5	26.9	408	2 S38343	bone morphogenetic
80	170.5	26.9	408	2 S58731	bone morphogenetic
81	170.5	26.9	420	2 I49541	bone morphogenetic
82	170	26.8	101	2 B36192	inhibin beta-B1 ch
83	169	26.7	101	2 C36192	inhibin beta-B2 ch
84	168	26.5	402	2 A45056	osteogenic protein
85	165.5	26.1	400	2 A49147	bone morphogenetic
86	165.5	26.1	401	2 JH0689	bone morphogenetic
87	164.5	25.9	357	2 A39364	GDF-1 embryonic gr
88	163.5	25.8	408	2 JH0801	bone morphogenetic
89	162.5	25.6	366	2 A46607	growth/differentia
90	160.5	25.3	366	2 A45402	transforming growt
91	159	25.1	373	2 PN0042	activin - fruit fl
92	158.5	25.0	472	1 BMHU3	bone morphogenetic
93	156.5	24.7	360	2 I53032	bone morphogenetic
94	149.5	23.6	350	2 T25451	transforming growt
95	148	23.3	366	2 T03907	TGF-beta-related p
96	140	22.1	427	2 A40735	TGF beta homolog d
97	135.5	21.4	309	2 JC5637	placental transfer
98	135.5	21.4	476	2 JC4646	bone morphogenetic
99	133.5	21.1	354	2 S29718	gene nodal protein
100	133.5	21.1	478	2 JC4838	bone morphogenetic


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QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
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Db 359 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 410

RESULT 4
A34939
transforming growth factor beta-3 precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34939; S25850; S36125; S36124; I51181
R:Jakowlew, S.B.; Dillard, P.J.; Kondalah, P.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 747-755, 1988
A:Title: Complementary deoxyribonucleic acid cloning of a novel transforming growth factor
A:Reference number: A34939; MUID:89096966
A:Accession: A34939
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-412 <JAK>
A:Cross-references: GB:M31154; NID:g212758; PIDN:AAA49089.1; PID:g212759
R:Burt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A:Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and
A:Reference number: S25850; MUID:92134496
A:Accession: S25850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <BUR>
A:Cross-references: EMBL:X58127; NID:g63815; PIDN:CAA41128.1; PID:g63816
A:Accession: S36125
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 119-172 <BU2>
A:Cross-references: EMBL:X60055; NID:g396688; PIDN:CAA42653.1; PID:g396689
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A:Accession: S36124
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 173-322, 'ELPT', 327-412 <BU3>
A:Cross-references: EMBL:X60091
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
R:Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.; Cubert, J.
Mol. Endocrinol. 6, 1285-1298, 1992
A:Title: Identification and characterization of the chicken transforming growth factor-beta
A:Reference number: I51181; MUID:93024487
A:Accession: I51181
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <JAK2>
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C:Genetics:
A:Introns: 216/1; 252/1; 309/2; 360/3
A:Note: list of introns may be incomplete
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-300/Domain: propeptide #status predicted <PRO>
F:301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
F:74,142/Binding site: carbohydrate (Asn) (covalent)

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Db 361 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412
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RESULT 5
S01825
transforming growth factor beta-3 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: S01825
R:Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.;
EMBO J. 7, 3737-3743, 1988
A:Title: A new type of transforming growth factor-beta, TGF-beta3.
A:Reference number: S01824; MUID:89091120
A:Accession: S01825
A:Molecule type: mRNA
A:Residues: 1-409 <DER>
A:Cross-references: EMBL:X14150; NID:g2127; PIDN:CAA32363.1; PID:g2128
C:Superfamily: inhibin
C:Keywords: growth factor
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-297/Domain: propeptide #status predicted <PRO>
F:298-409/Product: transforming growth factor beta-3 #status predicted <MAT>

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Best Local Similarity 98.2%; Pred. No. 1.2e-55;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
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Db 358 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 409
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RESULT 6
A39489
transforming growth factor beta-2 precursor - chicken
N:Alternate names: TGF-beta2
C:Species: Gallus gallus (chicken)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 16-Jul-1999
C:Accession: A39489; A61018; S25849
R:Burt, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A:Title: Molecular cloning and primary structure of the chicken transforming growth f
A:Reference number: A39489; MUID:92075163
A:Accession: A39489
A:Molecule type: DNA
A:Residues: 1-412 <BUR>
A:Cross-references: GB:X58071; NID:g63810; PIDN:CAA41101.1; PID:g833616; GB:X59082; G
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A:Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming
A:Reference number: A61018; MUID:90253805
A:Accession: A61018
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>
C:Genetics:
A:Introns: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3
C:Superfamily: inhibin
C:Keywords: growth factor; growth regulation; mitogen; transformation
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-300/Domain: propeptide #status predicted <PRO>
F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

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Best Local Similarity 79.5%; Pred. No. 2.6e-47;
Matches 89; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

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QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
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A;Reference number: A34005; MUID:88124824

A;Accession: A34005

A;Molecule type: mRNA

A;Residues: 1-414 <HAN>

A;Cross-references: GB:J03585; NID:g176495; PIDN:AAA35358.1; PID:g176496

A;Note: part of this sequence, including the amino end of the active peptide, confirm

R;Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.

DNA 7, 493-497, 1988

A;Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff

A;Reference number: A90960; MUID:89090808

A;Contents: annotation

A;Note: although they do not show the sequences, a clone identical yielding a sequenc

C;Superfamily: Inhibin

C;Keywords: alternative splicing; glycoprotein; growth factor; growth regulation; hom

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-302/Domain: propeptide #status predicted <PRO>

F;303-414/Product: transforming growth factor beta-2 #status predicted <MAT>

F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Best Local Similarity 79.5%; Pred. NO. 6.7e-47;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

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||| |||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||::||
Db 303 ALDAAYCFERNVDNCCLRPILYIDFKRLDGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 362

QY 61 VLGLYNTLNPEASPCPVQDDLEPLTILYYVGTRPKVEQLSNMVKSCKCS 112
|| |||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||::||
Db 363 VLSLYNTINPEASPCCVSQDLEPLTILYYIGTKPIEQLSNMIVKSCKCS 414

RESULT 9

A31249

transforming growth factor beta-2 precursor, short form - human

N;Alternate names: glioblastoma-derived T-cell suppressor factor

C;Species: Homo sapiens (man)

C;Date: 01-Dec-1989 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999

C;Accession: S06216; A31249

R;De Martin, R.; Haendler, B.; Hofer-Warbinek, R.; Gaugitsch, H.; Wrann, M.; Schluese

EMBO J. 6, 3673-3677, 1987

A;Title: Complementary DNA for human glioblastoma-derived T cell suppressor factor, a

A;Reference number: S06216; MUID:88111555

A;Accession: S06216

A;Molecule type: mRNA

A;Residues: 1-414 <DEM>

A;Cross-references: EMBL:Y00083; NID:g31959; PIDN:CAA68279.1; PID:g31960

R;Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.

DNA 7, 493-497, 1988

A;Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff

A;Reference number: A90960; MUID:89090808

A;Accession: A31249

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 101-130 <WEB>

C;Genetics: GDB:TGFB2

A;Gene: GDB:TGFB2

A;Cross-references: GDB:I20436; OMIM:190220

A;Map position: 1q41-lq41

C;Superfamily: Inhibin

C;Keywords: alternative splicing; growth factor

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-302/Domain: propeptide #status predicted <PRO>

F;303-414/Product: transforming growth factor beta-2 #status experimental <MAT>

Query Match 84.4%; Score 535; DB 2; Length 414;
Best Local Similarity 79.5%; Pred. NO. 6.7e-47;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLNEENCCVRPLYIDFRODLGKWKVHEPKGYVANFCSPCPYLRSADTTHTST 60

QY 1 ALDNTNYCFRNLNENCCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTHTST 60
||| |||||:::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 ALDAAYCFRNVDNCCRLPIYIDFKDLGWKIHEPKGINANFCAGACPYLWSSDTQHRSR 361
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLLEPLILYYVGRTPKVEQLSNMIVKSCKS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 VLSLYNTINPEASAPCCVSQDLDSLIIYIGNKPKEQLSNMIVKSCKS 413

RESULT 13

WFMS2
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 24-Nov-1999
C:Accession: A01396
J:Derivnck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
A>Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: GB:M13177; NID:g201952; PIDN:AAA40423.1; PID:g201953
A>Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a precursor polypeptide
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transformant
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.3%; Score 503; DB 1; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.le-43;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLNENCCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTHTST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 279 ALDNTNYCFNSTEKNCVRQIYIDFRDLGKWIHEPKGIHANFCGLGPCPYIWSLDTOYSK 338
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLLEPLILYYVGRTPKVEQLSNMIVKSCKS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 VLALYNQHNPGASAPCCVPALEPLIVYVVGKPKVEQLSNMIVKSCKS 390

RESULT 14

S10219
transforming growth factor beta-1 precursor - rat
N:Alternate names: TGF type 2; TGF-beta
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 24-Nov-1999
C:Accession: S10219; PT0023; S02267
R:Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A>Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
A:Reference number: S10219; MUID:90272425
A:Accession: S10219
A:Molecule type: mRNA
A:Residues: 1-390 <QIA>
A:Cross-references: EMBL:X52498; NID:g57341; PIDN:CAA36741.1; PID:g57342
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
J. Biochem. 106, 304-310, 1989
A>Title: Purification and structural analysis of a latent form of transforming growth fa
A:Reference number: PT0023; MUID:90036779
A:Accession: PT0023
A:Molecule type: protein
A:Residues: 30-32, 'X', 34-38, 'Q', 40-42, 'X', 44 <OKA>
R:Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989

R:Sauermann, U.; Meyermann, R.; Schluesener, H.J.

J. Neurosci. Res. 33, 142-147, 1992

A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning

A:Reference number: S37618; MUID:93085758

A:Accession: S37618

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <SAU>

A:Cross-references: EMBL:X58830; NID:g57475; PIDN:CAAA1634.1; PID:g57476

A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser

C:Superfamily: inhibin

Query Match 32.5%; Score 206; DB 2; Length 207;
Best Local Similarity 37.2%; Pred. No. 9.5e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCSPCPYLRSD---TTHS 59

Db 95 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPKYAANCYDCGCSPLNAHNMATNHA 153

Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCK 111

Db 154 IVQTLVHLNPEYVPKCCAPTCLNAISLVLFDDNSNVILKRYNMVVRACGC 206

RESULT 27

BMH06

bone morphogenetic protein 6 precursor - human

C:Species: Homo sapiens (man)

C:Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C:Accession: B39263

R:Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozni

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990

A:Title: Identification of transforming growth factor beta family members present in bon

A:Reference number: A39263; MUID:9108608

A:Accession: B39263

A:Molecule type: mRNA

A:Residues: 1-513 <CEL>

A:Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562

C:Genetics:

A:Gene: GDB:BMP6

A:Map position: 6pter-6qter

C:Superfamily: inhibin

C:Keywords: bone; glycoprotein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-374/Domain: propeptide #status predicted <PRO>

F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>

F:241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.5%; Score 206; DB 1; Length 513;

Best Local Similarity 37.2%; Pred. No. 2.5e-13;

Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCSPCPYLRSD---TTHS 59

Db 401 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPKYAANCYDCGCSPLNAHNMATNHA 459

Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCK 111

Db 460 IVQTLVHLNPEYVPKCCAPTCLNAISLVLFDDNSNVILKRYNMVVRACGC 512

RESULT 28

A54798

Vg-1-related protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A54798; A33925; S47442

R:Gitelman, S.E.; Koblin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.

J. Cell Biol. 126, 1595-1609, 1994

A:Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral b

A:Reference number: A54798; MUID:94375533

A:Accession: A54798

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-510 <GIT>

A:Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730

R:Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan,

Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989

A:Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transfer

A:Reference number: A33925; MUID:89282810

A:Accession: A33925

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 'M', 74, 'K', 76-85, 'P', 87-510 <LYO>

A:Cross-references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353

C:Superfamily: inhibin

Query Match 32.3%; Score 205; DB 2; Length 510;

Best Local Similarity 37.2%; Pred. No. 3.1e-13;

Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCSPCPYLRSD---TTHS 59

Db 398 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPKYAANCYDCGCSPLNAHNMATNHA 456

Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCK 111

Db 457 IVQTLVHLNPEYVPKCCAPTCLNAISLVLFDDNSNVILKRYNMVVRACGC 509

RESULT 29

I47072

inhibin beta-A chain precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 16-Jul-1999

C:Accession: I47072; B60856

R:Fleming, J.S.; Galloway, S.M.; Crawford, R.J.; Tisdall, D.J.; Greenwood, P.J.

Mol. Reprod. Dev. 40, 1-8, 1995

A:Title: Tissue-specific variation in the length of the 5' untranslated region of the

A:Reference number: I47072; MUID:95217464

A:Accession: I47072

A:Molecule type: mRNA

A:Residues: 1-425 <FL>

A:Cross-references: GB:LJ9218; NID:g310379; PIDN:AA041621.1; PID:g310380

R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenh

J. Endocrinol. 113, 213-221, 1987

A:Title: Isolation of inhibin from ovine follicular fluid.

A:Reference number: A60856; MUID:87224684

A:Accession: B60856

A:Molecule type: protein

A:Residues: 310-312, 'X', 314-319, 'XX', 322 <LEV>

C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.

C:Superfamily: inhibin

C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 32.2%; Score 204; DB 2; Length 425;

Best Local Similarity 38.3%; Pred. No. 3.3e-13;

Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRDLGK-WVHEPKGYANFCSPCP-----YLRSDTTHSTVLGYNTL 68

Db 320 CCKKQFYVSFK-DIGWQDWIIAPSGYHANYCEGCPSHIAGTSGSLSFSHTVINHYMR 378

Qy 69 --NPEASASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCKS 112

Db 379 GHSPPANLKKSCCVPTKLRMSMLYDDGQNIKKDQNNIVIEECGCS 425

RESULT 30

WFGGBA

Inhibin beta-A chain precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C:Accession: A01393
R:Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.; Nature 318, 659-663, 1985
A>Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
A:Reference number: A93371; MUID:86092207
A:Accession: A01393
A:Molecule type: mRNA
A:Residues: 1-424 <MAS>
A:Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003
C:Comment: The source of this protein is ovarian follicular fluid.
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
inferred forms of inhibin have been isolated (A and B) that differ in the amino-terminal
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follitropin
C:Superfamily: inhibin
C:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonadotropin releasing hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-308/Domain: propeptide #status predicted <PRO>
F:309-424/Product: inhibin beta-A chain #status predicted <MAT>
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.5%; Score 200; DB 1; Length 424;
Best Local Similarity 37.4%; Pred. No. 8.3e-13;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFDRLGHW-VVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNLT 68
|| : : : ||| | : : ||| | : : ||| | : : ||| | :
Db 319 CCKKOFFVSFK-DIGWNIIAPSGHYHANCCEGCPHIAGTSGSSLSFHSTVINHYMR 377
|| : : : ||| | : : ||| | : : ||| | : : ||| | :
Qy 69 --NPASASPCCVPDLEPLTLIYY-VGRTPKVEQLSNMVKSKCS 112
|| : : : ||| | : : ||| | : : ||| | : : ||| | :
Db 378 GHSPFANKSCCVPTKLPMSELYDDGQNIKKDIQNMIIVEECGS 424
|| : : : ||| | : : ||| | : : ||| | : : ||| | :

RESULT 31

S31440

Inhibin beta-A chain - mouse

N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A60087; I48265; S31440
R:Albano, R.M.; Godsavage, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack, J.M.; Development 110, 435-443, 1990
A>Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia ce
A:Reference number: A60087; MUID:92155098
A:Accession: A60087
A:Molecule type: protein
A:Residues: 309-311,'X','313-318,'XX','321-325 <AL2>
R:Albano, R.M.; Groome, N.; Smith, J.C.; Development 117, 711-723, 1993
A>Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A:Reference number: I48243; MUID:93321614
A:Accession: I48265
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-424 <RES>
A:Cross-references: EMBL:X69619; NID:g50145; PIDN:CAA49325.1; PID:g50146
C:Superfamily: inhibin

Query Match 31.5%; Score 200; DB 1; Length 424;
Best Local Similarity 37.4%; Pred. No. 8.3e-13;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFDRLGHW-VVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNLT 68
|| : : : ||| | : : ||| | : : ||| | : : ||| | :
Db 319 CCKKOFFVSFK-DIGWNIIAPSGHYHANCCEGCPHIAGTSGSSLSFHSTVINHYMR 377
|| : : : ||| | : : ||| | : : ||| | : : ||| | :
Qy 69 --NPASASPCCVPDLEPLTLIYY-VGRTPKVEQLSNMVKSKCS 112
|| : : : ||| | : : ||| | : : ||| | : : ||| | :

C:Accession: S30488; B23556; B24248; A30884; S33351; P00010
R:Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu, A.
DNA Seq. 2, 103-110, 1991
A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.
A:Reference number: S30488; MUID:92135888
A:Accession: S30488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <TAN>
A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA40805.1; PID:g825621
A:Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue 54 as Glu.
R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.
FEBS Lett. 206, 329-334, 1986
A:Title: Human inhibin genes. Genomic characterisation and sequencing.
A:Reference number: A91366; MUID:87005283
A:Accession: B23556
A:Molecule type: DNA
A:Residues: 311-426 <STE>
A:Cross-references: GB:X04447; NID:g33928; PIDN:CAA28041.1; PID:g33929
R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A:Title: Structure of two human ovarian inhibins.
A:Reference number: A90123; MUID:86186863
A:Accession: B24248
A:Molecule type: mRNA
A:Residues: 1-426 <MAS>
A:Cross-references: GB:M13436; NID:g186414; PIDN:AAA59168.1; PID:g307069
R:Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988
A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin.
A:Reference number: A30884; MUID:88190086
A:Accession: A30884
A:Molecule type: mRNA
A:Residues: 1-426 <MUR>
A:Cross-references: GB:J03634; NID:g181946; PIDN:AAA35787.1; PID:g181947
R:Berg, H.; Walter, M.; Northemann, W.
submitted to the EMBL Data Library, April 1993
A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhibin.
A:Reference number: S33351
A:Accession: S33351
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 311-376, 'AC', 380-426 <BER>
A:Cross-references: EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose, Y.
Biochem. Biophys. Res. Commun. 174, 1163-1168, 1991
A:Title: Purification of megakaryocyte differentiation activity from a human fibrous histiocyte.
A:Reference number: P00010; MUID:91144591
A:Accession: P00010
A:Molecule type: protein
A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 <FUJ>
A:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
bin beta-A and beta-B, respectively.
C:Genetics:
A:Gene: GDB:INHBA
A:Cross-references: GDB:119346; OMIM:147290
A:Map position: 7p15-7p13
A:Introns: 129/3
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-310/Domain: propeptide #status predicted <PRO>
F:311-426/Product: inhibin beta A chain #status experimental <MAT>
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.5%; Score 200; DB 1; Length 426;
Best Local Similarity 37.4%; Pred. No. 8, 3e-13;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLXYIDFRDLGKWK-WVHEPKGYANFCGPGCPYLRS-----YLRSDATHTSHVGLYNTL 68
Db 321 CCKKQFFVSKF-DIGWNDWIITAPSGYHANYCCEGCPSHIAGTSGSLSLFSHSTVINHYRMR 379

QY 69 --NPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVMVSKCKS 112
Db 380 GHSPFANLSCCVPTKLRPMMLYYDDGQNIKKDIQNMIIVERCGCS 426
RESULT 34
JC4151
activin beta D chain precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: JC4151
R:Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A:Title: Molecular cloning and functional analysis of a new activin beta subunit: a d
A:Reference number: JC4151; MUID:95275314
A:Accession: JC4151
A:Molecule type: mRNA
A:Residues: 1-367 <ODA>
A:Cross-references: DBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961513
A:Experimental source: embryo
C:Superfamily: inhibin
C:Keywords: glycoprotein; mesoderm
F:1-253/Domain: signal sequence #status predicted <SIG>
F:254-367/Product: activin beta D chain #status predicted <MAT>
F:64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.2%; Score 197.5; DB 2; Length 367;
Best Local Similarity 36.0%; Pred. No. 1.3e-12;
Matches 41; Conservative 25; Mismatches 35; Indels 13; Gaps 6;

QY 10 NLEEN---CCVRPLXYIDFRDLGKWK-WVHEPKGYANFCGPGCPYLRS-----ADTHTST 60
Db 256 NCDQSNLCCRKDYVDFK-DIGWNDWIITKPEGYQINCYMGLCPMHIIAGAPGMAASFHTT 314
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVMVSKCKS 112
Db 315 VLNLKANNIQTAVNSCCVPTKRRPLSMLEYF-DRNNNVLTKTDIADMIVEACGCS 367
RESULT 35
A43918
TGFB-beta-related protein 60A precursor - fruit fly (Drosophila melanogaster)
A:Alternate names: bone morphogenetic protein homolog precursor
C:Species: Drosophila melanogaster
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A43918; A41233
R:Doctor, J.S.; Jackson, P.D.; Rashka, K.E.; Visalli, M.; Hoffmann, F.M.
Dev. Biol. 151, 491-505, 1992
A:Title: Sequence, biochemical characterization, and developmental expression of a ne
A:Reference number: A43918; MUID:92290120
A:Accession: A43918
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-455 <DOC>
A:Cross-references: GB:M84795; NID:g156729; PIDN:AAA28307.1; PID:g156730
A:Note: sequence extracted from NCBI backbone (NCBI:106399, NCBIP:106400)
R:Wharton, K.A.; Thomsen, G.H.; Gelbart, W.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 9214-9218, 1991
A:Title: Drosophila 60A gene, another transforming growth factor beta family member,
A:Reference number: A41233; MUID:92021021
A:Accession: A41233
A:Molecule type: mRNA
A:Residues: 1-455 <WHA>
A:Cross-references: GB:M77012; NID:g156727; PIDN:AAA28306.1; PID:g156728
A:Comment: This protein is a member of the transforming growth factor beta family.
C:Genetics:
A:Gene: 60A
A:Cross-references: FlyBase:FBgn0024234
C:Superfamily: inhibin
C:Keywords: homodimer

Query Match
Best Local Similarity 30.8%; Score 195; DB 2; Length 455;
Matches 41; Conservative 19; Mismatches 37; Indels 6; Gaps 4;

QY 14 NCCVRPLIDFRQDLGW-KWVHEPKGYANFCSPGCPYLRSAD---TTHSTVLGLYNTLN 69
: : : ||||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :
Db 353 SCQMOTLYIDEK-DLGWHDWIIAPEGYGATCYSCSECFNPLNAHNMATNHAIVQTQLVHLE 411
: : : ||||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :

QY 70 PEASAPCCVPQDLEPILTIYYVG-RTPKVQEQLSNMVVKSKC 111
: : : |||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :
Db 412 PKVKPKCCAPTRLGALPVLYHLNDENVNLKKRYRNMIVKSGC 454

RESULT 36
JC4862
activin beta-A chain precursor - Japanese common newt
C:Species: Cynops pyrrhogaster (Japanese common newt)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 20-Jun-2000
C:Accession: JC4862
R:Yamamoto, T.; Nakayama, Y.; Abe, S.
Biochem. Biophys. Res. Commun. 224, 451-456, 1996
A:Title: Expression of activin beta subunit genes in sertoli cells of newt testes.
A:Reference number: JC4862; MUID:96295508
A:Accession: JC4862
A:Molecule type: mRNA
A:Residues: 1-413 <YAM>
A:Cross-references: GB:D84516; NID:g1502288; PIDN:BAAL2693.1; PID:g1502289
A:Experimental source: testes
C:Comment: This protein is secreted from Sertoli cells and plays a role in the regulation of spermatogenesis.
C:Superfamily: inhibin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:298-413/Product: activin beta-A chain #status predicted <MAT>

Query Match
Best Local Similarity 30.4%; Score 193; DB 2; Length 413;
Matches 41; Conservative 17; Mismatches 39; Indels 10; Gaps 6;

QY 15 CCVRPLIDFRQDLGW-KWVHEPKGYANFCSPGPCP-YLR-----SADTTHTSVLGLYNT- 67
: : : |||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :
Db 308 CCKKQFYVSFK-DIGWSDWVIAPPGYTANYCEGDPCPMYITGTSGSGPSFHAAVINQYMR 366
: : : |||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :

QY 68 -LNPEASAPCCVPQDLEPILTIYY-VGRTPKVQEQLSNMVVKSKCS 112
: : : |||| : |||| : |||| : |||| : |||| : |||| : |||| : |||| :

Db 367 GYSPTTSVKSCVPTTKURASMLIYDDGQNIIKRDIQNMVVEGCSS 413

RESULT 37
T43286
cet-1 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43286
R:Morita, K.; Chow, K.L.; Ueno, N.
Development 126, 1337-1347, 1999
A:Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis elegans.
A:Reference number: 22393; MUID:99146896
A:Accession: T43286
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-365 <MOR>
A:Cross-references: EMBL:AF074395; NID:g3328181; PIDN:AAC26791.1; PID:g3328182
C:Genetics:
A:Gene: cet-1
A:Map position: 5
C:Superfamily: inhibin

Query Match 30.2%; Score 191.5; DB 2; Length 365;
Best Local Similarity 39.6%; Pred. No. 5.2e-12;
Matches 42; Conservative 16; Mismatches 41; Indels 7; Gaps 5;

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Qy   12  ENCCVR-PLYIDFRODLGHWK-WVHEPKGYIYANFCSGPCPYLRSAD---TTHSTVLGLYN 66
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db   260  ESNLCRTDFYYDF-DLNNQDMIMAPKYDAYCQCQSCPMPAQLNATNHAIQSLLH 318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Qy   67  TLNPASASPCCVPODEPLTIYV-VGRTPKEQLSNMVVKSKCK 111
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db   319  SLRPEVPPCCVPTETSPLSILYMVDKVIVIREYADM RVESCGC 364
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 38
B40905
inhibit beta-A chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B40905; B40036
R:Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno,
Mol. Endocrinol. 1, 388-396, 1987
A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis
A:Reference number: A40905; WUID:90331931
A:Accession: B40905
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-424 <ESC>
R:Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.; Mayo, K.E.
Mol. Endocrinol. 1, 561-568, 1987
A:Title: Rat inhibit: molecular cloning of alpha- and beta-subunit complementary deox
A:Reference number: A40056; WUID:91042598
A:Accession: B40056
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-366, 'H', 368-424 <WOO>
A:Cross-references: GB:M37482; NID:g204936; PIDN:AAA41436.1; PID:g204937
C:Superfamily: inhibit

```

Query Match	30.1%	Score 191;	DB 1;	Length 424;
Best Local Similarity	36.4%;	Pred. No. 6.8e-12;		
Matches	39;	Conservative 21;	Mismatches 37;	Indels 10; Gaps 5;
Qy	15	CCVRLYIDFRDLGWK-VWHEPKGYANFCSGPCP-----YLRADTHTSTVLGLYNPL 68		
		: : : : : : : : : : : : :		
Db	319	CCKQFFVSFK-DIGWNDWIAPSGVHANYCEGBCPSHIACTSGSSLSFSSTVINHYRMR 377		
Qy	69	--NPASASPCCPQDLPLTILYV-VGRTPKVEQLSNMWVKSKCS 112		
		: : : : : : : : : : : : :		
Db	378	GHSPEANLKSCCVPTKLRPWSMLYDDGONIIKKDIONMIVEEGCS 424		

RESULT 39
I51284
bone morphogenetic protein-7 - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: I51284
R:Houston, B.; Thorp, B.H.; Burt, D.W.
J. Mol. Endocrinol. 13, 289-301, 1994.
A:Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick
A:Reference number: I51284; MUID:95200473
A:Accession: I51284
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <HOU>
A:Cross-references: GB: S77477; NID: g957233; PIDN: AAB33846.1; PID: g957234
C:Superfamily: inhibin

```

Query Match      30.0%; Score 190; DB 2; Length 313;
Best Local Similarity 34.8%; Pred. No. 6.3e-12;
Matches 40; Conservative 22; Mismatches 39; Indels 14; Gaps 5;

Qy 10 NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYANFCGPGPYLRSA---DTT 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 NIAENSDDORACKKHLYVSFR-DLGWODWIITAPEGYAAAYCYCEGAFIPYMNAFN 257

```


C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0690
 R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
 A:Reference number: JH0687; MUID:92378616
 A:Accession: JH0690
 A:Molecule type: mRNA
 A:Residues: 1-426 <NIS>
 A:Cross-references: GB:X63427; NID:964591; PIDN:CAA45021.1; PID:g64592
 A:Experimental source: oocyte
 C:Superfamily: inhibin
 C:Keywords: glycoprotein
 F:283-426/Product: bone morphogenetic protein 7 #status predicted <MAT>
 F:177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 187; DB 2; Length 426;
 Best Local Similarity 35.2%; Pred. No. 1.8e-11;
 Matches 38; Conservative 23; Mismatches 41; Indels 6; Gaps 4;
 QY 9 RNLEENCCVRPLYDFRDLGWK-WVHEPKGYANFCGPGCVLRS- --DTHSTVLGL 64
 Db 319 RFLQACKKHELFVSPR-DLGWODWIIAPGAYAYCDGECAPLNSFMNTHAIVOTL 377
 QY 65 YNTLNPEASAPCCVPQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
 Db 378 VHFNPETVPKCCATQTLNGISLVLYFDDSANVLLKKYKNWVQACGC 425

RESULT 45
 WFPGBB
 inhibin beta-B chain precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
 C:Accession: A01394
 R:Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.;
 Nature 318, 659-663, 1985
 A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
 Nature 318, 659-663, 1985
 A:Reference number: A93371; MUID:86092207
 A:Accession: A01394
 A:Molecule type: mRNA
 A:Residues: 1-349 <MAS>
 A:Cross-references: GB:X03267; NID:g2005; PIDN:CAA27021.1; PID:g2006
 C:Comment: The source of this protein is ovarian follicular fluid.
 C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid
 C:Comment: The mature protein has been isolated (A and B) that differ in the amino-terminal
 C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follit
 C:Superfamily: inhibin
 C:Keywords: follicle-inhibitor; glycoprotein; gonad
 F:1-234/Domain: propeptide (fragment) #status predicted <PRO>
 F:235-349/Product: inhibin beta-B chain #status predicted <MAT>
 F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.4%; Score 186.5; DB 1; Length 349;
 Best Local Similarity 37.4%; Pred. No. 1.6e-11;
 Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYDFRDLGWK-WVHEPKGYANFCGPGCP-YLR- ---SADTTHSTVLGLYNT- 67
 Db 245 CCRCQFFIDFRL-IGNSDWIIAPTGYGNYCEGCPAYLAGVPGSSASSTAVVNVQYRMR 303
 QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKVQ-LSNMVVKSKCS 112
 Db 304 GLNP-GTVNSCCIPTKLSTMSMLYFDDDEYNIVKRDVNPVIVECGCA 349

RESULT 46
 A40150
 inhibin beta-B chain precursor - human
 N:Alternate names: activin AB chain B
 C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
 C:Accession: A40150; C24248; A40156; S10751
 R:Mason, A.J.; Berkmeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
 Mol. Endocrinol. 3, 1352-1358, 1989
 A:Title: Activin B: precursor sequences, genomic structure and in vitro activities.
 A:Reference number: A40150; MUID:90114200
 A:Accession: A40150
 A:Molecule type: DNA
 A:Residues: 1-407 <MAS>
 A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
 R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986
 A:Title: Structure of two human ovarian inhibins.
 A:Reference number: A90123; MUID:86186863
 A:Accession: C24248
 A:Molecule type: mRNA
 A:Residues: 55-407 <MA2>
 A:Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417
 R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
 Mol. Endocrinol. 3, 939-948, 1989
 A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
 A:Reference number: A40156; MUID:89295443
 A:Accession: A40156
 A:Molecule type: mRNA
 A:Residues: 22-46, 'A', 48-407 <FEN>
 A:Cross-references: GB:M31632
 A:Experimental source: testis
 R:Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois,
 Biochim. Biophys. Acta 1039, 135-141, 1990
 A:Title: Purification and characterization of recombinant human activin B.
 A:Reference number: S10751; MUID:90304183
 A:Accession: S10751
 A:Molecule type: protein
 A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
 C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respo
 bin beta-A and beta-B, respectively.
 C:Genetics:
 A:Gene: GDB:INHBB
 A:Cross-references: GDB:119347; OMIM:147390
 A:Map position: 2cen-2q13
 C:Superfamily: inhibin
 C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-292/Domain: propeptide #status predicted <PRO>
 F:293/Product: inhibin beta-B chain #status predicted <MAT>
 F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.4%; Score 186.5; DB 1; Length 407;
 Best Local Similarity 37.4%; Pred. No. 1.9e-11;
 Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYDFRDLGWK-WVHEPKGYANFCGPGCP-YLR- ---SADTTHSTVLGLYNT- 67
 Db 303 CCRCQFFIDFRL-IGNSDWIIAPTGYGNYCEGCPAYLAGVPGSSASSTAVVNVQYRMR 361
 QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKVQ-LSNMVVKSKCS 112
 Db 362 GLNP-GTVNSCCIPTKLSTMSMLYFDDDEYNIVKRDVNPVIVECGCA 407

RESULT 47
 S50899
 betaB inhibin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S50899
 R:Thompson, D.A.; Cronin, C.N.; Martin, F.
 Eur. J. Biochem. 226, 751-764, 1994
 A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet
 y DNase I footprinting.
 A:Reference number: S50897; MUID:95112839
 A:Accession: S50899

[illegible]

Query Match 28.8%; Score 182.5; DB 2; Length 394;
Best Local Similarity 37.7%; Pred. No. 4.6e-11;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

Qy 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 288 KRLKSSCRHRPLVYDF-SDVGNDWIVAPPGYHAFYCHGECFPPLADHLNS--TNHAIQV 344

Qy 63 GLYNTLN---PEASASPCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 345 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVLKNYQDMVVEGCGC 393

RESULT 56
BMH2
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2A; rhBMP2
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B37278; PC2178
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 <W02>
A:Cross-references: GB:M22489; NID:gl79501; PIDN:AAA51834.1; PID:gl79502
R:Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Kataya
J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in silkw
A:Reference number: PC2178; MUID:94266754
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 'X', 297-304 <ISH>
A:Experimental source: cell line BOMo-15A1IC
R:Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.
Protein Sci. 4(Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2) a
A:Reference number: A56729
A:Contents: annotation
A:Note: Determination of amino ends of mature forms; dimers with long form chains have
C:Comment: This hormone is capable of inducing bone formation at ectopic morphological
C:Genetics:
A:Gene: GDB:BMP2; BMP2A
A:Cross-references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
C:Complex: homodimer, disulfide linked
C:Superfamily: inhibin
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-265/Domain: propeptide #status predicted <PRO>
F:266-396/Product: bone morphogenetic protein 2, long form #status predicted <MAT>
F:283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>
F:135,163,164,200/Binding site: carboxylic acid (Asn) (covalent) #status predicted
F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 28.8%; Score 182.5; DB 1; Length 396;
Best Local Similarity 37.7%; Pred. No. 4.7e-11;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

Qy 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 290 KRLKSSCRHRPLVYDF-SDVGNDWIVAPPGYHAFYCHGECFPPLADHLNS--TNHAIQV 346

Qy 63 GLYNTLN---PEASASPCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 347 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVLKNYQDMVVEGCGC 395

RESULT 57

JH0688
bone morphogenetic protein 2II precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0688
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in earl
A:Reference number: JH0687; MUID:92378616
A:Accession: JH0688
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
A:Experimental source: oocyte
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F:137,202,237,340/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 28.8%; Score 182.5; DB 2; Length 398;
Best Local Similarity 37.7%; Pred. No. 4.7e-11;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

Qy 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 292 KRLKSSCRHRPLVYDF-SDVGNDWIVAPPGYHAFYCHGECFPPLADHLNS--TNHAIQV 348

Qy 63 GLYNTLN---PEASASPCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 349 TLVNSVNTNIPKA-----CCVPTLSAISML-YLDENEKVLKNYQDMVVEGCGC 397

RESULT 58
JH0687
bone morphogenetic protein 2I precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0687; S16244
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in earl
A:Reference number: JH0687; MUID:92378616
A:Accession: JH0687
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: GB:X63424; NID:g64585; PIDN:CAA45018.1; PID:g64586
A:Experimental source: oocyte
R:Plessow, S.; Koester, M.; Knoechel, W.
Biochim. Biophys. Acta 1089, 280-282, 1991
A:Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
A:Reference number: S16244; MUID:91274367
A:Accession: S16244
A:Molecule type: mRNA
A:Residues: 1-6, 'S', 8-15, 'V', 17-232, 'N', 234-398 <PLE>
A:Cross-references: EMBL:X55031; NID:g64581; PIDN:CAA38850.1; PID:g64582
C:Superfamily: inhibin
C:Keywords: dimer; glycoprotein
F:285-398/Product: bone morphogenetic protein 2I #status predicted <MAT>
F:137,202,340/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 28.8%; Score 182.5; DB 2; Length 398;
Best Local Similarity 37.7%; Pred. No. 4.7e-11;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

Qy 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 292 KRLKSSCRHRPLVYDF-SDVGNDWIVAPPGYHAFYCHGECFPPLADHLNS--TNHAIQV 348

Qy 63 GLYNTLN---PEASASPCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 349 TLVNSVNTNIPKA-----CCVPTLSAISML-YLDENEKVLKNYQDMVVEGCGC 397

A;Molecule type: mRNA
A;Residues: 1-461 <PDB>
A;Cross-references: ENR
C;Superfamily: inhibin

A;Residues: I-461 <PON>
A;Cross-references: EMBL:Z48313; NID:g673496; PID:g673497
C;Superfamily: inhibin

Query Match	28.5%	Score 181;	DB 2;	Length 461;
Best Local Similarity	34.6%	pred. No. 7.8e-11;		
Matches	37;	Conservative 22;	Mismatches 42;	Indels 6; Gaps 4;
QY	10	NLENCCVRPLYIDFRQDLGW-KWVHEPKGYANPCSGPCPYLRSD---	TTHTSTVLGIY	65
		: : : : : : : : : : : :		
Db	355	NSDWQCKRKNLFVNF-EDLDQEWELIAPLGVAFCQCECAFFPLNGHANATNHAIVQTIV	413	
QY	66	NTLNPEASASCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC	111	
		: : : : : : : : :		
Db	414	HMGSPSHVPQCCATKLSPITVYIDDSRNVLKLYKNMVVRACCG	460	

RESULT 64

JC2466
inhibin beta-C chain precursor - human
N:Alternate names: activin beta C chain
C:Species: Homo sapiens (man)
C:Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
C:Accession: JC2466
R:Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A:Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC chain
A:Reference number: JC2466; MUID:95126961

A;Molecule type: mRNA
A;Residues: 1-352 <HOE

A; Cross-references: GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g669155
A; Experimental source: liver
C; Genetics:

A:Gene: GDB:INHBC
A:Cross-references: GDB:632884
A:Map position: 2cen-2q13
C:Superfamily: inhibin
C:Keywords: glycoprotein

F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-236/Domain: propeptide #status predicted <PRO>
F;237-352/Product: activin beta C #status predicted <M
F;110,143,161/Binding site: carbohydrate (Asn) (covalen

Query Match	28.4%	Score 180;	DB 2;
Best Local Similarity	37.4%	Pred. No. 7.4e-11;	Length 352;
Matches 40;	Conservative	19;	Mismatches 38;
			Indels 10;
			Gaps 5.

[illegible]

RESULT 65

JC5366
 activin beta C - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
 C:Accession: JC5366
 R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
 Biochem. Biophys. Res. Commun. 231, 655-661, 1997
 A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit
 A:Reference number: JC5366; MUID:97224404
 A:Accession: JC5366
 A:Molecule type: DNA
 A:Residues: 1-352 <FAN>

A;Cross-references: GB:U95962
C;Comment: Activin beta C and
C;Genetics:
A;Introns: 105/3
C;Superfamily: inhibin

Query Match	28.4%	Score 180;	DB 2;	Length 352;
Best Local Similarity	37.8%	Pred. No. 7.4e-11;		
Matches 42;	Conservative 20;	Mismatches 31;	Indels 18;	Gaps 7;

Qy 15 CCVRPLYIDFRQDLGWK-WWHEPKGYANFCSGPCPYLRSAD-----TTHSTVLGLYNT 67
|| : ||| :|| : :||| ||| :||| | : ||| |
Db 247 CCRQEFFFVDFR-EIGANDWIITPEGYAMNFTCGOCP-LHVAGMPCISASHTAVL---NL 301

QY 68 LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVMVKCKCS 112
 - - - - - | - - - - - ||| - - - - - ||| - - - - - ||| - - - - - ||| - - - - - ||| - - - - - |||
 Db 302 LKANAAGTTGRGSCCVPSTRRPLSLYYDRDSNIVKTIPTDMVVEACGCS 352

RESULT 66

S70580
 activin beta C precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S70580
 R:tau, A.L.; Nishimori, K.; Matsuk, M.M.
 Biochim. Biophys. Acta 1307, 145-148, 1996
 A:Title: Structural analysis of the mouse activin beta-C gene.
 A:Reference number: S70580; MUID:96283807

A:Accession: S70580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <LAU>
A:Cross-references: EMBL:U40772
C:Genetics:
A:Introns: 106/1
C:Superfamily: Inhibin

Query Match 28.4%; Score 180; DB 2; Length 352;
Best Local Similarity 37.8%; Pred. No. 7.4e-11;
Matches 42; Conservative 20; Mismatches 31; Indels 18; Gaps 7;

Qy 15 CCVRPLYIDFRQDLGWK-WWHEPKGYANFCSGPCPYLRSD-----TTHSTVLGLYNT 67
 || : ||| : || | : : ||| ||| : || | : : ||| |
 Db 247 CCRQEFFVDFR-ETGWNDWIIQPEGVAMNFCGQCP-LHVAGMPCISAFHITAVL---NL 301

Qy	68	LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVMVKCKCS	112
		: : : : ::	
Db	302	LKANAAAGTTGRCSCCVPTSRRRPLSLYYDRDSNIYKTIDPDMVVEACGCS	352

RESULT 67

S43295
bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N:Alternate names: growth and differentiation factor 6
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
R:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427

A; Residues: 1-125 <STO>
A; Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
C; Genetics:
A; Gene: Gdf6
C; Superfamily: inhibin
F; 1-5/Domain: polybasic protease recognition site #status predicted <P>
F; 6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) <P>
I; 1-125/Protein: bone morphogenetic protein homolog GDF6 (fragment) <P>

	Query Match	28.2%	Score 179;	DB 1:	Length 454;	
	Best Local Similarity	35.2%;	Pred. No. 1.2e-10;			
	Matches	37; Conservative	22; Mismatches	40; Indels	6; Gaps	4;
QY	12 EENCVRPLXIDFRODLGWK-WHEPKGYIYANFCGCPYLRSAD---	TTTSTVLGLYNT	67			
Db	350 KQACKHIELVSR-DLWQDWIIIAPEYAIFYCDGECFFLNAMNATNHAI	VQTLVHL	408			
QY	68 LNPPASAPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVKSKC	K	111			
Db	409 MFPHVHPKCPCAPTALNAISLVYPDDSSNVILKKRYNNVVRS	CGC	453			
RESULT	70					
S43296	bone morphogenetic protein-related protein (GDF7) - mouse					
C:	Species: Mus musculus (house mouse)					
C:	Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000					
C:	Accession: S43296					
R:	Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.					
A:	Title: Limb alterations in brachypodism mice due to mutations in a new member of th					
A:	Reference number: S43294; MUID:94195427					
A:	Accession: S43296					
A:	Status: preliminary					
A:	Molecule type: DNA					
A:	Residues: 1-151 <STO>					
A:	Cross-references: GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466					
C:	Superfamily: inhibin					
Query Match	27.8%; Score 176;	DB 2:	Length 151;			
Best Local Similarity	37.0%; Pred. No. 7.7e-11;					
Matches	40; Conservative	20; Mismatches	42; Indels	6; Gaps	5;	
QY	9 RNLEENCVRPLXIDFRODLGW-KWWHEPKGYIYANFCGCPY-LRS-	ADTTHSTVLGL	64			
Db	44 RRGSRCSRKSLHWDFK-ELGWDWIITAPLDYEAYHCEGVCDPFLRSHLEPTNHAIQT	L	102			
QY	65 YNTLNPEASAPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVKSKC	K	111			
Db	103 LNSMAPDAAPASCPCPARLSPISTILYIDAANNVVYKQVEDMVVEACGC	150				
RESULT	71					
B53452	cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)					
C:	Species: Bos primigenius taurus (cattle)					
C:	Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000					
C:	Accession: B53452					
R:	Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Ko					
J:	Biol. Chem. 269, 28227-28234, 1994					
A:	Title: Cartilage-derived morphogenetic proteins. New members of the transforming g					
A:	Reference number: A55452; MUID:95050604					
A:	Accession: B53452					
A:	Status: preliminary; not compared with conceptual translation					
A:	Molecule type: mRNA					
A:	Residues: 1-436 <CHA>					
A:	Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490					
C:	Superfamily: inhibin					

RESULT 81
I49541
bone morphogenetic protein 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49541; S29523; B34201
R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mund
J. Biol. Chem. 270, 28364-28373, 1995
A:Title: The mouse bone morphogenetic protein-4(BMP4) gene: Analysis of promoter utiliza
A:Reference number: I49541; MUID:96081880
A:Accession: I49541
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-420 <RES>
A:Cross-references: GB:I47480; NID:g994733; PIDN:AC37698.1; PID:g994734
R:Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
submitted to the EMBL Data Library, December 1990
A:Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) cDN
A:Reference number: S29523
A:Accession: S29523
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 13-420 <DIC>
R:Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, D.A
Peland, N.G.; Jenkins, N.A.
Genomics 6, 505-520, 1990
A:Title: Chromosomal localization of seven members of the murine TGF-beta superfamily su
A:Reference number: A34201; MUID:90228966
A:Accession: B34201
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 253-420 <DI2>
C:Genetics:
A:Gene: BMP-4
A:Introns: 11/1; 137/1
C:Superfamily: inhibin

Query Match 26.9%; Score 170.5; DB 2; Length 420;
Best Local Similarity 37.7%; Pred. No. 8.2e-10;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;
QY 9 RNLENCVRLYIDFRODLGK-WVHEPKGYANFCGPGCPY-----LRSDTTHSTVL 62
Db 314 RKNKNCRRHSLYVDF-SDVGNWDWIVAPPGYQAFYCHGDCFPFLADHLNS--TNHAIQV 370
QY 63 GLYTLN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 371 TLVNSVNSIPKA---CCVPTSLAISML-YLDEYDKVLKNTQEMVVEGCGC 419

RESULT 82
B36192
inhibin beta-B1 chain - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C:Accession: B36192
R:Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A:Title: Activins are expressed early in Xenopus embryogenesis and can induce axial meso
A:Reference number: A36192; MUID:91029481
A:Accession: B36192
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-101 <THO>
C:Superfamily: inhibin

Query Match 26.8%; Score 170; DB 2; Length 101;
Best Local Similarity 41.2%; Pred. No. 2e-10;
Matches 35; Conservative 14; Mismatches 26; Indels 10; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGCP-YLR-----SADTTHSTVLGLYNT- 67
Db 5 CCRQFYIDFRL-IGNDWIIAPAGYGYNGVCEGCPAYLAGVPGSASSFHTAVVNOYRMR 63
QY 68 -LNPEASAPCCVPQDLEPLTILY 91
Db 64 GLNP-GTVNSCCIPTKLTSMMLYF 87
RESULT 83
C36192
inhibin beta-B2 chain - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C:Accession: C36192
R:Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A:Title: Activins are expressed early in Xenopus embryogenesis and can induce axial m
A:Reference number: A36192; MUID:91029481
A:Accession: C36192
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: DNA
A:Residues: 1-101 <THO>
C:Superfamily: inhibin

Query Match 26.7%; Score 169; DB 2; Length 101;
Best Local Similarity 40.0%; Pred. No. 2.6e-10;
Matches 34; Conservative 15; Mismatches 26; Indels 10; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGCP-YLR-----SADTTHSTVLGLYNT- 67
Db 5 CCRQFYIDFRL-IGNDWIIAPAGYGYNGVCEGCPAYLAGVPGSASSFHTAVVNOYRMR 63
QY 68 -LNPEASAPCCVPQDLEPLTILY 91
Db 64 GLNP-GTVNSCCIPTKLTSMMLYF 87

RESULT 84
A45056
osteogenic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 8; OP-2
C:Species: Homo sapiens (man)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A45056
R:Ozekaynak, E.; Schneegelsberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier,
J. Biol. Chem. 267, 25220-25227, 1992
A:Title: Osteogenic protein-2. A new member of the transforming growth factor-beta su
A:Reference number: A45056; MUID:93094231
A:Accession: A45056
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-402 <OZK>
A:Cross-references: NID:g189389; PIDN:AAB01360.1; PID:g189390
A:Experimental source: hippocampus
A>Note: sequence extracted from NCBI backbone (NCBIP:120189)
C:Genetics:
A:Gene: GDB:BMP8; OP-2
A:Cross-references: GDB:I36392
C:Superfamily: inhibin

Query Match 26.5%; Score 168; DB 2; Length 402;
Best Local Similarity 38.2%; Pred. No. 1.4e-09;
Matches 39; Conservative 13; Mismatches 44; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGCPY-LRSA--DPTHTVLGLYNTLP 70
Db 301 CRRHLYVSF-ODLGLDWIAPQGYATYCEGCSFPDSCMNATNHALQSLVHLMPK 359
QY 71 EASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111


```
A:Molecule type: mRNA  
A:Residues: 1-360 <RES>  
A:Cross-references: GB:S77492; NID:g957225; PIDN:AAB33725.1; PID:g957226  
C:Superfamily: inhibin
```

Query Match 24.7%; Score 156.5; DB 2; Length 360;
Best Local Similarity 34.3%; Pred.No.1.9e-08;
Matches 37; Conservative 20; Mismatches 36; Indels 15; Gaps 7;

Qy 14 NCVVRPLYDFRODLGW-KWVHEPKGYANFCSGPC--PYLRS-ADTTHSTVLGLYNTLN 69
Dl 257 NCARYLKVDFF-ADIGSEWIISPKSFAYYCAGACQPMPKSLKPNSHAIQSIVRAVG 315

Qy 70 -----PEASAPCCVPQDLEPLTLILYY-VGRTPKVQEQLSNMVVKSKCK 111
Db 316 VVSIGE-----PCCVPEKMSSLSILFDEKNMNVLLKYVYPNNMTVDSCAC 359

RESULT 94
T25451
transforming growth factor beta homolog - Caenorhabditis elegans
C:Species:Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T25451
R:Bentley, D.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans, cosmid B0412.
A:Reference number: Z20037
A:Accession: T25451
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-350 <BEN>
A:CROSS-references: EMU:L080953; PIDN:AAB52554.1; GSDB:GNO0021
A:Experimental source: strain Bristol N2; clone B0412,
C:Genetics:
A:Gene: dai-7
A:Map position: 3
A:Introns: 43/3; 123/3; 184/2; 288/3
C:Superfamily: inhibin

Query Match 23.6%; Score 149.5; DB 2; Length 350;
Best Local Similarity 31.8%; Pred.No.9.3e-08;
Matches 34; Conservative 19; Mismatches 43; Indels 11; Gaps 6;

Qy 13 ENCVRPPLYIDFRODLGKKWWHEPKGYANFCSPCPY---LRSDATHTSHVT-LGLYNT 67
Db 248 KGCCLYLEIEF-EKGWDWTAVPRINAYNCRGDCCHYNNAHFNLAEFTGHAKIMRAHKV 306

Qy 68 LNPEASAPCCVPQDLEPLTLIYGRTPKVE--QLSNNVVVKSKCS 112
Db 307 SNPEIGY-CCHPTDYDIKL-IYNRDRGVSIANVMGIACCSCS 350

RESULT 95
T03907
TCGF-beta-related protein homolog F39G3.8 - Caenorhabditis elegans
C:Species:Caenorhabditis elegans
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
C:Accession: T03907
R:Du, Z.; Le, T.T.; Holmes, A.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F39G3.
A:Reference number: Z15131
A:Accession: T03907
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-366 <DUZ>
A:CROSS-references: EMU:AF016424; NID:g2291203; PIDN:AAB55333.1; PID:g2291211
C:Genetics:

A:Map position: V
A:Introns: 38/2; 86/2; 110/1; 161/2; 205/1; 229/2; 259/1

A:Note: F39G3.8
C:Superfamily: inhibin

Query Match 23.3%; Score 148; DB 2; Length 366;
Best Local Similarity 32.7%; Pred. No. 1.4e-07;
Matches 35; Conservative 21; Mismatches 45; Indels 6; Gaps 5;

Qy 10 NLEENCVRPLIDFRQDLGW-KWHEPKGYANFCSGPC--PYLRSAD-TTHSTVLGLY 65
| | : | : | | | | | | : | : | | | | : : : | : | : |
Db 260 NENRCQRKGLYVDF-DILGWKQWIAPEGFSAFYCSGDCSAPFSKEMNATSHAI VQSTL 318
| | : | : | | | | | | | : | : | | | | : : : | : | : |
Qy 66 NTLNPEASAPCCVPQDLPLTLILY-VGRTPKVEQLSNMVKSKCK 111
: : : : | | | | | | : : : : | : | | | |
Db 319 HVRVNPSTTPAKCASPLSGSYKILFDQNKQVQIKRYRDMVYDEGCG 365

RESULT 96
A40735
TGF beta homolog dsl-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A40735
R:Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.
Cell 73, 687-702, 1993
A:Title: Control of cell pattern in the neural tube: regulation of cell differentiation
A:Reference number: A40735; MUID:93272310
A:Accession: A40735
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-427 <BA>
A:Cross-references: GB:L12032; NID:G304379; PIDN:AAA48752.1; PID:G304380
A:Experimental source: spinal cord
A:Note: sequence extracted from NCBI backbone (NCBIN:132680, NCBI:P:132681)
C:Superfamily: inhibin

Query Match 22.1%; Score 140; DB 2; Length 427;
Best Local Similarity 31.8%; Pred. No. 1.1e-06;
Matches 35; Conservative 21; Mismatches 46; Indels 8; Gaps 5;

Qy 9 RNLENCVVR-PLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSADTT---HSTVLG 63
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 318 RSGIANHCRRSLHVNFK-EIGWDSWIIAPKDYAEAFCKGCGFFPLDVTNPTKHAIVQT 376
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 64 LYTLNPEASAPCCVPQDLPLTLILY--VGRTPKVEQLSNMVKSKCK 111
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 377 LVHLQNPKRASKACCVPTKLDALISLYKDDAGVPTLIYEGMKVAEGCG 426

RESULT 97
JC5697
Placental transforming growth factor-beta homolog - human
C:Species: Homo sapiens (man)
C:Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 17-Mar-1999
C:Accession: JC5697
R:Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.
J. Biochem. 122, 622-626, 1997
A:Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in
A:Reference number: JC5697; MUID:98006316
A:Accession: JC5697
A:Molecule type: mRNA
A:Residues: 1-309 <YOK>
A:Cross-references: DDBJ:AB000584
A:Experimental source: fibrosarcoma
C:Comment: This protein plays a role in reproduction.

Query Match 21.4%; Score 135.5; DB 2; Length 309;
Best Local Similarity 27.6%; Pred. No. 2.2e-06;
Matches 24; Conservative 15; Mismatches 47; Indels 1; Gaps 1;

Qy 26 QDLGW-KWHEPKGYANFCSGPCPYLRSADTTHTSTVLGLYNTLNPEASAPCCVPQDL 84

A:Note: F39G3.8
C:Superfamily: inhibin

Query Match 23.3%; Score 148; DB 2; Length 366;
Best Local Similarity 32.7%; Pred. No. 1.4e-07;
Matches 35; Conservative 21; Mismatches 45; Indels 6; Gaps 5;

Qy 10 NLEENCVRPLIDFRQDLGW-KWHEPKGYANFCSGPC--PYLRSAD-TTHSTVLGLY 65
| | : | : | | | | | | : | : | | | | : : : | : | : |
Db 260 NENRCQRKGLYVDF-DILGWKQWIAPEGFSAFYCSGDCSAPFSKEMNATSHAI VQSTL 318
| | : | : | | | | | | | : | : | | | | : : : | : | : |
Qy 66 NTLNPEASAPCCVPQDLPLTLILY-VGRTPKVEQLSNMVKSKCK 111
: : : : | | | | | | : : : : | : | | | |
Db 319 HVRVNPSTTPAKCASPLSGSYKILFDQNKQVQIKRYRDMVYDEGCG 365

RESULT 96
A40735
TGF beta homolog dsl-1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A40735
R:Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.
Cell 73, 687-702, 1993
A:Title: Control of cell pattern in the neural tube: regulation of cell differentiation
A:Reference number: A40735; MUID:93272310
A:Accession: A40735
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-427 <BA>
A:Cross-references: GB:L12032; NID:G304379; PIDN:AAA48752.1; PID:G304380
A:Experimental source: spinal cord
A:Note: sequence extracted from NCBI backbone (NCBIN:132680, NCBI:P:132681)
C:Superfamily: inhibin

Query Match 22.1%; Score 140; DB 2; Length 427;
Best Local Similarity 31.8%; Pred. No. 1.1e-06;
Matches 35; Conservative 21; Mismatches 46; Indels 8; Gaps 5;

Qy 9 RNLENCVVR-PLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSADTT---HSTVLG 63
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 318 RSGIANHCRRSLHVNFK-EIGWDSWIIAPKDYAEAFCKGCGFFPLDVTNPTKHAIVQT 376
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 64 LYTLNPEASAPCCVPQDLPLTLILY--VGRTPKVEQLSNMVKSKCK 111
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 377 LVHLQNPKRASKACCVPTKLDALISLYKKDAGVPTLIYEGMKVAEGCG 426

RESULT 97
JC5697
Placental transforming growth factor-beta homolog - human
C:Species: Homo sapiens (man)
C:Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 17-Mar-1999
C:Accession: JC5697
R:Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.
J. Biochem. 122, 622-626, 1997
A:Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in
A:Reference number: JC5697; MUID:98006316
A:Accession: JC5697
A:Molecule type: mRNA
A:Residues: 1-309 <YOK>
A:Cross-references: DDBJ:AB000584
A:Experimental source: fibrosarcoma
C:Comment: This protein plays a role in reproduction.

Query Match 21.4%; Score 135.5; DB 2; Length 309;
Best Local Similarity 27.6%; Pred. No. 2.2e-06;
Matches 24; Conservative 15; Mismatches 47; Indels 1; Gaps 1;

Qy 26 QDLGW-KWHEPKGYANFCSGPCPYLRSADTTHTSTVLGLYNTLNPEASAPCCVPQDL 84

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 30, 2001, 08:52:36 ; Search time 10.16 Seconds
(without alignments)
380.991 Million cell updates/sec

Title: TGFB3P
Perfect score: 634
Sequence: 1 ALDNTYCFRNLENCVRPL.....RTPKVEQLSNMVKSCSKX 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	99.8	410	1	TGF3_MOUSE
2	633	99.8	412	1	TGF3_HUMAN
3	630	99.4	412	1	TGF3_RAT
4	629	99.2	412	1	TGF3_CHICK
5	621	97.9	409	1	TGF3_PIG
6	539	85.0	412	1	TGF2_CHICK
7	535	84.4	412	1	TGF2_BOVIN
8	535	84.4	414	1	TGF2_HUMAN
9	535	84.4	435	1	TGF2_PIG
10	530	83.6	414	1	TGF2_MOUSE
11	516	81.4	413	1	TGF2_XENLA
12	503	79.3	390	1	TGF1_MOUSE
13	503	79.3	390	1	TGF1_RAT
14	500	78.9	315	1	TGF1_BOVIN
15	500	78.9	390	1	TGF1_CANFA
16	500	78.9	390	1	TGF1_CERAE
17	500	78.9	390	1	TGF1_HUMAN
18	500	78.9	390	1	TGF1_PIG
19	500	78.9	390	1	TGF1_SHEEP
20	499	78.7	390	1	TGF1_HORSE
21	488	77.0	390	1	TGF1_CAVPO
22	461	72.7	373	1	TGF1_CHICK
23	439	69.2	382	1	TGF1_XENLA
24	217	34.2	374	1	GDF8_BRARE
25	208.5	32.9	375	1	GDF8_PAPHA
26	208	32.8	350	1	IHBE_MOUSE
27	208	32.8	350	1	IHBE_RAT
28	207.5	32.7	375	1	GDF8_SHEEP
29	206	32.5	207	1	BMP6_RAT
30	206	32.5	426	1	IHBA_HORSE
31	206	32.5	513	1	BMP6_HUMAN
32	205	32.3	510	1	BMP6_MOUSE
33	204.5	32.3	375	1	GDF8_CHICK

34	204.5	32.3	375	1	GDF8_HUMAN
35	204.5	32.3	375	1	GDF8_MELGA
36	204.5	32.3	375	1	GDF8_PIG
37	204.5	32.3	376	1	GDF8_MOUSE
38	204.5	32.3	376	1	GDF8_RAT
39	204	32.2	355	1	DVRI_BRARE
40	204	32.2	405	1	IHBA_SHEEP
41	203	32.0	425	1	GDFB_MOUSE
42	203	32.0	407	1	GDFB_HUMAN
43	201.5	31.8	375	1	GDFB_BOVIN
44	200	31.5	424	1	IHBA_MOUSE
45	200	31.5	424	1	IHBA_PIG
46	200	31.5	424	1	IHBA_RAT
47	200	31.5	425	1	IHBA_BOVIN
48	200	31.5	426	1	IHBA_HUMAN
49	195.5	30.8	436	1	60A_DROVI
50	195	30.8	455	1	60A_DROME
51	191.5	30.2	391	1	IHBB_CHICK
52	191	30.1	424	1	IHBA_CHICK
53	190	30.0	360	1	DVRI_XENLA
54	189	29.8	431	1	BMP7_HUMAN
55	187	29.5	426	1	BMP7_XENLA
56	186.5	29.4	349	1	IHBB_PIG
57	186.5	29.4	407	1	IHBB_HUMAN
58	186.5	29.4	408	1	IHBB_BOVIN
59	184.5	29.1	255	1	IHBB_MOUSE
60	184.5	29.1	345	1	GDFB_RAT
61	183	28.9	430	1	BMP7_MOUSE
62	182.5	28.8	393	1	BMP2_RAT
63	182.5	28.8	394	1	BMP2_MOUSE
64	182.5	28.8	395	1	BMP2_RABIT
65	182.5	28.8	396	1	BMP2_DAMDA
66	182.5	28.8	396	1	BMP2_HUMAN
67	182.5	28.8	398	1	BMPA_XENLA
68	182.5	28.8	398	1	BMPB_XENLA
69	182	28.7	495	1	GDF5_MOUSE
70	182	28.7	501	1	GDF5_HUMAN
71	181	28.5	461	1	DVRI_STRPU
72	180	28.4	352	1	IHBC_HUMAN
73	180	28.4	352	1	IHBC_MOUSE
74	180	28.4	621	1	DECA_DROPS
75	179	28.2	125	1	GDF6_MOUSE
76	179	28.2	452	1	BMP5_MOUSE
77	179	28.2	454	1	BMP5_HUMAN
78	176	27.8	151	1	GDF7_MOUSE
79	175	27.6	436	1	GDF6_BOVIN
80	174.5	27.5	424	1	BM10_HUMAN
81	174	27.4	372	1	DECA_TRICA
82	174	27.4	372	1	GDF1_HUMAN
83	172	27.1	588	1	DECA_DROME
84	172	27.1	593	1	DECA_DROSI
85	171.5	27.1	353	1	BMP2_CHICK
86	171	27.0	399	1	BM8B_MOUSE
87	170.5	26.9	405	1	BMP4_CHICK
88	170.5	26.9	408	1	BMP4_DAMDA
89	170.5	26.9	408	1	BMP4_HUMAN
90	170.5	26.9	408	1	BMP4_MOUSE
91	170.5	26.9	408	1	BMP4_RAT
92	169.5	26.7	409	1	BMP4_RABIT
93	169	26.7	383	1	UNIV_STRPU
94	168.5	26.6	420	1	BM10_MOUSE
95	168	26.5	399	1	BM8A_MOUSE
96	168	26.5	402	1	BMP8_HUMAN
97	165.5	26.1	401	1	BMP4_XENLA
98	164.5	25.9	357	1	GDF1_MOUSE
99	162.5	25.6	366	1	GDF3_MOUSE
100	160	25.2	364	1	GDF3_HUMAN

ALIGNMENTS

RESULT 1

```

TGFB3_MOUSE
ID  TGFB3_MOUSE  STANDARD;          PRT;    410 AA.
AC  P17125;
DT  01-AUG-1990 (Rel. 15, Created)
DT  01-AUG-1990 (Rel. 15, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
GN  TGFB3.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  MEDLINE=90190650; PubMed=2628730;
RX  Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT  "Complementary DNA cloning of the murine transforming growth
RT  factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT  of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT  adult tissues.";
RL  Mol. Endocrinol. 3:1926-1934(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9100714; PubMed=2206556;
RX  Denhez F., Lafyatis R., Kondaiiah P., Roberts A.B., Sporn M.B.;
RT  "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT  mTGF-beta 3.";
RL  Growth Factors 3:139-146(1990).
CC  -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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CC  -----
DR  EMBL; M32745; AAA40422.1; -.
DR  PIR; A41397; A41397.
DR  PIR; A61039; A61039.
DR  HSP; P10600; ITGK.
DR  MGD; MGI:98727; Tgfb3.
DR  InterPro; IPR001111; -.
DR  InterPro; IPR001839; -.
DR  InterPro; IPR002400; -.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGF-beta; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Mitogen; Glycoprotein; Signal.
FT  SIGNAL 1 23
FT  PROPEP 24 298
FT  CHAIN 299 410
FT  DISULFID 305 314
FT  DISULFID 313 376
FT  DISULFID 342 407
FT  DISULFID 346 409
FT  DISULFID 375 375
FT  CARBOHYD 72 72
FT  CARBOHYD 133 133
FT  CARBOHYD 140 140
FT  SITE 259 261
SQ  SEQUENCE 410 AA; 46884 MW; 250F7048CA432BD6 CRC64;

Query Match 99.8%; Score 633; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPKGYANFCSGPCPYLRSADTTTST 60
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Db 299 ALDITNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPKGYANFCSGPCPYLRSADTTTST 358
QY 61 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 359 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 410
  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
TGFB3_MOUSE
ID  TGFB3_MOUSE  STANDARD;          PRT;    412 AA.
AC  P10600;
DT  01-JUL-1989 (Rel. 11, Created)
DT  01-JUL-1989 (Rel. 11, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
GN  TGFB3.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=88263019; PubMed=3164476;
RX  ten Dijke P., Hansen P., Iwata K., Pieler C., Foulkes J.G.;
RT  "Identification of another member of the transforming growth factor
RT  type beta gene family.";
RL  Proc. Natl. Acad. Sci. U.S.A. 85:4715-4719(1988).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Placenta;
RX  MEDLINE=89091120; PubMed=3208746;
RX  Derynck R., Lindquist P.B., Lee A., Wen D., Tamm J., Graycar J.L.,
RT  Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L., Chen E.Y.;
RT  "A new type of transforming growth factor-beta, TGF-beta 3.";
RL  EMBO J. 7:3737-3743(1988).
RN  [3]
RP  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 301-412.
RX  MEDLINE=96416253; PubMed=8819159;
RX  Mittl P.R., Priestle J.P., Cox D.A., McMaster G., Cerletti N.,
RA  Grutter M.G.;
RT  "The crystal structure of TGF-beta 3 and comparison to TGF-beta 2:
RT  implications for receptor binding.";
RL  Protein Sci. 5:1261-1271(1996).
CC  -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; J03241; AAA61161.1; -.
DR  EMBL; X14149; CAA32362.1; -.
DR  EMBL; X14885; CAA33024.1; ALT_INIT.
DR  EMBL; X14886; CAA33024.1; JOINED.
DR  EMBL; X14887; CAA33024.1; JOINED.
DR  EMBL; X14888; CAA33024.1; JOINED.
DR  EMBL; X14889; CAA33024.1; JOINED.
DR  EMBL; X14890; CAA33024.1; JOINED.
DR  EMBL; X14891; CAA33024.1; JOINED.
DR  PIR; S01824; S01824.
DR  PIR; A36169; A36169.
DR  PDB; ITGJ; 1J-JAN-97.
DR  PDB; ITGK; 12-MAR-97.
DR  MIM; 190230; -.
DR  InterPro; IPR001111; -.
DR  InterPro; IPR001839; -.
DR  InterPro; IPR002400; -.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGF-beta; 1.

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DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1;
KW Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 300 TRANSFORMING GROWTH FACTOR BETA 3.
FT CHAIN 301 412
FT DISULFID 307 316
FT DISULFID 315 378
FT DISULFID 344 409
FT DISULFID 348 411
FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 261 263 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 412 AA; 47328 MW; 3CAD3548D3AE178 CRC64;

Query Match 99.8%; Score 633; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 60
|||||
DB 301 ALDNTNCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 360
|||||

QY 61 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|||||
DB 361 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412
|||||

RESULT 3
TGF3_RAT
ID TGF3_RAT STANDARD; PRT; 412 AA.
AC Q07258.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
GN TGF3 OR TGF-B3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Lung;
RX MEDLINE=95155340; PubMed=7852342;
RA Wang J., Kuliszewski M., Yee W., Sedlackova L., Xu J., Tseu I.,
RA Post M.;
RT "Cloning and expression of glucocorticoid-induced genes in fetal rat
RT lung fibroblasts. Transforming growth factor-beta 3."
RL J. Biol. Chem. 270:2722-2728(1995).
RN [2]
RP SEQUENCE OF 159-213 FROM N.A.
RX MEDLINE=93286190; PubMed=8509457;
RA McKinnon R.D., Piras G., Ida J., Dubois-Dalq M.;
RT "A role for TGF-beta in oligodendrocyte differentiation."
RL J. Cell Biol. 121:1397-1407(1993).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: U03491; AAA67915.1; -.
DR EMBL: X71903; CAA50722.1; -.
DR PIR: B40699; B40699.
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DR PIR: S36042; S36042.
DR HSSP: P10600; ITGK.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR InterPro: IPR002400; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 300 POTENTIAL.
FT CHAIN 301 412 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 315 378 BY SIMILARITY.
FT DISULFID 344 409 BY SIMILARITY.
FT DISULFID 348 411 BY SIMILARITY.
FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 261 263 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 412 AA; 47116 MW; 24FD7D899090AA9D CRC64;

Query Match 99.4%; Score 630; DB 1; Length 412;
Best Local Similarity 99.1%; Pred. No. 3.3e-60;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 60
|||||
DB 301 ALDNTNCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCGPGCYLRSADTTHST 360
|||||

QY 61 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|||||
DB 361 VLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412
|||||

RESULT 4
TGF3_CHICK
ID TGF3_CHICK STANDARD; PRT; 412 AA.
AC P16047;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
GN TGF3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89096966; PubMed=3211158;
RA Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
RT "Complementary deoxyribonucleic acid cloning of a novel transforming
RT growth factor-2 messenger ribonucleic acid from chick embryo
RT chondrocytes."
RL J. Mol. Endocrinol. 2:747-755(1988).
RN [2]
RP SEQUENCE OF 1-117 FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Blood;
RX MEDLINE=92134496; PubMed=1840616;
RA Burt D.W., Dey B.R., Paton I.R.;
RT "Comparative analysis of human and chicken transforming growth
RT factor-beta 2 and -beta 3 promoters."
RL J. Mol. Endocrinol. 7:175-183(1991).
RN [3]
RP SEQUENCE OF 1-117 FROM N.A.
RX MEDLINE=93024487; PubMed=1406706;
RA Jakowlew S.B., Lechleider R., Geisler A.G., Kim S.J.,
RA Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
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RT Identification and characterization of the chicken transforming
RT growth factor-beta 3 promoter."
RL Mol. Endocrinol. 6:1285-1298(1992).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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DR EMBL; M31154; AAA49089.1; -
DR EMBL; X58127; CAA41128.1; -
DR EMBL; X60055; CAA42653.1; -
DR EMBL; S46000; AAB23575.1; -
DR PIR; A34939; A34939.
DR HSSP; P10600; ITGK.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 300
FT CHAIN 301 412 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 307 316 BY SIMILARITY.
FT DISULFID 315 378 BY SIMILARITY.
FT DISULFID 344 409 BY SIMILARITY.
FT DISULFID 348 411 BY SIMILARITY.
FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 261 263 CELL ATTACHMENT SITE (POTENTIAL).
FT SEQUENCE 412 AA; 47184 MW; E15266B79D3F30F7 CRC64;

Query Match 99.2%; Score 629; DB 1; Length 412;
Best Local Similarity 99.1%; Pred. No. 4.2e-60;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGPYLRSADTTHST 60
Db 301 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGPYLRSADTTHST 360

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 361 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 5
TGF3_PIG 5
ID TGF3_PIG STANDARD; PRT; 409 AA.
AC P15203;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
GN TGF3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID-9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE-89091120; PubMed-3208746;

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RA Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,
RA Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
RA Chen E.Y.;
RT "A new type of transforming growth factor-beta, TGF-beta 3."
RL EMBL J. 7:3737-3743(1988).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
DR EMBL; X14150; CAA32363.1; -
DR PIR; S01825; S01825.
DR HSSP; P10600; ITGK.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 18
FT PROPEP 19 297
FT CHAIN 298 409 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 304 313 BY SIMILARITY.
FT DISULFID 312 375 BY SIMILARITY.
FT DISULFID 341 406 BY SIMILARITY.
FT DISULFID 345 408 BY SIMILARITY.
FT DISULFID 374 374 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).
FT SEQUENCE 409 AA; 46814 MW; B4900235B5CC955E CRC64;

Query Match 97.9%; Score 621; DB 1; Length 409;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGPYLRSADTTHST 60
Db 298 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGPYLRSADTTHSS 357

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 358 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 409

RESULT 6
TGF2_CHICK 6
ID TGF2_CHICK STANDARD; PRT; 412 AA.
AC P30371;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
GN TGF2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID-9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-Blood;
RX MEDLINE-92075163; PubMed-1683775;

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RA Burt D.W., Paton I.R.;
RT "Molecular cloning and primary structure of the chicken transforming
RT growth factor-beta 2 gene.";
RL Cell Biol. 10:723-734(1991).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X58071; CAA41101.1; -.
DR EMBL: X59082; CAA41101.1; JOINED.
DR EMBL: X59081; CAA41101.1; JOINED.
DR EMBL: X59080; CAA41101.1; JOINED.
DR PIR: A39489; A39489.
DR HSP: P08112; 1TFG.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 300
FT CHAIN 301 412
FT DISULFID 307 316
FT DISULFID 315 378
FT DISULFID 344 409
FT DISULFID 348 411
FT DISULFID 377 377
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 240 240
SQ SEQUENCE 412 AA; 47606 MW; 93E759BF1BD958DC CRC64;

Query Match 85.0%; Score 539; DB 1; Length 412;
Best Local Similarity 79.5%; Pred. No. 1.9e-50;
Matches 89; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLNCCVRLPYIDFRDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
DB 301 ALDAAACYFRNVQDNCCLRPYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 360

QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 361 VLSLNTINPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 7
TGFB2_BOVIN
ID TGFB2_BOVIN STANDARD; PRT: 112 AA.
AC P21214;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (MILK GROWTH FACTOR)
DE (MGF).
GN TGFB2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
```

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RN RP
SEQUENCE.
RC TISSUE=Milk;
RA MEDLINE=92189724; PubMed=1799413;
RX Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.;
RT "Separation, purification, and sequence identification of TGF-beta 1
RT and TGF-beta 2 from bovine milk.";
RL J. Protein Chem. 10:565-575(1991).
[2]
RN RP
SEQUENCE OF 1-30.
RC TISSUE=Bone;
RA MEDLINE=87137406; PubMed=3469199;
RX Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.Y., Bentz H.,
RA Graycar J.;
RT "Cartilage-inducing factor-B is a unique protein structurally and
RT functionally related to transforming growth factor-beta.";
RL J. Biol. Chem. 262:1946-1949(1987).
[3]
RN RP
SEQUENCE OF 1-19.
RC TISSUE=Milk;
RA MEDLINE=91224126; PubMed=2026157;
RX Cox D.A., David A., Buerk R.R.;
RT "Isolation and characterization of milk growth factor, a
RT transforming-growth-factor-beta 2-related polypeptide, from bovine
RT milk.";
RL Eur. J. Biochem. 197:353-358(1991).
[4]
RN RP
SUBUNITS.
RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
RL J. Biol. Chem. 267:2325-2328(1992).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
CC AND OF TGF-BETA 2/3 HAVE BEEN FOUND IN BONE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR PIR: S15389; S15389.
DR HSP: P08112; 1TFG.
DR InterPro: IPR001839; -.
DR InterPro: IPR002400; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Milk.
FT DISULFID 7 16
FT DISULFID 15 78
FT DISULFID 44 109
FT DISULFID 48 111
FT DISULFID 77 77
SQ SEQUENCE 112 AA; 12719 MW; 5142C7432C4EBC1C CRC64;

Query Match 84.4%; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.3e-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLNCCVRLPYIDFRDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
DB 1 ALDAAACYFRNVQDNCCLRPYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 60

QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 61 VLSLNTINPEASAPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112

RESULT 8
TGFB2_HUMAN
ID TGFB2_HUMAN STANDARD; PRT: 414 AA.
AC P08112; Q15581;
DT 01-AUG-1988 (Rel. 08, Created)
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QY      1 ALDRTNYCFRNLEENCCVRPLYIDFRQDLGWKWHIEPKGYANFCSGPCPYLRSADTTHST 60
    ||| |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      303 ALDAAYCFRNVQDCCLRLPIDFKRIDLGWKWIEHPKGYNANFCAGACPYLWSSDTOHTK 362
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 VLGLNTLNPEASAPCCVPDLEPLTLTYVVGTRTPKVEQLSNMVKSKCS 112
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      363 VLSLYNTINPEASAPCCVSQDLEPLTLTYIGNTPKIEQLSNMIVKSKCS 414
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
TFG2_XENLA
ID TGF2_XENLA STANDARD; PRT; 413 AA.
AC P17247;
DT 01-AUG-1990 (Rel. 15, Created)
DD 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DEF TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
GN TGFβ2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20245678; PubMed=2336403;
RX Rebert M.L., Bhatia-Dey N., Dawid I.B.;
RA "The sequence of TGF-beta 2 from Xenopus laevis.";
RL Nucleic Acids Res. 18:2185-2185(1990).
RC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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-----
DR EMBL; X51817; CAA36116.1; -.
DR EMBL; X51817; CAA36117.1; ALT_INIT.
DR PIR; S09510; S09510.
DR HSSP; P08112; ITFG.
DR InterPro; IPRO01111; -.
DR InterPro; IPRO01839; -.
DR InterPro; IPRO02400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFβ-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Mitogen; Glycoprotein; Growth factor.
FT SIGNAL 1
FT PROPEP 19
FT CHAIN 20 301
FT CHAIN 302 413
FT DISULFID 308 317
FT DISULFID 316 379
FT DISULFID 345 410
FT DISULFID 349 412
FT DISULFID 378 378
FT CARBOHYD 72 72
FT CARBOHYD 140 140
FT CARBOHYD 241 241
SQ SEQUENCE 413 AA; 47639 MW; 6127715B38734010 CRC64;
TRANSFORMING GROWTH FACTOR BETA 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC... ) (POTENTIAL).
N-LINKED (GLCNAC... ) (POTENTIAL).
N-LINKED (GLCNAC... ) (POTENTIAL).
SEQUENCE 413 AA; 47639 MW; 6127715B38734010 CRC64;

Query Match 81.4%; Score 516; DB 1; Length 413;
Best Local Similarity 76.8%; Pred. No. 5.4e-48;
Matches 86; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY      1 ALDRTNYCFRNLEENCCVRPLYIDFRQDLGWKWHIEPKGYANFCSGPCPYLRSADTTHST 60

```



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DR InterPro: IPR002400; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
FT SEQUENCE 390 AA; 44310 MW; 4381A51B711D689E CRC64;

Query Match 79.3%; Score 503; DB 1; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.3e-46;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRDGLGWKWHPEKGYANFCGPPYLSADTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 279 ALDNTNCFSTKNCVRLPYIDFRDGLGWKWHPEKGYANFCGPPYLSADTHST 338
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :

QY 61 VLGLYNTLNPASASCCVPPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 339 VLALYQHNPGASASCCVPPQALEPLIVYVGRTPKVEQLSNMVKCKCS 390

RESULT 13
TGFL_RAT
ID TGFL_RAT STANDARD; PRT; 390 AA.
AC P17246;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
GN TGFBI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Heart;
RX MEDLINE=90272425; PubMed=2349108;
RA Qian S.W., Kondalath P., Roberts A.B., Sporn M.B.;
RT "cDNA cloning by PCR of rat transforming growth factor beta-1.";
RL Nucleic Acids Res. 18:3059-3053(1990).
CC -|- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -|- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -|- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X52498; CAA36741.1; -.
DR PIR: S10219; S10219.

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DR HSSP: P01137; lKLC.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR InterPro: IPR002400; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
FT SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRC64;

Query Match 79.3%; Score 503; DB 1; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.3e-46;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRDGLGWKWHPEKGYANFCGPPYLSADTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 279 ALDNTNCFSTKNCVRLPYIDFRDGLGWKWHPEKGYANFCGPPYLSADTHST 338
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :

QY 61 VLGLYNTLNPASASCCVPPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 339 VLALYQHNPGASASCCVPPQALEPLIVYVGRTPKVEQLSNMVKCKCS 390

RESULT 14
TGFL_BOVIN
ID TGFL_BOVIN STANDARD; PRT; 315 AA.
AC P18341;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (FRAGMENT).
GN TGFBI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91042552; PubMed=3153459;
RA van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.;
RT "Complementary deoxyribonucleic acid cloning of bovine transforming
RT growth factor-beta 1.";
RL Mol. Endocrinol. 1:693-698(1987).
RN [2]
RP SUBUNITS.
RC TISSUE=Bone;
RX MEDLINE=92119307; PubMed=173936;
RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
RL J. Biol. Chem. 267:2325-2328(1992).
CC -|- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -----

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FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.
FT DISULFID 326 389 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT DISULFID 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
FT CONFLICT 6 7 LR -> PG (IN REF. 3).
FT CONFLICT 114 114 L -> V (IN REF. 3).
FT CONFLICT 180 180 R -> G (IN REF. 3).
FT CONFLICT 237 237 N -> NA (IN REF. 3).
SQ SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;

Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.6e-46;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKWHEPKGYANFCSPGCPYLRSDTTHST 60
||||| : ||||| ||||| ||||| ||||| ||||| ||||| : ||| :
DB 279 ALDTNYCFSTTEKNCVRLYIDFRKDLGKWKWHEPKGYHANFCLGCPYIWSLDFTQYSK 338

QY 61 VLGLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
||||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||
DB 339 VLALYNQHNPGASAPCCVQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 19
TGFI_SHEEP
ID TGFI_SHEEP STANDARD; PRT; 390 AA.
AC P50414;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
GN TGFB1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95121932; PubMed=7821809;
RA Woodall C.J., McLaren L.J., Watt N.J.;
RT "Sequence and chromosomal localisation of the gene encoding ovine
latent transforming growth factor-beta 1.";
RL Gene 150:371-373(1994).
RN [2]
RP SEQUENCE OF 281-390 FROM N.A.
RX STRAIN=MERINO; TISSUE=Skin;
RC MEDLINE=95268698; PubMed=7749621;
RA Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RT "Growth factor expression in skin during wool follicle development.";
RL Comp. Biochem. Physiol. 110B:697-705(1995).
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC EMBL; X76916; CAA54242.1; -.
DR EMBL; L36038; AAA31526.1; -.
DR HSSP; P01137; IKLC.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 278 POTENTIAL.
FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.
FT DISULFID 326 389 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 390 AA; 44291 MW; 1C247299484D0E57 CRC64;

Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.6e-46;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKWHEPKGYANFCSPGCPYLRSDTTHST 60
||||| : ||||| ||||| ||||| ||||| ||||| ||||| : ||| :
DB 279 ALDTNYCFSTTEKNCVRLYIDFRKDLGKWKWHEPKGYHANFCLGCPYIWSLDFTQYSK 338

QY 61 VLGLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
||||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||
DB 339 VLALYNQHNPGASAPCCVQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 20
TGFI_HORSE
ID TGFI_HORSE STANDARD; PRT; 390 AA.
AC O19011;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
GN TGFB1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=98185507; PubMed=9524819;
RA Pena-Goncalves M.N., Onions D.E., Nicolson L.;
RT "Cloning and sequencing of equine transforming growth factor-beta 1
(TGF-beta-1) cDNA.";
RL DNA Seq. 7:375-378(1997).
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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Matches 77; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
QY 6 YCFRNLNCCVRLPYIDFRODLGKWKWHEPKGYANFCSPYLRSDTTHSTVGLGLY 65
Db 276 YCFGNNGPNCVKPLIYINFRDLGKWKWHEPKGYEANTGLGNCPYIWSMDTQYSKVLISY 335

QY 66 NTLNPEASASCCVQDLEPLTILYVGRTPKVQSLNNMVKSKCS 112
Db 336 NONNPGASISCCVQDLEPLTILYVGRTPKVQSLNNMVKSKCS 382

RESULT 24
ID GDF8_BRARE STANDARD; PRT; 374 AA.
AC 042222;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; AF019626; AAB86693.1; -.
CC ZFIN; ZDB-GENE-990415-165; mstn.
CC InterPro; IPR001111; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 22 POTENTIAL.
CC PROPEP 23 265 POTENTIAL.
CC CHAIN 266 374 GROWTH/DIFFERENTIATION FACTOR 8.
CC DISULFID 280 339 BY SIMILARITY.
CC DISULFID 308 371 BY SIMILARITY.
CC DISULFID 312 373 BY SIMILARITY.
CC DISULFID 338 372 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 374 AA; 42060 MW; 6302BC6C86562576 CRC64;

Query Match 34.2%; Score 217; DB 1; Length 374;
Best Local Similarity 40.0%; Pred. No. 5.2e-16;
Matches 44; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 7 CFRNLNCCVRLPYIDFRODLGKWKWHEPKGYANFCSPYLRSDTTHSTVGLG 63
Db 271 CDENSESRRCRYPLTVDF-EDFGWDWIAPKRYKANYCSECDYMLQKYPHPTH----- 324

Matches 77; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
QY 6 YCFRNLNCCVRLPYIDFRODLGKWKWHEPKGYANFCSPYLRSDTTHSTVGLGLY 65
Db 276 YCFGNNGPNCVKPLIYINFRDLGKWKWHEPKGYEANTGLGNCPYIWSMDTQYSKVLISY 335

QY 66 NTLNPEASASCCVQDLEPLTILYVGRTPKVQSLNNMVKSKCS 112
Db 336 NONNPGASISCCVQDLEPLTILYVGRTPKVQSLNNMVKSKCS 382

RESULT 24
ID GDF8_BRARE STANDARD; PRT; 374 AA.
AC 042222;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL; AF019626; AAB86693.1; -.
CC ZFIN; ZDB-GENE-990415-165; mstn.
CC InterPro; IPR001111; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 22 POTENTIAL.
CC PROPEP 23 265 POTENTIAL.
CC CHAIN 266 374 GROWTH/DIFFERENTIATION FACTOR 8.
CC DISULFID 280 339 BY SIMILARITY.
CC DISULFID 308 371 BY SIMILARITY.
CC DISULFID 312 373 BY SIMILARITY.
CC DISULFID 338 372 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 374 AA; 42060 MW; 6302BC6C86562576 CRC64;

Query Match 34.2%; Score 217; DB 1; Length 374;
Best Local Similarity 40.0%; Pred. No. 5.2e-16;
Matches 44; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

QY 7 CFRNLNCCVRLPYIDFRODLGKWKWHEPKGYANFCSPYLRSDTTHSTVGLG 63
Db 271 CDENSESRRCRYPLTVDF-EDFGWDWIAPKRYKANYCSECDYMLQKYPHPTH----- 324

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QY 64 LYNTLNPEASASCCVQDLEPLTILYVGRTPKV-EQLSNMVVSKSKCS 112
Db 325 LVNKASPRGTAGCCTPTKMSPINMLYFNGKEQIIYKIPSMVVDRCGS 374

RESULT 25
ID GDF8_PAPHA STANDARD; PRT; 375 AA.
AC 018828;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; AF019619; AAB86686.1; -.
CC InterPro; IPR001111; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 23 POTENTIAL.
CC PROPEP 24 266 POTENTIAL.
CC CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
CC DISULFID 281 340 BY SIMILARITY.
CC DISULFID 309 372 BY SIMILARITY.
CC DISULFID 313 374 BY SIMILARITY.
CC DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 375 AA; 42688 MW; 7B49B90ACAB926EA CRC64;

Query Match 32.9%; Score 208.5; DB 1; Length 375;
Best Local Similarity 40.4%; Pred. No. 4.3e-15;
Matches 42; Conservative 15; Mismatches 38; Indels 9; Gaps 4;

QY 12 EENCVCVRPLYIDFRODLGKWKWHEPKGYANFCSPYLRSDTTHSTVGLYNTLN 69
Db 278 ESRCCRYPLTVDF-EALGWDWIAPKRYKANYCSECEVFLOKYPHPTH-----LVHQAN 331

QY 70 PEASASCCVQDLEPLTILYVGRTPKV-EQLSNMVVSKSKCS 112
Db 332 PRCSAGCCTPTKMSPINMLYFNGKEQIIYKIPAMVVDRCGS 375

RESULT 26
ID IHBE_MOUSE STANDARD; PRT; 350 AA.

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[illegible]

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AC P55102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96031670; PubMed=7548399;
RA Yoshida S., Takanouchi K., Hasegawa T., Ikeda A., Suzuki M.,
RA Chang K., Matsuyama S., Nishihara M., Takahashi M.;
RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
RT subunit.";
RL J. Vet. Med. Sci. 57:469-473(1995).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; D50326; BRA08862.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINBA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 310 INHIBIN BETA A CHAIN.
FT CHAIN 311 426 BY SIMILARITY.
FT DISULFID 314 322 BY SIMILARITY.
FT DISULFID 321 391 BY SIMILARITY.
FT DISULFID 350 423 BY SIMILARITY.
FT DISULFID 354 425 BY SIMILARITY.
FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 426 AA; 47709 MW; E481060B8368A77D CRC64;

Query Match 32.5%; Score 206; DB 1; Length 426;
Best Local Similarity 38.3%; Pred. No. 9e-15;
Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRLYIDFRODLGK-WVHEPKGYANFCGPGP-----YLRADTTHSTVLGLYNTL 68
Db 321 CKKQFFVSKF-DIGWNOWIITAPSHYCEGEGSHIAGTSGSLSPHSTVINQYRLR 379
Qy 69 --NPEASAPCCVPQDLPTLLTYL-VGRTPKVEQLSNMVKSKCS 112
Db 380 GHNPFANKSCCVPTKLRLPMSMLYDDGQNTIKKDIQNIVVECGCS 426
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RESULT 31
BMP6_HUMAN STANDARD; PRT; 513 AA.
ID BMP6_HUMAN
AC P22004;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6).
GN BMP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=91088608; PubMed=2263636;
RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA Wang E.A., Wozney J.M.;
RT "Identification of transforming growth factor beta family members
RT present in bone-inductive protein purified from bovine bone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; M60315; AAA36737.1; -.
DR PIR; B39263; B39263.
DR HSSP; P18075; IBMP.
DR MIM; 112266; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 381 POTENTIAL.
FT CHAIN 382 513 BONE MORPHOGENETIC PROTEIN 6.
FT DISULFID 412 478 BY SIMILARITY.
FT DISULFID 441 510 BY SIMILARITY.
FT DISULFID 445 512 BY SIMILARITY.
FT DISULFID 477 477 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 241 241 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 513 AA; 57225 MW; 3F19155B36049278 CRC64;

Query Match 32.5%; Score 206; DB 1; Length 513;
Best Local Similarity 37.2%; Pred. No. 1.e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFERNLENCVRLPLYIDFRODLGK-WVHEPKGYANFCGPGPYLRSD--TTHS 59
Db 401 SDINSELSTACKRHLYVSF-QDLGWQDWIITAPKGYAANYDCGECGCFPLNAHNATNHA 459
Qy 60 TVLGLYNTLNPEASAPCCVPQDLPTLLTYL-VGRTPKV-EQLSNMVKSKC 111
Db 460 IVOTLVHLMNPEVVPKCCAPTKLNAISLVLYFDNSNVILKKYRNMVVRGCC 512
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RESULT 32
BMP6_MOUSE
ID BMP6_MOUSE STANDARD; PRT; 510 AA.
AC P20722;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6) (VG-1-RELATED PROTEIN)
DE (VGR-1).
GN BMP6 OR BMP-6 OR VGR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94375533; PubMed=8089189;
RA Gitelman S.E., Kobrin M.S., Ye J.Q., Lopez A.R., Lee A., Derynck R.;
RT "Recombinant Vgr-1/BMP-6-expressing tumors induce fibrosis and
RT endochondral bone formation in vivo.";
RL J. Cell Biol. 126:1595-1609(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97222480; PubMed=9069123;
RA Gitelman S.E., Kobrin M., Lee A., Fet V., Lyons K., Hogan B.L.M.,
RA Derynck R.;
RT "Structure and sequence of the mouse Bmp6 gene.";
RL Mamm. Genome 8:212-214(1997).
RN [3]
RN SEQUENCE OF 73-510 FROM N.A.
RX MEDLINE=89282810; PubMed=2734307;
RA Lyons K., Graycar J.L., Lee A., Hashmi S., Lindquist P.B., Chen E.Y.,
RA Hogan B.L.M., Derynck R.;
RT "Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the
RT transforming growth factor beta gene superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4554-4558(1989).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS. LOW LEVELS SEEN IN
CC THE KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X80992; CAA56917.1;
CC EMBL; U73520; AAB18235.1;
CC EMBL; U73515; AAB18235.1; JOINED.
CC EMBL; U73516; AAB18235.1; JOINED.
CC EMBL; U73517; AAB18235.1; JOINED.
CC EMBL; U73518; AAB18235.1; JOINED.
CC EMBL; U73519; AAB18235.1; JOINED.
CC EMBL; J04566; AAA40548.1;
CC PIR; A33925; A33925.
CC HSSP; P18075; IBMP.
CC MGD; MGI:88182; Bmp6.
CC InterPro; IPR001111;
CC InterPro; IPR001839;
CC InterPro; IPR002400;
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00250; TGF-BETA_1; 1.
CC SIGNAL; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 378 POTENTIAL.

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FT CHAIN 379 510 BONE MORPHOGENETIC PROTEIN 6.
FT DISULFID 409 475 BY SIMILARITY.
FT DISULFID 438 507 BY SIMILARITY.
FT DISULFID 442 509 BY SIMILARITY.
FT CARBOHYD 474 474 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 73 73 K -> M (IN REF. 3).
FT CONFLICT 75 75 E -> K (IN REF. 3).
FT CONFLICT 86 86 L -> P (IN REF. 3).
SQ SEQUENCE 510 AA; 56431 MW; 910B68531289FCD2 CRC64;

Query Match 32.3%; Score 205; DB 1; Length 510;
Best Local Similarity 37.2%; Pred. No. 1.4e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

QY 4 TNYCFRNLENCVVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPYLRSAD---TTHS 59
Db 398 SDYNGSELKTACKKHELYVSF-QDLGWQDWITAPKGYANYCDGECSPPLNAHMHATNHA 456

QY 60 TVLGLYNTLNPEASAPCCVPQDPLETLILYVGRTPKV-EQLSNMVKSKC 111
Db 457 IVQTLVHLMNPEYVPCPCAPTCLNAISLVLYFDNSNVILKRYNMVVRACGC 509

RESULT 33
ID GDF8_CHICK STANDARD; PRT; 375 AA.
AC O42220;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update).
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF019621; AAB86688.1;
CC InterPro; IPR001111;
CC InterPro; IPR001839;
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF-BETA_1; 1.
CC SIGNAL; Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.

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FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 374 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42707 MW; DA732DB9426E4D4F CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLIYDFRODLGKWKVHEPKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTH-----LVHQAN 331
QY 70 PEASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCS 112
DB 332 PRGSAGCCTPTKMSPINLDFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 34
GDF8_HUMAN
ID GDF8_HUMAN STANDARD; PRT; 375 AA.
AC O14793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; AF019627; AAB86694.1; -.
DR MIM; 601788; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 374
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLIYDFRODLGKWKVHEPKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTH-----LVHQAN 331
QY 70 PEASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCS 112
DB 332 PRGSAGCCTPTKMSPINLDFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 34
GDF8_HUMAN
ID GDF8_HUMAN STANDARD; PRT; 375 AA.
AC O14793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; AF019627; AAB86694.1; -.
DR MIM; 601788; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 374
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

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Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLIYDFRODLGKWKVHEPKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTH-----LVHQAN 331
QY 70 PEASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCS 112
DB 332 PRGSAGCCTPTKMSPINLDFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 35
GDF8_MELGA
ID GDF8_MELGA STANDARD; PRT; 375 AA.
AC O42221;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; AF019625; AAB86692.1; ALT_INIT.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42784 MW; D2AEAB732AE84E77 CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLIYDFRODLGKWKVHEPKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTH-----LVHQAN 331
QY 70 PEASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVKSKCS 112

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Query Match	32.3%	Score 204.5	DB 1	Length 375
Best Local Similarity	39.4%	Pred. No. 1.1e-14		
Matches	41	Conservative	15	Mismatches 39; Indels 9; Gaps 4

QY	12	EENCCVRLYIDFRQDLGKWKVHEPKGYANFCGPGCP--YLSRADTHTHTVGLGYTLN 69
DB	278	ESRCCRYPLTVDF-EAFGWDIIAPKRYKANYGSGECEFVLFQKYPHTH-----LVHQAN 331
QY	70	PEASAPCCVPQDLEPLTYLYVGRTPKV-EQLSNMVMVVKSCKS 112
DB	332	PRSGAGCCCTPTKSPINMLYFNGKEQIIYKIPAMVVDRCGS 375

RESULT 37				
GDF8_MOUSE				
ID	GDF8_MOUSE	STANDARD;	PRT;	376 AA.
AC	O08689;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).			
GN	GDF8 OR MSTN.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CD-1; TISSUE=Skeletal muscle;			
RX	MEDLINE=97284412; PubMed=9139826;			
RA	McPherron A.C., Lawler A.M., Lee S.-J.;			
RT	"Regulation of skeletal muscle mass in mice by a new TGF-beta superfamily member."			
RL	Nature 387:83-90(1997).			
CC	-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.			
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.			
CC	-!- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT, DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION CONTINUES IN ADULTHOOD.			
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			

EMBL; U04005; AAC53167.1; -	
HSSP; P18075; IBMP.	
MGI; 95691; Mstn.	
InterPro; IPR001111; -	
InterPro; IPR001839; -	
Pfam; PF00019; TGF-beta; 1.	
Pfam; PF00688; TGF-beta; 1.	
PROSITE; PS00250; TGF_BETA_1; 1.	
Growth factor; Cytokine; Glycoprotein; Signal.	
SIGNAL	1 24 POTENTIAL.
PROPEP	25 267 POTENTIAL.
CHAIN	268 376 GROWTH/DIFFERENTIATION FACTOR 8.
DISULFID	282 341 BY SIMILARITY.
DISULFID	310 373 BY SIMILARITY.
DISULFID	314 375 BY SIMILARITY.
DISULFID	340 340 INTERCHAIN (BY SIMILARITY).
CARBOHYD	72 72 N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE	376 AA; 42921 MW; 3E19814DDG2C08BE CRC64;

EMBL; AF019623; AAB86690.1; -	
EMBL; AF188635; AAF02770.1; -	
EMBL; AF188636; AAF02771.1; -	
EMBL; AF188637; AAF02772.1; -	
EMBL; AF188638; AAF02773.1; -	
EMBL; AF033855; AAC08035.1; -	
EMBL; AF093798; AAC62489.1; -	
InterPro; IPR001111; -	
InterPro; IPR001839; -	
Pfam; PF00019; TGF-beta; 1.	
Pfam; PF00688; TGF-beta; 1.	
PROSITE; PS00250; TGF_BETA_1; 1.	
Growth factor; Cytokine; Glycoprotein; Signal.	
SIGNAL	1 23 POTENTIAL.
PROPEP	24 266 POTENTIAL.
CHAIN	267 375 GROWTH/DIFFERENTIATION FACTOR 8.
DISULFID	281 340 BY SIMILARITY.
DISULFID	309 372 BY SIMILARITY.
DISULFID	313 374 BY SIMILARITY.
DISULFID	339 339 INTERCHAIN (BY SIMILARITY).
CARBOHYD	71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE	375 AA; 42791 MW; 0F658685EFD3A318 CRC64;

DB	332	PRSGAGCCCTPTKSPINMLYFNGKEQIIYKIPAMVVDRCGS 375
QY	15-JUL-1999 (Rel. 38, Created)	
DT	15-JUL-1999 (Rel. 38, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).	
GN	GDF8 OR MSTN.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Skeletal muscle;	
RX	MEDLINE=98024153; PubMed=9356471;	
RA	McPherron A.C., Lee S.-J.;	
RT	"Double muscling in cattle due to mutations in the myostatin gene."	
RL	Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=DURC, HAMPSHIRE, MEISHAN, & YORKSHIRE; TISSUE=Skeletal muscle;	
RT	Voelker G.R., Controy J.C., Wheeler M.B.;	
RT	"Porcine myostatin cDNA sequences: Durc, Hampshire, Meishan and Yorkshire pigs."	
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RP	SEQUENCE OF 1-10 AND 36-375 FROM N.A.	
RC	TISSUE=Muscle;	
RX	Daneau I., Silversides D.W.;	
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	
CC	-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.	
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).	
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	

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Query Match 32.3%; Score 204.5; DB 1; Length 376;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLVIDFRQDLGKWKVHEPKGYANFCSGPCP--YLRSDTTHSTVLGLYNTLN 69
DB 279 ESRCCRYPLTVDF-EAFGWDWIATPRYKRYANCYSGCEFFVLQKYPH-----LVHQAN 332

QY 70 PEASAPCCVPQDLEPLTILYVGRTPKV-EQLSNMVVSKCS 112
DB 333 PRGSAGPCCPTPKMSPINLMYFNKGRIIYKIPAMVVDRCGCS 376

RESULT 38
GDF8_RAT
ID GDF8_RAT STANDARD; PRT; 376 AA.
AC O35312;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1].
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019624; AAB86691.1; -
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24
FT PROPEP 25 267
FT CHAIN 268 376
FT DISULFID 282 341
FT DISULFID 310 373
FT DISULFID 314 375
FT DISULFID 340 340
FT CARBOHYD 72 72
FT SEQUENCE 376 AA; 42829 MW; 933043D8C8C3294B CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 376;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLVIDFRQDLGKWKVHEPKGYANFCSGPCP--YLRSDTTHSTVLGLYNTLN 69
DB 279 ESRCCRYPLTVDF-EAFGWDWIATPRYKRYANCYSGCEFFVLQKYPH-----LVHQAN 332
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QY 70 PEASAPCCVPQDLEPLTILYVGRTPKV-EQLSNMVVSKCS 112
DB 333 PRGSAGPCCPTPKMSPINLMYFNKGRIIYKIPAMVVDRCGCS 376

RESULT 39
DVR1_BRARE
ID DVR1_BRARE STANDARD; PRT; 355 AA.
AC P35621;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DVR-1 PROTEIN PRECURSOR.
GN VGL OR DVR-1.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1].
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94009920; PubMed=8405668;
RA Helde K.A., Grunwald D.J.;
RT "The DVR-1 (Vgl) transcript of zebrafish is maternally supplied and
RT distributed throughout the embryo.";
RL Dev. Biol. 159:418-426(1993).
CC -!- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC -!- SUBUNIT: HOMODIMER (PROBABLE).
CC -!- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
CC DISTRIBUTED AMONG ALL BLASTOMERES.
CC -!- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
CC GASTRULA.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; U00931; AAC27347.1; -
DR HSSP; P18075; IBMP.
DR ZFIN; ZDB-GENE-980526-389; vgl.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 15
FT PROPEP 16 240
FT CHAIN 241 355
FT DISULFID 254 320
FT DISULFID 283 352
FT DISULFID 287 354
FT DISULFID 319 319
FT CARBOHYD 108 108
FT CARBOHYD 179 179
FT CARBOHYD 296 296
FT SEQUENCE 355 AA; 40201 MW; 0ED5B9850EBFB222 CRC64;

Query Match 32.2%; Score 204; DB 1; Length 355;
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FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 425 AA; 47565 MW; C910F7F64FF82F67 CRC64;

Query Match 32.2%; Score 204; DB 1; Length 425;
Best Local Similarity 38.3%; Pred. No. 1.5e-14;
Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRPLIDFRQDLGWR-VWHEPKGYVANCSPGCP-----YLRSDTTHSTVLGLNYTL 68
Db 320 CCKQKQVTSFK-DIGWMDWIAPSGYHIANCEGCEPSHIAGTSGSLSFSTVINHYRMR 378
QY 69 --NPEASASPCVQDLEPLTILY-VGRTPKVBQLSNMVVKCKCS 112
Db 379 GHSPFANLKSCCVPTKLRPSMLYDDGQNIKDIQNMIVECCCS 425

RESULT 41
ID GDFB_MOUSE STANDARD; PRT; 405 AA.
AC Q921M4: Q9OX55: Q9R221;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN 11).
GN GDF11 OR BMP11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177155; PubMed=10075854;
RA Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in *Xenopus* embryos.";
RL Dev. Biol. 208:222-232(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RN MEDLINE=993118097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11.";
RL Nat. Genet. 22:260-264(1999).
RN [3]
RP SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGF-beta superfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD. INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
RC STRAIN=FRIESIAN; TISSUE=Muscle; and Embryo;
RX MEDLINE=97458167; PubMed=9314496;
RA Kambadur R., Sharma M., Smith T.P.L., Bass J.J.;
RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
RT Piedmontese cattle.";
RL Piedmontese cattle.
RL Genome Res. 7:910-916(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.
RC STRAIN=HOLSTEIN; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
CC SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES
CC M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
CC HINDLIMB MUSCLES.
CC -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
CC LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
CC DAY 31 UP UNTIL LATE GESTATION.
CC -!- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
CC PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
CC DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTSE
CC CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
CC NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN
CC MUSCLE MASS OF 20-25%.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AF019761; AAB81508.1; -.
DR EMBL; AF019620; AAB86687.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
FT SIGNAL 1 18
FT PROPEP 19 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 47 47
FT CARBOHYD 71 71
FT VARIANT 94 94
FT VARIANT 313 313
FT CONFLICT 14 14
FT CONFLICT 14 14
SQ SEQUENCE 375 AA; 42520 MW; E1B791AD92DA9E6 CRC64;

Query Match 31.8%; Score 201.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 2.4e-14;
Matches 41; Conservative 14; Mismatches 40; Indels 9; Gaps 4;

QY 12 EENCVRPLYIDFRODLGKWKVHEPKGYANFCSPCP--YLRSADTTHSTVGLYNTLN 69
Db 278 ESRCCRYPLTVDF-EAFGWDIITAPKRYKANYSGCECFVLOKYPPTH-----LVHQAN 331

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QY 70 PEASAPCCVQDLEPLTILYVGRTPKV-BQLSNMVVKSCKS 112
| | | | | : | : | | | : | : | | |
Db 332 PRGSAGCCTPTKMSPINMLYFNGEQIIVKIPAMVVDRCGS 375

RESULT 44
IHBA_MOUSE
ID IHBA_MOUSE STANDARD; PRT; 424 AA.
AC Q04938;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93321614; PubMed=8330535;
RA Albano P.M., Groome N., Smith J.C.;
RT "Activins are expressed in preimplantation mouse embryos and in ES
RT and EC cells and are regulated on their differentiation.";
RL Development 117:711-723(1993).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; X69619; CAA49325.1; -.
DR PIR; S31440; S31440.
DR HSSP; P18075; IBMP.
DR MGD; MGI:96570; Inhba.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINBA.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 155 165
FT CONFLICT 14 14
SQ SEQUENCE 424 AA; 47392 MW; 80C251B8754A7213 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 424;

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Best Local Similarity 37.4%; Pred. No. 3.9e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCGPGCP-----YLSADTHTSTVLGLYNTL 68
   || : : : || : || : || : || : || : || : || : || : || : || : || : ||
Db 319 CCKQFFVSEK-DIGWNDWIAPSGYHANYCEGECPSHAGTSGSLSFSHTVINHYMR 377
   || : : : || : || : || : || : || : || : || : || : || : || : || : ||

QY 69 --NPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVKSKCKS 112
   || : || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 378 GHSPFANLSCCVPKLRPMSMLYDDGQNIKKDIQNMIIVECGCS 424
   || : || : || : || : || : || : || : || : || : || : || : || : || : ||

RESULT 45
IHBA_PIG
ID IHBA_PIG STANDARD; PRT; 424 AA.
AC P03970;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RT factor-beta.";
RL Nature 318:659-663(1985).
RN [2]
RP SEQUENCE OF 309-323.
RC TISSUE=Follicular fluid;
RX MEDLINE=92355604; PubMed=1644823;
RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
RA Arizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
RT "Isolation and characterization of native activin B.";
RL J. Biol. Chem. 267:16385-16389(1992).
CC CC
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; X03266; CAA27020.1; -.
CC PIR; A01393; WFPGBA.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR000491; -.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00670; INHIBINB.
```

```
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 308 INHIBIN BETA A CHAIN.
FT PROPEP 309 424
FT DISULFID 312 320 BY SIMILARITY.
FT DISULFID 319 389 BY SIMILARITY.
FT DISULFID 348 421 BY SIMILARITY.
FT DISULFID 352 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 424 AA; 47476 MW; 436BC62226FDAF52 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 424;
Best Local Similarity 37.4%; Pred. No. 3.9e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCGPGCP-----YLSADTHTSTVLGLYNTL 68
   || : : : || : || : || : || : || : || : || : || : || : || : || : ||
Db 319 CCKQFFVSEK-DIGWNDWIAPSGYHANYCEGECPSHAGTSGSLSFSHTVINHYMR 377
   || : : : || : || : || : || : || : || : || : || : || : || : || : ||

QY 69 --NPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVKSKCKS 112
   || : || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 378 GHSPFANLSCCVPKLRPMSMLYDDGQNIKKDIQNMIIVECGCS 424
   || : || : || : || : || : || : || : || : || : || : || : || : || : ||

RESULT 46
IHBA_RAT
ID IHBA_RAT STANDARD; PRT; 424 AA.
AC P18331;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042598; PubMed=3153478;
RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
RT "Rat inhibin: molecular cloning of alpha- and beta-subunit
RT complementary deoxyribonucleic acids and expression in the ovary.";
RL Mol. Endocrinol. 1:561-568(1987).
CC CC
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; M37482; AAA41436.1; -.
CC PIR; B40056; B40056.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR000491; -.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC
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DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta-propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
SQ SEQUENCE 424 AA; 47406 MW; B2DAF791FA50984 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 424;
Best Local Similarity 37.4%; Pred. No. 3.9e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRQDLGK-WVHEPKGYANFCGPGP-----YLRSDTHTSTVLGLYNTL 68
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 319 CCKKQFFVSVFK-DIGNDWIITAPSGYHANYCEGCPHSHAGTSGSLFSFHVNIHYMR 377
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 69 --NPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSCKCS 112
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 378 GHSPFANLKSCCVPTKLRPMSMLYDDGQNIKKDIQNMIIVECGCS 424
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 47
IHBA_BOVIN STANDARD; PRT; 425 AA.
AC P07995;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=Liver.
RC MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting";
RL Eur. J. Biochem. 226:751-764(1994).
RN [2]
SQ SEQUENCE OF 258-425 FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wattenhall R.E.H., Burger H.G., de Kretser D.M.;
RT "Cloning and sequence analysis of cDNA species coding for the two
RT subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.

CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U16239; AAB60627.1;
CC EMBL: U16238; AAB60627.1; JOINED.
CC EMBL: M13274; AAA97415.1;
CC PIR: B25732; B25732.
CC HSSP: P18075; 1BMP.
CC InterPro: IPR000491;
CC InterPro: IPR001111;
CC InterPro: IPR001839;
CC InterPro: IPR002400;
CC Pfam: PF00019; TGF-beta; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PRINTS: PR00670; INHIBINB.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein;
Signal.
FT SIGNAL 1 20
FT PROPEP 21 309
FT CHAIN 310 425
FT DISULFID 313 321
FT DISULFID 320 390
FT DISULFID 349 422
FT DISULFID 353 424
FT DISULFID 389 389
FT CARBOHYD 165 165
SQ SEQUENCE 425 AA; 47521 MW; 2DB799D7197CDA37 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 425;
Best Local Similarity 37.4%; Pred. No. 4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRQDLGK-WVHEPKGYANFCGPGP-----YLRSDTHTSTVLGLYNTL 68
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 320 CCKKQFFVSVFK-DIGNDWIITAPSGYHANYCEGCPHSHAGTSGSLFSFHVNIHYMR 378
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 69 --NPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSCKCS 112
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 GHSPFANLKSCCVPTKLRPMSMLYDDGQNIKKDIQNMIIVECGCS 425
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 48
IHBA_HUMAN STANDARD; PRT; 426 AA.
AC P08476; Q14599;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID
DE DIFFERENTIATION PROTEIN) (EDF).
GN INHBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86186863; PubMed=3754442;
RA Mason A.J., Niall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins.";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
RN [2]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE=88190086; PubMed=3267209;
RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
RT "Erythroid differentiation factor is encoded by the same mRNA as that
of the inhibin beta A chain.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92135888; PubMed=1777673;
RA Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukamizu A.;
RT "Structure and sequence analysis of the human activin beta A subunit
gene.";
RN DNA Seq. 2:103-110(1991).
[4]
RP SEQUENCE OF 311-426 FROM N.A.
RX MEDLINE=87005283; PubMed=3758355;
RA Stewart A.G., Milbrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
RT "Human inhibin genes. Genomic characterisation and sequencing.";
RN FEBS Lett. 206:329-334(1986).
[5]
RP SEQUENCE OF 311-426 FROM N.A.
RC TISSUE=Testis;
RA Berg H., Walter M., Northmann W.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN AB IS A DIMER OF BETA-A.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
[6]
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CC EMBL; M13436; AAA59168.1; -
CC EMBL; X04447; CAA28041.1; -
CC EMBL; X57578; CAA40805.1; -
CC EMBL; X57579; CAA40805.1; JOINED.
CC EMBL; J03634; AAA35787.1; -
CC EMBL; A14422; CAA01159.1; -
CC EMBL; X72498; CAA51163.1; -
CC PIR; A30884; A30884.
CC PIR; B24248; B24256.
CC PIR; B23556; B23556.
CC PIR; S30488; S30488.
CC HSSP; P18075; LBMP.
CC MIM; 147290; -.
CC InterPro; IPR000491; -.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00670; INHIBINB.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 310
FT CHAIN 311 426
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423
INHIBIN BETA A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

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FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
FT CONFLICT 377 379
SQ SEQUENCE 426 AA; 47442 MW; 201CDEDF99CB6919 CRC64;
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
RMR -> AC (IN REF. 5).
201CDEDF99CB6919 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 426;
Best Local Similarity 37.4%; Pred. No. 4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFQDLGKWK-WVHEPKGYANFCGPGCP-----YLRADTHTSTVGLYNTL 68
|| : : : : : || : : || : : || : : || : : || : : || : : || : : ||
Db 321 CCKQKQFFVSFK-DIGWNDWIAPSGYHANYCEGCPHSIAGTSGSLSFHSTVINHRMR 379

QY 69 --NPEASASPCVQDLEPLILY-VGTRPKVEOLSNMNVKSKCS 112
|| : : : : : || : : || : : || : : || : : || : : || : : || : : ||
Db 380 GHSPFANLKSCCVTKLRPMMLYDDQNIKKDIQNIWIVECGCS 426

RESULT 49
60A_DROVI
ID 60A_DROVI STANDARD; PRT; 436 AA.
AC Q24735;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 60A PROTEIN PRECURSOR (GLASS BOTTOM BOAT PROTEIN).
GN GBB OR 60A OR TGF-beta-60A.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305349; PubMed=8688461;
Du W., Doctor J.S.;
RT "Isolation and sequence of the Drosophila virilis 60 A gene, a
transforming growth factor-beta superfamily member related to
vertebrate bone morphogenetic proteins.";
RL Biochim. Biophys. Acta 1307:273-279(1996).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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-----
CC EMBL; U48595; AAC47262.1; -.
CC HSSP; P18075; LBMP.
CC FlyBase; FBgn0015681; Dvir\gbb.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 27
FT PROPEP 28 317
FT CHAIN 318 436
FT DISULFID 335 401
FT DISULFID 364 433
FT DISULFID 368 435
FT DISULFID 400 400
FT CARBOHYD 102 102
FT CARBOHYD 114 114
POTENTIAL.
60A PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

```

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Pittman K.A., Nixon K., Nusser D.R., Pacieb J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Sinden-Klamos I., Simpson M., Skupsis M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; *;
*The genome sequence of *Drosophila melanogaster*.";
Science 287:2185-2195(2000).
-|- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-|- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH PEAKS
OF TRANSCRIPTION DURING EARLY EMBRYOGENESIS, IN PUPAE, AND IN
ADULT MALES.
-|- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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EMBL; M77012; AAA28306.1; -;
EMBL; M84795; AAA28307.1; -;
EMBL; AE003462; AAF47075.1; -;
PIR; A41233; A41233.
PIR; A43918; A43918.
HSP; P18075; 1BMP.
Flybase; FBgn024234; gbb.
InterPro; IPRO01111; -;
InterPro; IPRO01839; -;
InterPro; IPRO02400; -;
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFB-propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
SIGNALL 36
PROPEP 37 335 POTENTIAL.
CHAIN 336 455 60A PROTEIN.
DISULFID 354 420 BY SIMILARITY.
DISULFID 383 452 BY SIMILARITY.
DISULFID 387 454 BY SIMILARITY.
DISULFID 419 419 INTERCHAIN (BY SIMILARITY).
CARBOHYD 238 238 N-LINKED (GLCNAC..) (POTENTIAL).
CARBOHYD 250 250 N-LINKED (GLCNAC..) (POTENTIAL).
CARBOHYD 396 396 N-LINKED (GLCNAC..) (POTENTIAL).
SEQUENCE 455 AA; 51687 MW; C8FA795556341F94 CRC64;

ary Match 30.8%; Score 195; DB 1; Length 455;
t Local Similarity 39.8%; Pred. No. 1-5e-13;
ches 41; Conservative 19; Mismatches 37; Indels 6; Gaps 4;

14 NCVRLPYIDPRQDLGW-KVVHEPKGYANFCSGPCPLRSAD---TTHTSTVLGYNLN 69
:|::||||||-|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
353 SCQMQLTYIDFK-DLGHWDWTIAAPGAGFYCGECNFPNLNAHMNATNHAIVQTLVHLE 411

70 PEASAPCCVPQDELPTILYYVG-RTPKVEQLSNVMVKSCCK 111
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
412 PKKVPKCPCAPTRGUALPVLYHLNDENVNLUKKYRNMIKVCSCG 454

RESULT 51

KW	Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein.
FT	NON_TER 1 1
FT	PROPEP <1 234
FT	CHAIN 235 349
FT	DISULFID 238 246
FT	DISULFID 245 314
FT	DISULFID 274 346
FT	DISULFID 278 348
FT	DISULFID 313 313
FT	CARBOHYD 35 35
SQ	SEQUENCE 349 AA; 39354 MW; C57IEA91ADA5DE77 CRC64;
Query Match	
Best Local Similarity 29.4%; Score 186.5; DB 1; Length 349;	
Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps	
QY	15 CCVRPLYIDRFQDLGWR-WVHEPKGYANFCSPGCP-YLR----SADTTHSTVLGLYNT-67
DB	245 CCRQPFIDFRL-IGWSDWIIATGYGNYGEGSCPAYLAGVPGSASSPHTAVVNOYRMR 303
QY	68 -LNPEASASCCVPQDLEPTILYVGRTPKVEQ-LSNVVVKSKCKS 112
DB	304 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVECGCA 349
RESULT 57	
INBB_HUMAN	
ID	INBB_HUMAN STANDARD; PRT; 407 AA.
AC	P09529;
DT	01-MAR-1989 (Rel. 10, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
GN	INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE=90114200; PubMed=2575216;
RA	Mason A.J., Berkemeier L.M., Schmelzer C.H., Schwall R.H.;
RA	"Activin B: precursor sequences, genomic structure and in vitro
RT	activities";
RL	Mol. Endocrinol. 3:1352-1358(1989).
RL	[2]
RX	SEQUENCE OF 22-407 FROM N.A.
RX	MEDLINE=89295443; PubMed=2739657;
RA	Feng Z.M., Bardin C.W., Chen C.L.;
RT	"Characterization and regulation of testicular inhibin beta-subunit
RL	mRNA";
RL	Mol. Endocrinol. 3:939-948(1989).
RL	[3]
RX	SEQUENCE OF 55-407 FROM N.A.
RX	MEDLINE=86186863; PubMed=3754442;
RA	Mason A.J., Niall H.D., Seeburg P.H.;
RT	"Structure of two human ovarian inhibins.";
RL	Biochem. Biophys. Res. Commun. 135:957-964(1986).
CC	-I- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC	SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC	ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC	IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC	-I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC	INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC	ACTIVIN AB IS A DIMER OF BETA-A.
CC	ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC	-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
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CC	tion between the Swiss Institute of Bioinformatics and the EMBL outstat-
CC	the European Bioinformatics Institute. There are no restrictions on

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CC EMBL; M31669; AAA59451.1; -.
CC EMBL; M31668; AAA59451.1; JOINED.
CC EMBL; M31682; AAA59170.1; -.
CC EMBL; M13437; AAA59169.1; -.
CC PIR; C24248; C24248.
CC HSSP; P18075; LBMP.
CC MIW; 147390; -.
CC InterPro; IPR000381; -.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00671; INHIBINB.
CC DISULFID 371 371 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 93 93 N-LINKED (GLCNAC... ) (POTENTIAL).
CC CONFLICT 47 47 S -> A (IN REF. 2).
CC SEQUENCE 407 AA; 45121 MW; 90316C83597BA6B4 CRC64;

Query Match 29.4%; Score 186.5; DB 1; Length 407;
Best Local Similarity 37.4%; Pred. No. 1.1e-12;
Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFRQDLGKWK-WVHEPKGYANFCGPGCP-YLR-----SADTHTSTVLGLYNT- 67
Db 303 CCQQOFFIDFRL-IGWNDWIIAPTGYGNYCEGSCPAYLAGVPGSASSFHTAVVNOYRMR 361
QY 68 -LNPEASAPCCVPQDLPLTILYVGRTPKVEQ-LSNMVVKSCKCS 112
Db 362 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVNPVNIIVECGCA 407

RESULT 58
ID INHB_BOVIN STANDARD; PRT; 408 AA.
AC P42917;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
GN INHBB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95112839; PubMed=7813465;
RX Thompson D.A., Cronin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting."
RL Eur. J. Biochem. 226:751-764(1994).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPOLYPEPTIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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```



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GN BMP7 OR BMP-7 OR OP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91354237; PubMed=1715687;
RT Oezkaynak E., Schneegelsberg P.N.J., Oppermann H.;
RL "Murine osteogenic protein (OP-1): high levels of mRNA in kidney.";
RL Biochem. Biophys. Res. Commun. 179:116-123(1991).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
CC AND BONE HOMEOSTASIS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; X56906; CAA40222.1; -.
CC PIR; J01184; J01184.
CC HSSP; P18075; I BMP.
CC MGD; MG1:103302; Bmp7.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 231 POTENTIAL.
FT CHAIN 292 430 BONE MORPHOGENETIC PROTEIN 7.
FT DISULFID 329 395 BY SIMILARITY.
FT DISULFID 358 427 BY SIMILARITY.
FT DISULFID 362 429 BY SIMILARITY.
FT DISULFID 394 394 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 430 AA; 49283 MW; 486C36DD97754047 CRC64;

Query Match 28.9%; Score 183; DB 1; Length 430;
Best Local Similarity 35.3%; Pred. No. 2.7e-12;
Matches 36; Conservative 22; Mismatches 38; Indels 6; Gaps 4;

QY 15 CCVRPLIDFRQDLGNK-WVHEPKGYANFCSPGCPYLRSA---DTHSTVGLYNTLNP 70
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 CRKHLYVSFR-DLGWQDIIAPEGAAAYCEGACAPPLSNMNTNHAIVQTLVHPINP 387
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 71 EASASPCVPQDLPLTILYVGRTPKV-EQLSNMVVKSCKC 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 388 DTVPKCCAPTQLNAISLVYFDDSSNVLKKNRMVVRACG 429
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 62
BMP2_RAT
ID BMP2_RAT STANDARD; PRT; 393 AA.
AC P49001;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).

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GN BMP2 OR BMP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone;
RT Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL; Z5868; CAA81088.1; -.
CC HSSP; P18075; I BMP.
CC InterPro; IPR001111; -.
CC InterPro; IPR001839; -.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 279 BONE MORPHOGENETIC PROTEIN 2.
FT CHAIN 280 393 BY SIMILARITY.
FT DISULFID 293 358 BY SIMILARITY.
FT DISULFID 322 390 BY SIMILARITY.
FT DISULFID 326 392 BY SIMILARITY.
FT DISULFID 357 357 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 393 AA; 44383 MW; 7D20865852E0F213 CRC64;

Query Match 28.8%; Score 182.5; DB 1; Length 393;
Best Local Similarity 37.7%; Pred. No. 2.7e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

QY 9 RNLENCVRPLIDFRQDLGNK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 KRLSSCKRHPLIYVDF-SDVGWMDWIVAPPGYHAFYCHGECFPPLADHLNS--TNHAI 343
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 63 GLYNTLN---PEASASPCVPQDLPLTILYVGRTPKV-EQLSNMVVKSCKC 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 TLVSNVSKIPKA---CCVTELSAISML-YLDENEKVLKKNYQDMVVEGCGC 392
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 63
BMP2_MOUSE
ID BMP2_MOUSE STANDARD; PRT; 394 AA.
AC P21274;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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OS Dama dama (Fallow deer) (Cervus dama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=30532;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Antler;
 RX MEDLINE=97157076; PubMed=9003457;
 RA Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
 RA Harris S.E.;
 RT "Bone morphogenetic protein 2 transcripts in rapidly developing deer
 RT antler tissue contain an extended 5' non-coding region arising from a
 RT distal promoter.";
 RL Biochim. Biophys. Acta 1350:47-52(1997).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ001817; CAA05033.1; -;
 DR HSP; P18075; IBMF.
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 282 BY SIMILARITY.
 FT CHAIN 283 396 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID 296 361 BY SIMILARITY.
 FT DISULFID 325 393 BY SIMILARITY.
 FT DISULFID 329 395 BY SIMILARITY.
 FT DISULFID 360 360 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 396 AA; 44646 MW; 5FE23A0AC7F91572 CRC64;
 Query Match 28.8%; Score 182.5; DB 1; Length 396;
 Best Local Similarity 37.7%; Pred. No. 2.8e-12;
 Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;
 QY 9 RNLENCVRLYIDRQDLGNK-WVHEPKGYVANCSPGCV- - - - -LRSDTHTSTVL 62
 DB 290 KRLKSCXKRLPLVDFP-SDGVNDWVIAFGYHAFYGCPCPLADHLNS--TNHAIQV 346
 QY 63 GLYNTLN---PEASAPCCVPQDLEPLTILYVGRPKV---EQLSNNVKSCKC 111
 DB 347 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVKLVKQYQDVMVEGCGC 395
 RESULT 66
 ID BMP2_HUMAN STANDARD; PRT; 396 AA.
 AC P12643;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
 GN BMP2 OR BMP2A.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89072730; PubMed=3201241;
 RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 RT activities.";
 RL Science 242:1528-1534(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.;
 RT "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Blakey S.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.
 RX MEDLINE=99175323; PubMed=10074410;
 RA Scheufler C., Sebald W., Huelsmeyer M.;
 RT "Crystal structure of human bone morphogenetic protein-2 at 2.7 A
 RT resolution.";
 RL J. Mol. Biol. 287:103-115(1999).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND
 CC COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
 CC LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
 CC SMALL INTESTINE.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: M22489; AAA51834.1; -;
 DR EMBL: AF040249; AAF21646.1; -;
 DR EMBL: AL035668; CAB82007.1; -;
 DR PIR; B37278; B37278.
 DR PDB; 3BMP; 12-MAR-00.
 DR TM; 112261; -;
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
 KW 3D-structure.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 282 BONE MORPHOGENETIC PROTEIN 2.
 FT CHAIN 283 396
 FT DISULFID 296 361
 FT DISULFID 325 393
 FT DISULFID 329 395
 FT DISULFID 360 360 INTERCHAIN.
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 396 AA; 44702 MW; 20653A3987B25E60 CRC64;
 Query Match 28.8%; Score 182.5; DB 1; Length 396;
 Best Local Similarity 37.7%; Pred. No. 2.8e-12;
 Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

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QY 9 RNLEENCCVRPLYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 290 KRLKSSCKRRHPLYVDF-SDVGWMDWIVAPPGYHAFYCHGCEPPLADHLNS--TNHAIQV 346
QY 63 GLYNTLN---PEASASPCVPODLEPLTLTYVVGRTPKV--EQLSNMVMVKCKC 111
Db 347 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVVLLKNYQDMVVEGCGC 395

RESULT 67
BMPA_XENLA
ID BMPA_XENLA STANDARD; PRT; 398 AA.
AC P25703;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91274367; PubMed=2054389;
RA Plessow S., Koester M., Knoechel W.;
RT "cDNA sequence of Xenopus laevis bone morphogenetic protein 2
(BMP-2)".
RL Biochim. Biophys. Acta 1089:280-282(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92378616; PubMed=1510675;
RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos."
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; X55031; CAA38850.1; -
DR EMBL; X63424; CAA45018.1; -
DR PIR; S16244; S16244.
DR PIR; JH0687; JH0687.
DR HSSP; P18075; LBMP.
DR InterPro; IPR001839; -
DR InterPro; IPR001111; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 23
FT PROPEP 24 284
FT CHAIN 285 398
FT DISULFID 298 363
FT DISULFID 327 395
FT DISULFID 331 397
FT DISULFID 362 362
FT CARBOHYD 137 137
FT CARBOHYD 202 202
FT CARBOHYD 340 340
FT CONFLICT 7 7
FT CONFLICT 16 16
FT CONFLICT 233 233

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SQ SEQUENCE 398 AA; 45575 MW; 150AC64A47D2E15F CRC64;

Query Match 28.8%; Score 182.5; DB 1; Length 398;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

QY 9 RNLEENCCVRPLYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 292 KRLKSSCKRRHPLYVDF-SDVGWMDWIVAPPGYHAFYCHGCEPPLADHLNS--TNHAIQV 348

QY 63 GLYNTLN---PEASASPCVPODLEPLTLTYVVGRTPKV--EQLSNMVMVKCKC 111
Db 349 TLVNSVNTNIPKA-----CCVPTLSAISML-YLDENEKVVLLKNYQDMVVEGCGC 397

RESULT 68
BMPB_XENLA
ID BMPB_XENLA STANDARD; PRT; 398 AA.
AC P30884;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92378616; PubMed=1510675;
RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos."
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; X63425; CAA45019.1; -
DR PIR; JH0688; JH0688.
DR HSSP; P18075; LBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
DR PROSITE; PS00250; TGF_beta_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 23
FT PROPEP 24 284
FT CHAIN 285 398
FT DISULFID 298 363
FT DISULFID 327 395
FT DISULFID 331 397
FT DISULFID 362 362
FT CARBOHYD 137 137
FT CARBOHYD 202 202
FT CARBOHYD 237 237
FT CARBOHYD 340 340
FT CONFLICT 7 7
FT CONFLICT 16 16
FT CONFLICT 233 233

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Query Match 28.8%; Score 182.5; DB 1; Length 398;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;

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DR Pfam; PF00688; Tgfb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 381
FT CHAIN 382 501 GROWTH/DIFFERENTIATION FACTOR 5.
FT DISULFID 400 466 BY SIMILARITY.
FT DISULFID 429 498 BY SIMILARITY.
FT DISULFID 433 500 BY SIMILARITY.
FT DISULFID 465 465 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 38 38 S -> T (IN REF. 1).
FT CONFLICT 254 258 VPSR -> ARGG (IN REF. 1).
FT CONFLICT 276 276 A -> S (IN REF. 1).
FT CONFLICT 321 321 T -> A (IN REF. 1).
FT CONFLICT 384 384 S -> L (IN REF. 1).
SQ SEQUENCE 501 AA; 55640 MW; EF631EA03417A348 CRC64;

Query Match 28.7%; Score 182; DB 1; Length 501;
Best Local Similarity 37.0%; Pred. No. 4e-12;
Matches 40; Conservative 23; Mismatches 39; Indels 6; Gaps 5;

QY 9 RNLENCVRLYIDFRODLGW-KWHEPKGYANFCGPGPY-IRS--ADTHSTVLGL 64
Db 394 NKLKARCSKALHVNFK-DMGWDWIIAPLEAYEAFHCEGLCEFFLRSHLEPTNHAIVQL 452

QY 65 YNTLNPEASASPCVPQDLEPLTILYYVGRTPKV-EQLSNMNVVKSCKC 111
Db 453 MNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMVVESC GC 500

RESULT 71
DVRL_STRPU STANDARD; PRT; 461 AA.
AC P48969;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE DVR-1 PROTEIN HOMOLOG PRECURSOR.
GN DVRL1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponce M.R., Micol J.L., Davidson E.H.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; Z48313; CAA88306.1; -
CC HSP; P18075; IBMP.
CC InterPro; IPR001111; -
CC InterPro; IPR001839; -
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; Tgfb_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
KW PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; signal.
FT SIGNAL 1 30 POTENTIAL.

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FT PROPEP 31 338 POTENTIAL.
FT CHAIN 339 461 DVR-1 PROTEIN HOMOLOG.
FT DISULFID 360 426 BY SIMILARITY.
FT DISULFID 389 458 BY SIMILARITY.
FT DISULFID 393 460 BY SIMILARITY.
FT DISULFID 425 425 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51881 MW; 2573D54B6625F7EF CRC64;

Query Match 28.5%; Score 181; DB 1; Length 461;
Best Local Similarity 34.6%; Pred. No. 4.7e-12;
Matches 37; Conservative 22; Mismatches 42; Indels 6; Gaps 4;

QY 10 NLENCVRLYIDFRODLGW-KWHEPKGYANFCGPGPYLRSAD---TTHSTVLGLY 65
Db 355 NSDWQCKRKNLFVNF-EDLDWQEWIIAPLGVAFYCGCECAFFLGHANATNHAIVOTLV 413

QY 66 NTLNPEASASPCVPQDLEPLTILYY-VGRTPKVEQLSNMNVVKSCKC 111
Db 414 HHSMPSHVPPCCAPTKLSPIITVLYYDDSRNVVLKYYKNMVRACGC 460

RESULT 72
IHBC_HUMAN STANDARD; PRT; 352 AA.
ID IHBC_HUMAN
AC P55103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
GN INHBC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95126961; PubMed=7826378;
RA Hoetten G., Neidhardt H., Schneider C., Pohl J.;
RT "Cloning of a new member of the TGF-beta family: a putative new
RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
CC -1- FUNCTION: INHIBINS ARE GONADAL GLYCOPETIDES THAT INHIBIT THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
CC DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; X82540; CAA57890.1; -
CC HSP; P18075; IBMP.
CC MIM; 601233; -
CC InterPro; IPR001318; -
CC InterPro; IPR001839; -
CC InterPro; IPR002400; -
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00672; INHIBINBC.
CC PROSITE; PS00250; TGF_BETA_1; 1.

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RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
CC
CC -1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM. FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC
CC -1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED
CC WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
CC AND MIDGUT MESODERM (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL: U63856; AAC47553.1; -
CC FlyBase; FBgn0018547; Dpse\dpp.
CC InterPro; IPR001111; -
CC InterPro; IPR001839; -
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFb.propeptide; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Developmental protein; Differentiation; Glycoprotein;
CC Signal.
CC SIGNAL 1 15 POTENTIAL.
CC PROPEP 16 479 BY SIMILARITY.
CC CHAIN 480 621 DECAPENTAPLEGIC PROTEIN.
CC DISULFID 520 586 BY SIMILARITY.
CC DISULFID 549 618 BY SIMILARITY.
CC DISULFID 553 620 BY SIMILARITY.
CC DISULFID 585 585 INTERCHAIN (BY SIMILARITY).
CC DOMAIN 45 57 POLY-ALA.
CC DOMAIN 88 92 POLY-ASN.
CC DOMAIN 95 104 POLY-ASN.
CC DOMAIN 163 173 POLY-GLN.
CC DOMAIN 483 495 POLY-GLY.
CC CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 621 AA; 69038 MW; 3FD7141FB5509651 CRC64;

Query Match 28.4%; Score 180; DB 1; Length 621;
Best Local Similarity 38.5%; Pred. No. 8.2e-12;
Matches 42; Conservative 13; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLENCVRLYIDFRODLGW-KWVHEPKGYANFCSPGCPYLRSD-THSTHTVLG 63
Db 514 KNHEETCRRLHYVDF-ADVGDWDWIVAPGYDAYCHGKCPF-PLADHFNSTNHAVQT 571

QY 64 LYNTLNPEASPCVPPDLEPLTILYVGR-TPKVEQLSNMVKSKC 111
Db 572 LVNNLPGKVPKACVPPQLDSVAMLYLNDQSTVVVLYKNYQEMTVVGGCG 620

RESULT 75
GDF6_MOUSE ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).

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GN GDF6 OR GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL: U08338; AAA18779.1; -
CC HSSP; P18075; LBMP.
CC MGD; MGI:95689; Gdf6.
CC InterPro; IPR001839; -
CC Pfam; PF00019; TGF-beta; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein.
CC NON_TER 1 1 POTENTIAL.
CC PROPEP <1 5 GROWTH/DIFFERENTIATION FACTOR 6.
CC CHAIN 6 125 BY SIMILARITY.
CC DISULFID 24 90 BY SIMILARITY.
CC DISULFID 53 122 BY SIMILARITY.
CC DISULFID 57 124 BY SIMILARITY.
CC DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
CC SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 28.2%; Score 179; DB 1; Length 125;
Best Local Similarity 38.2%; Pred. No. 2e-12;
Matches 39; Conservative 20; Mismatches 37; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGW-KWVHEPKGYANFCSPGCPY-LRS-ADTHSTVLGLYNTLP 70
Db 24 CSRKPLHVNFK-ELGWDWDWIIAPLEYEAVHCEGVCDFPLRSHLEPTNHAITQILMNSMDP 82

QY 71 EASAPCCVPPDLEPLTILYVGRTPKVEQLSNMVKSKC 111
Db 83 GSTPPSCCVPTKLTPTISILYIDAGNNVVYKQYEDMVVESC 124

RESULT 76
BMP5_MOUSE ID BMP5_MOUSE STANDARD; PRT; 452 AA.
AC P49003;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).
GN BMP5 OR BMP-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/KW;
RX MEDLINE=95046894; PubMed=7958439;
RA King J.A., Marker P.C., Seung K.J., Kingsley D.M.;

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RT  "BMP5 and the molecular, skeletal, and soft-tissue alterations in
RL  short ear mice.";
RN  Dev. Biol. 166:112-122(1994).
RP  -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC  -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L41145; AAA64612.1; -.
DR  HSSP; P18075; 1BMP.
DR  MGD; MGI:88181; Bmp5.
DR  InterPro; IPR001111; -.
DR  InterPro; IPR001839; -.
DR  InterPro; IPR002400; -.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGF-beta; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
DR  Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT  SIGNAL 1 25
FT  PROPEP 26 320
FT  CHAIN 321 452
FT  DISULFID 351 417
FT  DISULFID 380 449
FT  DISULFID 384 451
FT  DISULFID 416 416
FT  CARBOHYD 209.
FT  CARBOHYD 325.
FT  CARBOHYD 343.
FT  CARBOHYD 393.
FT  CARBOHYD 393.
SQ  SEQUENCE 452 AA; 51511 MW; AAD9521EC94A78D5 CRC64;

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Query Match 28.2%; Score 179; DB 1; Length 452;
Best Local Similarity 35.2%; Pred. No. 7.5e-12;
Matches 37; Conservative 22; Mismatches 40; Indels 6; Gaps 4;

QY 12 EENCCVRPLYIDFRDLGWK-WVHEPKGYANFCSPGCPYLRSD---TTHSTVLGLYNT 67
DB 348 KQACKKHELYVSFR-DLGWDQWIIAPEGYAFCGECFPLNAHMNATNHAIVQTLVHL 406
QY 68 LNPEASAPCCVPQDLEPLTILYVVGRTPKV-EOLSNMVKSKC 111
DB 407 MFPDHPKPCCAPTKLNAISLVLYFDDSSNVILKKYRNWVRSGC 451

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RESULT 77
BMP5_HUMAN
ID BMP5_HUMAN STANDARD; PRT; 454 AA.
AC P22003; Q9NTW5;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).
GN BMP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=91088608; PubMed=2263636;
RA Celeste A.J., Iannazi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA Wang E.A., Wozney J.M.;
RT "Identification of transforming growth factor beta family members

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RT  present in bone-inductive protein purified from bovine bone.";
RL  Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
RN  [2]
RP  SEQUENCE OF 279-454 FROM N.A.
RA  Tracey A.;
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC  -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC  -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LIVER.
CC  -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M60314; AAA36736.1; -.
DR  EMBL; AL133386; CAB81657.1; -.
DR  PIR; A39263; A39263.
DR  HSSP; P18075; 1BMP.
DR  MIM; 112265; -.
DR  InterPro; IPR001111; -.
DR  InterPro; IPR001839; -.
DR  InterPro; IPR002400; -.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGF-beta; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
DR  Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT  SIGNAL 1 30
FT  PROPEP 31 322
FT  CHAIN 323 454
FT  DISULFID 353 419
FT  DISULFID 382 451
FT  DISULFID 386 453
FT  DISULFID 418 418
FT  CARBOHYD 211 211
FT  CARBOHYD 327 327
FT  CARBOHYD 345 345
FT  CARBOHYD 395 395
SQ  SEQUENCE 454 AA; 51736 MW; 631277413CC22EE CRC64;

Query Match 28.2%; Score 179; DB 1; Length 454;
Best Local Similarity 35.2%; Pred. No. 7.5e-12;
Matches 37; Conservative 22; Mismatches 40; Indels 6; Gaps 4;

QY 12 EENCCVRPLYIDFRDLGWK-WVHEPKGYANFCSPGCPYLRSD---TTHSTVLGLYNT 67
DB 350 KQACKKHELYVSFR-DLGWDQWIIAPEGYAFCGECFPLNAHMNATNHAIVQTLVHL 408
QY 68 LNPEASAPCCVPQDLEPLTILYVVGRTPKV-EOLSNMVKSKC 111
DB 409 MFPDHPKPCCAPTKLNAISLVLYFDDSSNVILKKYRNWVRSGC 453

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RESULT 78
GDF7_MOUSE
ID GDF7_MOUSE STANDARD; PRT; 151 AA.
AC P43029;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).
GN GDF7 OR GDF-7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF-beta superfamily.";
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; U08339; AAA18780.1; -.
DR HSP; P18075; IBMP.
DR MGD; MGI:95690; Gdf7.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein.
FT NON_TER 1 5
FT PROPEP <1 5
FT CHAIN 6 151
FT DISULFID 50 116
FT DISULFID 79 148
FT DISULFID 83 150
FT DISULFID 115 115
FT DOMAIN 1 5
FT DOMAIN 16 41
FT SEQUENCE 151 AA; 15697 MW; 0E496ACB5827759 CRC64;

Query Match 27.8%; Score 176; DB 1; Length 151;
Best Local Similarity 37.0%; Pred. No. 5e-12;
Matches 40; Conservative 20; Mismatches 42; Indels 6; Gaps 5;

QY 9 RNLENCVRLPYIDFRODLGW-KWHEPKGYANFCGPGPY-LRS--ADTHSTVLGL 64
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 44 RGRSRCSKSLHVDK-ELGWDWIIAPDYAEVHCYGVCDPLRSHLEPTNHAIQTL 102
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 YNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVVKSCK 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 LNSMAPDAAPASCVPARLSPISILYIDAANNVYKQYEDMVVEACG 150
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 79
GDF6_BOVIN STANDARD; PRT; 436 AA.
AC P55106;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
DE MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT).
GN GDF6 OR CDMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RA "Cartilage-derived morphogenetic proteins. New members of the
RT

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transforming growth factor-beta superfamily predominantly expressed
in long bones during human embryonic development.";
J. Biol. Chem. 269:28227-28234(1994).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; U13651; AAA61416.1; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein.
FT NON_TER 1 316
FT PROPEP <1 316
FT CHAIN 317 436
FT DISULFID 335 401
FT DISULFID 364 433
FT DISULFID 368 435
FT DISULFID 400 400
FT CARBOHYD 27 27
FT CARBOHYD 89 89
FT SEQUENCE 436 AA; 47873 MW; B0688E12EF8AE91D CRC64;

Query Match 27.6%; Score 175; DB 1; Length 436;
Best Local Similarity 37.3%; Pred. No. 1.9e-11;
Matches 38; Conservative 19; Mismatches 39; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGW-KWHEPKGYANFCGPGPY-LRS--ADTHSTVLGLYNTLP 70
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 335 CSKKPLHVNFK-ELGWDWIIAPDYAEVHCYGVCDPLRSHLEPTNHAIQTLMSMDP 393
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 EASAPCCVQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 394 GSTPTSCCVPTKLTPTISILYIDAGNNVYNEVEEMVVEGCG 435
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 80
BM10_HUMAN STANDARD; PRT; 424 AA.
AC O95393;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 10 PRECURSOR (BMP-10).
GN BMP10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Celeste A.J.;
RT "Homo sapiens bone morphogenetic protein 10 (BMP-10) mRNA.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF101441; AAC77462.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00669; INHIBIN.
DR PROSITE; PS00250; TGF_BETA_1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
KW SIGNAL 21 POTENTIAL.
FT PROPEP 22 316 POTENTIAL.
FT CHAIN 317 424 BONE MORPHOGENETIC PROTEIN 10.
FT DISULFID 323 389 BY SIMILARITY.
FT DISULFID 352 421 BY SIMILARITY.
FT DISULFID 356 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 424 AA; 48047 MW; 3FDB3B7221BB2254 CRC64;

Query Match 27.5%; Score 174.5; DB 1; Length 424;
Best Local Similarity 37.6%; Pred. No. 2.1e-11;
Matches 41; Conservative 15; Mismatches 46; Indels 7; Gaps 5;

QY 9 RNLENCVVR-PLYIDFQDLGW-KWHEPKGYANFCGPGPYLRS---ADTHTSTVLG 63
DB 316 RNAKGKRTPLLYIDFQ-ETGWDSWIAPGGEYAEKRGVGNLYLAELHTPTKHAIIQA 374
QY 64 LYNTLNPEASPCVCPQDLPLETLTY-VGRTPKVEQLSNMVKSKC 111
DB 375 LVHLKNSOKASACVPTKLEPILSYLDKGVVTKFYEGMAVSECGC 423

RESULT 81
DECA_TRICA STANDARD; PRT; 372 AA.
AC Q26974;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN PRECURSOR.
GN DPP.
OS Tribolium castaneum (Red flour beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tribolium.
OX NCBI_TaxID=7070;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanchez-Salazar J., Pletcher M.T., Bennett R.L., Brown S.J.,
RA Dandamudi T.J., Denell R.E., Doctor J.S.;
RA "The Tribolium decapentaplegic gene is similar in sequence, structure,
FT and expression to the Drosophila dpp gene.";
RL Dev. Genes Evol. 206:237-246(1996).
CC CC
CC -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER, DISULFIDE-LINKED (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; U63132; AAB38392.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1.
KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW SIGNAL 21 POTENTIAL.
FT PROPEP 21 ? POTENTIAL.
FT CHAIN 271 372 DECAPENTAPLEGIC PROTEIN.
FT DISULFID 271 337 BY SIMILARITY.
FT DISULFID 300 369 BY SIMILARITY.
FT DISULFID 304 371 BY SIMILARITY.
FT DISULFID 336 336 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 372 AA; 42435 MW; C9991AB75D2E3173 CRC64;

Query Match 27.4%; Score 174; DB 1; Length 372;
Best Local Similarity 35.8%; Pred. No. 2.1e-11;
Matches 39; Conservative 17; Mismatches 45; Indels 8; Gaps 5;

QY 9 RNLENCVVR-PLYIDFQDLGW-KWHEPKGYANFCGPGPYL---RSADTHTSTVLG 64
DB 265 KNLKDCRRQMYVDF-GSVGNDWIAPLGDAYCGGECEYPIDHMTTTHAIVQSL 323
QY 65 YNTLNPEASPCVCPQDLPLETLTYVVGRTPKV--EQLSNMVKSKC 111
DB 324 VNSMKPREVPGCCVPTQLGQMSML-YLGSDGSVILKNYKEMVVGCGC 371

RESULT 82
GDF1_HUMAN STANDARD; PRT; 372 AA.
AC P27539; O43344;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).
GN GDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91239545; PubMed=2034669;
RA Lee S.-J.;
RA "Expression of growth/differentiation factor 1 in the nervous system:
RT conservation of a bicistronic structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Gordon L., Christensen M., Kyle A., Ramirez M., Stillwagen S.,
RA Ganes J., Danganan L., Bruce R., Quan G., Montgomery M., Ow D.,
RA Kobayashi A., Nolan M., Trong S., Olsen A.O., Carrano A.V.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY MEDIATE CELL DIFFERENTIATION EVENTS DURING EMBRYONIC
CC DEVELOPMENT.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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RESULT 84
DECA_DROSI STANDARD; PRT; 593 AA.
AC P91706;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
GN DPP.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NET DPI;
RX MEDLINE=97225212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL Genetics 145:297-309(1997).
CC -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED
CC WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
CC AND MIDGUT MESODERM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; U63854; AAC47554.1; -
DR FlyBase; FBgn0013673; Ds1m\dpp.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA.1; 1.
DR Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW Signal.
FT SIGNAL 1 15 POTENTIAL.
FT PROPEP 16 461 BY SIMILARITY.
FT CHAIN 462 593 DECAPENTAPLEGIC PROTEIN.
FT DISULFID 492 558 BY SIMILARITY.
FT DISULFID 521 590 BY SIMILARITY.
FT DISULFID 525 592 BY SIMILARITY.
FT DISULFID 557 557 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 593 AA; 66248 MW; F0BDB21209F44380 CRC64;

Query Match 27.1%; Score 172; DB 1; Length 593;
Best Local Similarity 35.8%; Pred. No. 5.6e-11;
Matches 39; Conservative 16; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLEENCCVRPLYIDPRDLGW-KWVHEPKGYANFCGPGCYLRSD-----TTHSTVLG 63

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DB 486 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGVDAYCHGKCF-PLADHFNSTNHAVQT 543
QY 64 LYLTLNPEASASPCVCPODLEPLTILYVGR-TPKVEQLSNMVKSKC 111
DB 544 LVNNMFGKVPKACCVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVGGCG 592

RESULT 85
BMP2_CHICK STANDARD; PRT; 353 AA.
ID BMP2_CHICK
AC Q90751;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (FRAGMENT).
GN BMP2 OR BMP-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RT patterning in the developing chick limb.";
RL Development 120:209-218(1994).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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-----
EMBL; X75914; CAA53513.1; -
DR HSPP; P18075; lBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA.1; 1.
DR Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
KW NON_TER 1 1
FT PROPEP <1 239 BY SIMILARITY.
FT CHAIN 240 353 BONE MORPHOGENETIC PROTEIN 2.
FT DISULFID 253 318 BY SIMILARITY.
FT DISULFID 282 350 BY SIMILARITY.
FT DISULFID 286 352 BY SIMILARITY.
FT DISULFID 317 317 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 353 AA; 40347 MW; 8DBB46CD0EBD769B CRC64;

Query Match 27.1%; Score 171.5; DB 1; Length 353;
Best Local Similarity 38.5%; Pred. No. 3.7e-11;
Matches 42; Conservative 18; Mismatches 30; Indels 19; Gaps 8;

QY 14 NCCVRPLYIDPRDLGW-KWVHEPKGYANFCGPGCY-----LRSDTHTSTVLGLYNT 67
DB 252 SKRRLPLYVDF-NDVGWDDWIVAPPGYSFAFYCHGCEPPLADHLNS--TNHAIQTVLNS 308
QY 68 LN---PEASAPCCVPQDLEPLTILYVGRPKV--EQLSNMVKSKC 111

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Db 309 VNSKIPKA-----CCVPTLSAISM-LYLDENEKVLKNYQDMVVEGCGC 352

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RESULT 86
ID BM8B_MOUSE
AC P55105;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 8B PRECURSOR (BMP-8B).
GN BMP8B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Placenta;
RX MEDLINE=97000308; PubMed=8843393;
RA Zhao G.Q., Hogan B.L.;
RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that
RL Mech. Dev. 57:159-168(1996).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
CC AND BONE HOMEOSTASIS (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; U39545; AB17573.1; -
DR HSSP; P18075; lBMP.
DR MGD; MGI:107335; Bmp8b.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 260
FT CHAIN 261 399
FT DISULFID 298 364
FT DISULFID 327 396
FT DISULFID 331 398
FT DISULFID 363 363
FT CARBOHYD 155 155
FT CARBOHYD 340 340
FT SEQUENCE 399 AA; 44752 MW; 44752 MW; EPA0B7B8C7EC4839 CRC64;

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Query Match 27.0%; Score 171; DB 1; Length 399;
 Best Local Similarity 40.0%; Pred. No. 4.7e-11;
 Matches 42; Conservative 16; Mismatches 39; Indels 8; Gaps 6;

QY 13 ENCCVRLPYIDPRDLGW-KWHEPKGYANFCGCPY--LBSA--DTHSTVLGLYNTL 68
 Db 296 EVCRTGELVGFGR-DLGWLDSDIAPQGYSAVYAGECIYPLNSMNSNTHATMQALVHLM 354
 QY 69 NPEASAPCCVPQDLPLTLIYVGRTPKV--EQLSNMVKSKC 111

Db 355 KPDIIPKVCVPFELSALSLEY-DRNNNVILRRRNMVVOACGC 398

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RESULT 87
ID BMP4_CHICK
AC Q90752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
GN BMP4 OR BMP-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RL patterning in the developing chick limb.";
CC Development 120:209-218(1994).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; X75915; CAA53514.1; -
DR HSSP; P18075; lBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 291
FT CHAIN 292 405
FT DISULFID 305 370
FT DISULFID 334 402
FT DISULFID 338 404
FT DISULFID 369 369
FT CARBOHYD 144 144
FT CARBOHYD 208 208
FT CARBOHYD 347 347
FT CARBOHYD 362 362
FT SEQUENCE 405 AA; 46057 MW; 544302DBA0A40F81 CRC64;

```

Query Match 26.9%; Score 170.5; DB 1; Length 405;
 Best Local Similarity 37.7%; Pred. No. 5.4e-11;
 Matches 43; Conservative 18; Mismatches 34; Indels 19; Gaps 8;

QY 9 RNLEENCVRPLYIDPRDLGMK-WVHEPKGYANFCGCPY-----LRSADTHSTVL 62
 Db 299 RKNKNCRRHRLYVDF-SDVGWNDWIVAPGYQAFYCHGDCPPLADHLNS--TNHAIQV 355

QY 63 GLYNTLN----PEASAPCCVPQDLPLTLIYVGRTPKV--EQLSNMVKSKC 111
 Db 356 TLVNSYNSSIPKA-----CCVPTLSAISM-LYLDENEKVLKNYQDMVVEGCGC 404


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FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 152 152 V -> A (IN REF. 2).
SQ SEQUENCE 408 AA; 46555 MW; 79801179DBB98204 CRC64;

Query Match 26.9%; Score 170.5; DB 1; Length 408;
Best Local Similarity 37.7%; Pred. No. 5.5e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

Qy 9 RNLENCVVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
Db 302 RKKKNCRHRSLSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCFPPLADHLNS--TNHAIQV 358

Qy 63 GLYNTLN---PEASASPCVQDPLEPLTILYVGRTPKV--EQLSNMVVKSCKC 111
Db 359 TLVNSVNSSIPKA-----CCVPTLSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407

RESULT 90
BMP4_MOUSE
ID BMP4_MOUSE STANDARD; PRT; 408 AA.
AC P21275;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93282803; PubMed=8507180;
RA Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
RT "Murine bone morphogenetic protein-4 gene: existence of multiple
promoters and exons for the 5'-untranslated region.";
RL Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93365172; PubMed=8358941;
RA Takaoka K., Yoshikawa H., Hashimoto J., Masuhara K., Miyamoto S.,
RA Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
RT "Gene cloning and expression of a bone morphogenetic protein derived
from a murine osteosarcoma.";
RL Clin. Orthop. Relat. Res. 294:344-352(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Liver;
RX Feng J.Q., Chen D., Cooney A.J., Tsai M., Harris M.A., Tsai S.Y.,
Feng M., Mundy G.R., Harris S.E.;
RT "The mouse bone morphogenetic protein-4 gene. Analysis of promoter
utilization in fetal rat calvarial osteoblasts and regulation by
COUP-TF1 orphan receptor.";
RL J. Biol. Chem. 270:28364-28373(1995).
RN [5]
RP SEQUENCE OF 241-408 FROM N.A.
RX MEDLINE=90228966; PubMed=1970330;
RA Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
RA Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
RA Stracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
RA Jenkins N.A.;
RT "Chromosomal localization of seven members of the murine TGF-beta
superfamily suggests close linkage to several morphogenetic mutant
loci.";
RL Genomics 6:505-520(1990).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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EMBL; X56848; CAA40179.1; -
EMBL; S65032; AAB28021.1; -
EMBL; L47480; AAC37698.1; ALT_INIT.
EMBL; D14814; BAA03555.1; -
PIR; B34201; B34201.
PIR; S29523; S29523.
HSP; P18075; IBM.
MGD; MGI:88180; Bmp4.
InterPro; IPR001111; -
InterPro; IPR001839; -
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 292
FT CHAIN 293 408 BONE MORPHOGENETIC PROTEIN 4.
FT DISULFID 308 373 BY SIMILARITY.
FT DISULFID 337 405 BY SIMILARITY.
FT DISULFID 341 407 BY SIMILARITY.
FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 407 407 C -> S (IN REF. 2).
SQ SEQUENCE 408 AA; 46496 MW; 35053D844624EF9D CRC64;

Query Match 26.9%; Score 170.5; DB 1; Length 408;
Best Local Similarity 37.7%; Pred. No. 5.5e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

Qy 9 RNLENCVVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
Db 302 RKKKNCRHRSLSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCFPPLADHLNS--TNHAIQV 358

Qy 63 GLYNTLN---PEASASPCVQDPLEPLTILYVGRTPKV--EQLSNMVVKSCKC 111
Db 359 TLVNSVNSSIPKA-----CCVPTLSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407

RESULT 91
BMP4_MOUSE
ID BMP4_MOUSE STANDARD; PRT; 408 AA.
AC Q06826;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93385158; PubMed=8373807;
RA Chen D., Feng J.Q., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
RT "Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal
rat calvarial cell.";

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RL Biochim. Biophys. Acta 1174:289-292(1993).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z22607; CAAB0329.1; -.
CC InterPro: IPR001839; -.
CC PIR: S33173; S33173.
CC PIR: S38343; S38343.
CC HSP: P18075; LBMP.
CC InterPro: IPR001111; -.
CC InterPro: IPR001839; -.
CC Pfam: PF00019; TGF-beta; 1.
CC PROSITE: PS00250; TGF_BETA.1; 1.
CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
CC SIGNAL 1 19
CC PROPEP 20 292
CC CHAIN 293 408
CC DISULFID 308 373
CC DISULFID 337 405
CC DISULFID 341 407
CC DISULFID 372 372
CC CARBOHYD 144 144
CC CARBOHYD 209 209
CC CARBOHYD 350 350
CC CARBOHYD 365 365
CC SEQUENCE 408 AA; 46540 MW; 61E92B48D5624F3 CRC64;
CC -----
CC Query Match 26.9%; Score 170.5; DB 1; Length 408;
CC Best Local Similarity 37.7%; Pred. No. 5.5e-11;
CC Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;
CC -----
CC QY 9 RNLEENCVRPLXIDFRQDLGK-WVHEPKGYANFCSPGCPY-----LRASDTHTSTVL 62
CC Db 302 RKKKNCRRHSLYVDF-SDVGNDWIVAPGQAFYCHGDCPPLADHLNS--TNHAIQV 358
CC -----
CC QY 63 GLYNTLN----PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
CC Db 359 TLVNSVNSSIPKA----CCVPTLSAISML-YLDEYDKVVLKKNYQEMVVEGCGC 407
CC -----
CC RESULT 92
CC BMP4_RABIT
CC ID BMP4_RABIT STANDARD; PRT; 409 AA.
CC AC Q46576;
CC DT 15-JUL-1999 (Rel. 38, Created)
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
CC GN BMP4 OR BMP-4.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC OX NCBI_TaxID=9986;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;
CC RA Wan X.L., Sears J., Chen S., Sears M.;
CC RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
CC RT epithelium."
CC RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

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CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF042497; AAB97467.1; -.
CC InterPro: IPR001111; -.
CC InterPro: IPR001839; -.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGF_beta_propeptide; 1.
CC PROSITE: PS00250; TGF_BETA.1; 1.
CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
CC SIGNAL 1 19
CC PROPEP 20 293
CC CHAIN 294 409
CC DISULFID 309 374
CC DISULFID 338 406
CC DISULFID 342 408
CC DISULFID 373 373
CC CARBOHYD 144 144
CC CARBOHYD 209 209
CC CARBOHYD 351 351
CC CARBOHYD 366 366
CC SEQUENCE 409 AA; 46641 MW; 35557561447AD625 CRC64;
CC -----
CC Query Match 26.7%; Score 169.5; DB 1; Length 409;
CC Best Local Similarity 38.1%; Pred. No. 7e-11;
CC Matches 43; Conservative 17; Mismatches 36; Indels 17; Gaps 8;
CC -----
CC QY 9 RNLEENCVRPLXIDFRQDLGK-WVHEPKGYANFCSPGCPYLSRAD----TTHSTVLG 63
CC Db 303 RKKKNCRRHSLYVDF-SDVGNDWIVAPGQAFYCHGDCPFLADHFNSTHAIQV 360
CC -----
CC QY 64 LYNTLN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
CC Db 361 LVNSVNSSIPKA----CCVPTLSAISML-YLDEYDKVVLKKNYQEMVVEGCGC 408
CC -----
CC RESULT 93
CC UNIV_STRPU
CC ID UNIV_STRPU STANDARD; PRT; 383 AA.
CC AC P48970;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
CC DE UNIVIN PRECURSOR.
CC OS Strongylocentrotus purpuratus (Purple sea urchin).
CC OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
CC OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
CC OC Strongylocentrotus.
CC OX NCBI_TaxID=7668;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=95046897; PubMed=7958442;
CC RA Stenzel P., Angerer L.M., Smith B.J., Angerer R.C., Vale W.W.;
CC RT "The univin gene encodes a member of the transforming growth
CC RT factor-beta superfamily with restricted expression in the sea urchin
CC RT embryo."
CC RN Dev. Biol. 166:149-158(1994).
CC CC -1- FUNCTION: COULD HAVE A CRITICAL ROLE IN EARLY DEVELOPMENTAL
CC CC DECISIONS IN THE SEA URCHIN EMBRYO.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS OF EXPRESSION IN THE EGG AND
CC PREHATCHING BLASTULA. DURING LATE CLEAVAGE STAGES, IT ACCUMULATES
CC PROGRESSIVELY TO A CIRCUM-EQUATORIAL BAND. DURING GASTRULATION IT
CC IS DETECTED PRIMARILY IN THE PRESUMPTIVE FOREGUT AND CILIATED

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[illegible]

RT "Genes for bone morphogenetic proteins are differentially transcribed
RL in early amphibian embryos.";
RN Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
RP [2]
RX CHARACTERIZATION.
RA MEDLINE=93048825; PubMed=1425343;
RA Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hogan B.L.;
RT "DVR-4 (bone morphogenetic protein-4) as a posterior-ventralizing
RT factor in Xenopus mesoderm induction.";
RL Development 115:639-647(1992).
CC -!- FUNCTION: POSTERIOR-VENTRALIZING FACTOR IN XENOPUS MESODERM
CC INDUCTION. INDUCES POSTERIOVENTRAL MESODERM AND COUNTERACTS
CC DORSALIZING SIGNALS SUCH AS ACTIVIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL; X63426; CAA45020.1; -.
DR PIR; JH0689; JH0689.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 287
FT CHAIN 288 401
FT BY SIMILARITY.
FT DISULFID 301 366
FT BY SIMILARITY.
FT DISULFID 330 398
FT BY SIMILARITY.
FT DISULFID 334 400
FT BY SIMILARITY.
FT DISULFID 365 365
FT INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 141 141
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 204 204
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 358 358
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 401 AA; 45988 MW; 3580DEC4B9890047 CRC64;

Query Match 26.1%; Score 165.5; DB 1; Length 401;
Best Local Similarity 36.8%; Pred. No. 1.8e-10;
Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVRLYIDFRODLGK-WVHEPKGYANFGSGPCPY-----LRSDTTHSTVL 62
DB 295 RKNKHKRRHSLYVDF-SDVGNNDIVAPPGVQAFYCHGDCPFPLADHLNS--TNHAIQV 351

QY 63 GLYNTLN---PEASAPCCVQDLEPLTILYVGRTPKV--EQLSNMVKSKKC 111
DB 352 TLVNSVNSIPKA-----CCVPTLSAISML-YLDEYDKWLKLNQYEMVVEGCGC 400

RESULT 98
GDF1_MOUSE
ID GDF1_MOUSE STANDARD; PRT; 357 AA.
AC P20863;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).
GN GDF1 OR GDF-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=91133438; PubMed=1704486;
RA Lee S.-J.;
RT "Identification of a novel member (GDF-1) of the transforming growth
RT factor-beta superfamily.";
RL Mol. Endocrinol. 4:1034-1040(1990).
CC [2]
CC SEQUENCE FROM N.A.
RX MEDLINE=91239545; PubMed=2034669;
RA Lee S.-J.;
RT "Expression of growth/differentiation factor 1 in the nervous system:
RT conservation of a bicistronic structure.";
CC Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
CC -!- FUNCTION: MAY MEDIATE CELL DIFFERENTIATION EVENTS DURING EMBRYONIC
CC DEVELOPMENT.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN THE NERVOUS
CC SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M57639; AAA37674.1; -.
DR EMBL; M62301; AAA37676.1; -.
DR PIR; A35683; A35683.
DR HSSP; P18075; IBMP.
DR MGD; MGI:95683; Gdf1.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 23
FT PROPEP 24 237
FT CHAIN 238 357
FT EMERSONIC GROWTH/DIFFERENTIATION FACTOR
FT BY SIMILARITY.
FT DISULFID 251 322
FT BY SIMILARITY.
FT DISULFID 280 354
FT BY SIMILARITY.
FT DISULFID 284 356
FT BY SIMILARITY.
FT DISULFID 321 321
FT INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 191 191
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 145 145
FT C -> S (IN REF. 2).
SQ SEQUENCE 357 AA; 38676 MW; DE341F046226C1EE CRC64;

Query Match 25.9%; Score 164.5; DB 1; Length 357;
Best Local Similarity 35.5%; Pred. No. 2.1e-10;
Matches 38; Conservative 17; Mismatches 41; Indels 11; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFGSGPCPY---LRSD---TTHSTVLGLYN 66
DB 251 CTRRLHVSFR-EVGHWRVVIAPRGFLANFCQGTALPETLRGPGPPALNHAVLRALMH 309

QY 67 TLNPEASA-SPCCVQDLEPLTILYVGRTPKV-EQLSNMVKSKKC 111
DB 310 AAAPTGAGSPCCVPERLSPISVLFDFDSDNVVLRHVEDWVDECCG 356

RESULT 99
GDF3_MOUSE
ID GDF3_MOUSE STANDARD; PRT; 366 AA.
AC Q07104;

DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR (GDF-3) (VG-1-RELATED
DE PROTEIN 2).
CN GDF3 OR GDF-3 OR VGR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155193; PubMed=8429021;
RA McPherron A.C., Lee S.-J.;
RT "GDF-3 and GDF-9: two new members of the transforming growth
RT factor-beta superfamily containing a novel pattern of cysteines.";
RL J. Biol. Chem. 268:3444-3449(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93125570; PubMed=1480182;
RA Jones C.M., Simon-Chazottes D., Guenet J.-L., Hogan B.L.;
RT "Isolation of Vgr-2, a novel member of the transforming growth
RT factor-beta-related gene family";
RL Mol. Endocrinol. 6:1961-1968(1992).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST
CC TO OTHER MEMBERS OF THIS FAMILY, CAN NOT BE DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -!- TISSUE SPECIFICITY: PRIMARILY IN ADULT BONE MARROW, SPLEEN, THYMUS
CC AND ADIPOSE TISSUE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L06443; AA53034.1; -;
DR EMBL; S52658; AAB24876.1; -;
DR PIR; A46607; A46607.
DR HSSP; P18075; LBMP.
DR MGD; MGI:95686; Gdf3.
DR InterPro; IPR001111; -;
DR InterPro; IPR001839; -;
DR InterPro; IPR002400; -;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 22
FT PROPEP 23 252
FT CHAIN 253 366
FT DISULFID 266 331
FT DISULFID 295 363
FT DISULFID 113 113
FT CARBOHYD 308 308
FT CARBOHYD 165 165
FT CONFLICT 167 168
FT CONFLICT 313 313
FT CONFLICT 313 313
SQ SEQUENCE 366 AA; 41527 MW; EB2D7CBB4FA63E71 CRC64;

Query Match 25.6%; Score 162.5; DB 1; Length 366;
Best Local Similarity 35.1%; Pred. No. 3.5e-10;
Matches 40; Conservative 21; Mismatches 34; Indels 19; Gaps 7;
QY 5 NYCERNLENCVRLYIDFRODLGW-KWHEPKGYANFCGCP- ----YLRSDTTH 58
Db 264 NCFCHR- ----QLFINF-QDLGWHKWIAPKGMFMANCHGECFPMSTYLNSSN--Y 312

QY 59 STVLGLYNTLNPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVVKSCK 111
Db 313 AFQALMHMADPKVPKA-VCVPTKLSPLSMYQSDKNVILRHVEDMVVDECG 365
RESULT 100
GDF3_HUMAN STANDARD; PRT; 364 AA.
AC Q9NR23;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR (GDF-3).
GN GDF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorenz B., White K.E., Econs M.J., Strom T.M.;
RT "Transcripts in human map region 12p13.3";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST
CC TO OTHER MEMBERS OF THIS FAMILY, CAN NOT BE DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
DR EMBL; AF263538; AAF91389.1; -;
DR InterPro; IPR001839; -;
DR InterPro; IPR002405; -;
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 24
FT PROPEP 25 250
FT CHAIN 251 364
FT DISULFID 264 329
FT DISULFID 293 361
FT DISULFID 297 363
FT CARBOHYD 112 112
FT CARBOHYD 306 306
FT CONFLICT 306 306
SQ SEQUENCE 364 AA; 41387 MW; E0D2EA86E2B73A0B CRC64;
Query Match 25.2%; Score 160; DB 1; Length 364;
Best Local Similarity 34.3%; Pred. No. 6.5e-10;
Matches 36; Conservative 22; Mismatches 39; Indels 8; Gaps 6;
QY 13 ENCCVR-PLVIDFQDLGW-KWHEPKGYANFCGCP- ---LRSADTTHSVGLYNT 67
Db 261 KNLCRRQLFINFR-DLGWHKWIAPKGMFMANCHGECFPMSTYLNSSN- 319
QY 68 LNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
Db 320 VDPEIPA-QVCPTKLSPLSMYQSDKNVILRHVEDMVVDECG 363
Search completed: October 30, 2001, 08:54:30
Job time: 114 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 30, 2001, 08:52:11 ; Search time 18.1 Seconds
 (without alignments)
 825,993 Million cell updates/sec

Title: TGFB3P
 Perfect score: 634
 Sequence: 1 ALDTNCFERNLENCVRL.....RTPKVEQLSNMVKSCRSX 113

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
 425026

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SPTREMBL16:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.rodent:*
- 12: sp.unclassified:*
- 13: sp.vertibrate:*
- 14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	84.4	442	Q15579	Q15579 homo sapien
2	530	83.6	414	Q9R298	Q9R298 rattus norv
3	530	83.6	414	Q9R281	Q9R281 rattus norv
4	530	83.6	442	Q9WU08	Q9WU08 rattus norv
5	528	83.3	414	Q9R2B8	Q9R2B8 rattus norv
6	500	78.9	112	Q02730	Q02730 oryctolagus
7	491	77.4	390	Q9TUM8	Q9TUM8 equus caball
8	489	77.1	361	Q9R854	Q9R854 cyprinus ca
9	488	77.0	130	Q08714	Q08714 mesocricetu
10	482	76.0	399	Q9ERB7	Q9ERB7 mesocricetu
11	463	73.0	81	Q9N1S3	Q9N1S3 capreolus c
12	435	68.6	91	Q9WVZ1	Q9WVZ1 capra hircu
13	422	66.6	101	Q9R184	Q9R184 meriones un
14	412	65.0	86	Q28241	Q28241 cervus elap
15	404	63.7	382	Q93449	Q93449 oncorhynch
16	396	62.5	382	Q9PWA9	Q9PWA9 morone chry
17	375	59.1	376	Q9PTG2	Q9PTG2 cyprinus ca
18	339	53.5	76	Q9QW26	Q9QW26 rattus sp.
19	329	51.9	87	Q42306	Q42306 carassius a

20	230	36.3	50	6	Q28240	Q28240 cervus elap
21	223	35.2	62	13	Q9DEP5	Q9DEP5 scophthalmu
22	213.5	33.7	373	13	Q9DDI8	Q9DDI8 salar
23	208	32.8	354	13	Q9YGV1	Q9YGV1 xenopus lae
24	207	32.6	373	13	Q90723	Q90723 gallus gall
25	207	32.6	373	13	Q98950	Q98950 gallus gall
26	204.5	32.3	162	6	Q9TSF2	Q9TSF2 sus scrofa
27	204.5	32.3	375	6	Q9GM97	Q9GM97 equus caball
28	204	32.2	361	5	Q96504	Q96504 branchiosto
29	204	32.2	411	5	Q9U418	Q9U418 branchiosto
30	200	31.5	426	4	Q9HBP0	Q9HBP0 homo sapien
31	198	31.2	404	13	Q9PW65	Q9PW65 carassius a
32	197.5	31.2	367	13	Q91696	Q91696 xenopus lae
33	196.5	31.0	185	6	Q9MZ18	Q9MZ18 ovis aries
34	193	30.4	413	13	Q98860	Q98860 cynops pyrr
35	192	30.3	614	5	P91720	P91720 dirosophila
36	191.5	30.2	365	5	O02424	O02424 caenorhabdi
37	191.5	30.2	365	5	O76514	O76514 caenorhabdi
38	190	30.0	313	13	Q91403	Q91403 gallus gall
39	190	30.0	398	13	Q918T6	Q918T6 gallus gall
40	190	30.0	412	13	O12938	O12938 brachydanio
41	189	29.8	115	13	Q9DGF2	Q9DGF2 cyprinus ca
42	189	29.8	115	13	Q9DGE8	Q9DGE8 oryzias lat
43	189	29.8	177	4	Q9H512	Q9H512 homo sapien
44	189	29.8	438	5	Q9GT26	Q9GT26 anopheles s
45	188.5	29.7	370	13	Q91350	Q91350 xenopus lae
46	188	29.7	96	13	Q9W759	Q9W759 cairina mos
47	188	29.7	399	13	Q9W753	Q9W753 xenopus lae
48	188	29.7	405	5	Q9U5E8	Q9U5E8 ptychodera
49	188	29.7	432	13	Q9PTF9	Q9PTF9 brachydanio
50	187	29.5	345	13	Q9DFV1	Q9DFV1 eleutheroda
51	187	29.5	413	13	Q9DGN4	Q9DGN4 xenopus lae
52	186	29.3	178	5	Q25211	Q25211 junonia coe
53	186	29.3	261	13	Q9W6C0	Q9W6C0 brachydanio
54	185.5	29.3	115	13	Q9DGE9	Q9DGE9 cyprinus ca
55	185.5	29.3	390	13	Q91597	Q91597 xenopus lae
56	185.5	29.3	683	5	Q94580	Q94580 halocynthia
57	185	29.2	126	13	Q93573	Q93573 gallus gall
58	185	29.2	204	5	Q9XZ69	Q9XZ69 tripeustes
59	185	29.2	351	11	Q9WUK5	Q9WUK5 rattus norv
60	184.5	29.1	352	13	Q9PWR8	Q9PWR8 carassius a
61	184.5	29.1	393	13	Q90261	Q90261 brachydanio
62	183.5	28.9	115	13	Q9DGF1	Q9DGF1 cyprinus ca
63	183.5	28.9	115	13	Q9DGE6	Q9DGE6 oryzias lat
64	183.5	28.9	138	13	Q9W6T9	Q9W6T9 brachydanio
65	183	28.9	424	13	Q9TGH7	Q9TGH7 xenopus lae
66	183	28.9	500	13	Q9W6G0	Q9W6G0 gallus gall
67	182.5	28.8	99	13	Q93254	Q93254 pagrus majo
68	181.5	28.6	115	13	Q9DGF0	Q9DGF0 cyprinus ca
69	179.5	28.3	395	13	Q9PWG6	Q9PWG6 anguilla ja
70	179.5	28.3	411	13	O57573	O57573 brachydanio
71	179.5	28.3	411	13	O13108	O13108 brachydanio
72	179.5	28.3	411	13	O93369	O93369 brachydanio
73	179	28.2	443	5	O76851	O76851 halocynthia
74	179	28.2	453	13	P87373	P87373 gallus gall
75	178	28.1	115	13	Q9DGE7	Q9DGE7 oryzias lat
76	178	28.1	417	5	O9XXQ7	O9XXQ7 lytechinus
77	177.5	28.0	364	13	Q9PVK1	Q9PVK1 gallus gall
78	177.5	28.0	386	13	O13109	O13109 brachydanio
79	177	27.9	289	5	O9XTQ8	O9XTQ8 strongyloce
80	174.5	27.5	400	13	O57574	O57574 brachydanio
81	173	27.3	191	5	Q26468	Q26468 schistocerc
82	173	27.3	400	5	O76147	O76147 dugesia jap
83	172.5	27.2	586	5	O9VQG9	O9VQG9 drosophila
84	172	27.1	301	5	O97390	O97390 crassostrea
85	172	27.1	428	5	O16123	O16123 brugia paha
86	172	27.1	428	5	O16134	O16134 brugia mala
87	172	27.1	588	5	Q9VQC6	Q9VQC6 drosophila
88	171.5	27.1	102	13	Q90390	Q90390 carassius a
89	170.5	26.9	337	6	Q9MZV5	Q9MZV5 canis fami
90	169	26.7	120	13	Q9W6T8	Q9W6T8 brachydanio
91	169	26.7	257	13	O42303	O42303 brachydanio
92	168.5	26.6	104	13	Q98861	Q98861 cynops pyrr

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93 168.5 26.6 400 13 013107 brachydanio
94 168.5 26.6 421 11 0921V8 mus musculus
95 167.5 26.4 102 13 09DEF1 Q9det1 oncorhynch
96 165.5 26.1 400 13 073818 O73818 xenopus lae
97 165.5 26.1 400 13 091703 Q91703 xenopus lae
98 165 26.0 324 13 09YHW9 Q9yhw9 gallus gall
99 164 25.9 102 13 090388 Q90388 carassius a
100 162 25.6 83 13 P79707 P79707 cygnops pyrr

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ALIGNMENTS

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RESULT 1
Q15579 ID Q15579 PRELIMINARY; PRT; 442 AA.
AC Q15579;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA-2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAMOXIFEN-TREATED PROSTATIC ADENOCARCINOMA;
RX MEDLINE=88166349; PubMed=3162414;
RA Madisen L., Webb N.R., Rose T.M., Marquardt H., Ikeda T., Twardzik D.,
RA Seyedin S., Purchio A.F.;
RT "Transforming growth factor-beta 2: cDNA cloning and sequence
RT analysis.";
RL DNA 7:1-8(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TAMOXIFEN-TREATED PROSTATIC ADENOCARCINOMA;
RX MEDLINE=89090808; PubMed=2850146;
RA Webb N.R., Madisen L., Rose T.M., Purchio A.F.;
RT "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts
RT two different precursor proteins produced by alternative mRNA
RT splicing.";
RL DNA 7:493-497(1988).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; M19154; AAA50404.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 20 POTENTIAL.
FT CHAIN 331 442 POTENTIAL.
SQ SEQUENCE 442 AA; 50573 MW; 5D7A3C2ED51753D5 CRC64;

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Query Match 84.4%; Score 535; DB 4; Length 442;
Best Local Similarity 79.5%; Pred. No. 1.8e-52;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCGCPYLRSDATTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 331 ALDAAVCFRNVDNCCRLPYIDFRODLGKWKVHEPKGYANFCACPYLWSSDTQHSR 390

QY 61 VLGLYNTLNPEASPCVPPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 391 VLSLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 442

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RESULT 2
Q9R298 ID Q9R298 PRELIMINARY; PRT; 414 AA.
AC Q9R298;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TGF-BETA 2 SHORT FORM PRECURSOR.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=MUSCLE;
RA Koishi K., Daizell K.G.B., McLennan I.S.;
RT "Structure and expression of TGF-beta 2 messages in the rat muscle.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF153013; AAD34160.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 414 AA; 47727 MW; 485DFC04EC0CA291 CRC64;

Query Match 83.6%; Score 530; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 6.3e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCGCPYLRSDATTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 ALDAAVCFRNVDNCCRLPYIDFRODLGKWKVHEPKGYANFCACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASPCVPPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VLSLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 414

RESULT 3
Q9R281 ID Q9R281 PRELIMINARY; PRT; 414 AA.
AC Q9R281;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Plisov S.V., Ivanov S.V., Plisova T.M., Lerman M., Perantoni A.O.;
RT "Rat transforming growth factor-beta2, complete coding sequence.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF135598; AAD24484.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.

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SQ SEQUENCE 414 AA; 47711 MW; 485DE768E720B2D1 CRC64;

Query Match 83.6%; Score 530; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 6.3e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSPGCPYLRSDTTHST 60
DB 303 ALDAAFCFRVQNCCLRLPYIDFKRDLGKWKVHEPKGYANFCACACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 363 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 414

RESULT 4
Q9WUQ8 PRELIMINARY; PRT; 442 AA.
AC Q9WUQ8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TGF-BETA 2 LONG FORM PRECURSOR.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RA Koishi K., Dalzell K.G.B., McLennan I.S.;
RT "Structure and expression of TGF-beta 2 messages in the rat muscle.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF153012; AAD34159.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-B; 1.
KW Glycoprotein.
SQ SEQUENCE 442 AA; 50533 MW; 69C81A19CE06C253 CRC64;

Query Match 83.6%; Score 530; DB 11; Length 442;
Best Local Similarity 78.6%; Pred. No. 6.7e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSPGCPYLRSDTTHST 60
DB 331 ALDAAFCFRVQNCCLRLPYIDFKRDLGKWKVHEPKGYANFCACACPYLWSSDTQHTK 390

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 391 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 442

RESULT 5
Q9R2B8 PRELIMINARY; PRT; 414 AA.
AC Q9R2B8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TGF-BETA2 PROTEIN.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RA Konrad L., Albrecht M., Amueller G.;
RT "The rat TGF-beta2 gene: Sequence analysis and expression pattern in the rat testis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AJ132718; CAB42003.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-B; 1.
KW Glycoprotein.
SQ SEQUENCE 414 AA; 47689 MW; 3AEF0912F5B550D5 CRC64;

Query Match 83.3%; Score 528; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 1.1e-51;
Matches 88; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCSPGCPYLRSDTTHST 60
DB 303 ALDAAFCFRVQNCCLRLPYIDFKRDLGKWKVHEPKGYANFCACACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 363 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 414

RESULT 6
ID 002730 PRELIMINARY; PRT; 112 AA.
AC 002730; O97501;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGF-B1 OR TGF-BETA-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 2-99 FROM N.A.
RA Inoue K., Kawabe Y., Kodama T.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; AF000133; AAB53806.1; -.
DR EMBL; AB020217; BAA36950.1; -.
DR HSP; P01137; 1KLA.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1

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FT CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 7 16 BY SIMILARITY.
FT DISULFID 15 78 BY SIMILARITY.
FT DISULFID 44 109 BY SIMILARITY.
FT DISULFID 48 111 BY SIMILARITY.
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 2 3 LD -> FS (IN REF. 2).
FT CONFLICT 85 92 PLPIVYV -> ATAHRVTL (IN REF. 2).
SQ SEQUENCE 112 AA; 12795 MW; 53C5B7D4635A6F3 CRC64;

Query Match 78.9%; Score 500; DB 6; Length 112;
Best Local Similarity 76.8%; Pred. No. 4e-49;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTNCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHST 60
Db 1 ALDNTNCFSSTEKNCVRLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 60

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 61 VLALYNQHNPGASAPCCVPQALEPLIVYVGRKPKVEQLSNMIVRSCKS 112

RESULT 7
Q9TUM8 PRELIMINARY; PRT; 390 AA.
AC Q9TUM8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1.
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NIXON A.J., Brower-Toland B.T., Sandell L.J.;
RA "Molecular cloning of equine transforming growth factor beta 1 reveals
RT a divergent nucleotide structure that encodes a novel bioactive
RT peptide among mammalian species.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF175709; AAD49431.1; -.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
SQ SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match 77.48%; Score 491; DB 6; Length 390;
Best Local Similarity 75.9%; Pred. No. 1.5e-47;
Matches 85; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ALDNTNCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHST 60
Db 279 ALDNTNCFSSTEKNCVRLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 338

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 339 VLALYNQHNPGASAPCCVPQVLEPLIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 8
Q98854 PRELIMINARY; PRT; 361 AA.
ID Q98854

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AC Q98854;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT).
GN TGFb2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=HEART;
RX MEDLINE=97354301; PubMed=9210595;
RA Sumathi K., Desai K.V., Kondaiah P.;
RT "Isolation of transforming growth factor-beta2 cDNA from a fish,
RT Cyprinus carpio by RT-PCR.";
RL Gene 191:103-107(1997).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U66874; AAB62983.1; -.
DR HSSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1
FT PROPEP <1 257
FT CHAIN 258 361 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 264 273 BY SIMILARITY.
FT DISULFID 272 335 BY SIMILARITY.
FT DISULFID 334 334 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 361 361
SQ SEQUENCE 361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;

Query Match 77.1%; Score 489; DB 13; Length 361;
Best Local Similarity 77.9%; Pred. No. 2.4e-47;
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ALDNTNCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSADTTHST 60
Db 258 ALDAAFCFRNVQDNCRLSLYIDFRKDLGKWKVHEPKGYANFCAGACPYLWSADTQHSN 317

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNM 104
Db 318 ILGLYNTLNPEASPCVCSQDLEPLTILYIGTKPKIEQLSNM 361

RESULT 9
ID Q08714 PRELIMINARY; PRT; 130 AA.
AC Q08714; O70331;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGFb1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=LVG (SYR);
RX MEDLINE=93304479; PubMed=8317544;
RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA Elovic A., McBride J., Gallagher G., Todd R.;
RT "Sequential expression of transforming growth factors alpha and beta 1
RT by eosinophils during cutaneous wound healing in the hamster.";
RL Am. J. Pathol. 143:130-142(1993).
RN [2]
RP SEQUENCE OF 26-115 FROM N.A.
RC STRAIN=SYRIAN; TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis";
RL Infect. Immun. 66:2135-2142(1998).
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
CC EMBL; X60296; CAA42838.1; -.
DR HSP; P01137; IRLA.
DR InterPro; IPR001839; -.
DR Pfam; PF000019; TGF-beta; 1.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 18
FT CHAIN 19 130 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 25 34 BY SIMILARITY.
FT DISULFID 33 96 BY SIMILARITY.
FT DISULFID 66 129 BY SIMILARITY.
FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 93 93 G -> S (IN REF. 2).
SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;

Query Match 77.0%; Score 488; DB 11; Length 130;
Best Local Similarity 75.9%; Pred. No. 1.1e-47;
Matches 85; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
Db 19 ALDNYCFSTERNCCVRQYIDFRDLGKWKVHEPKGYHANFCLGPCPYIWSLDTOYSK 78

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
Db 79 VLALYNOHNEFGASGCGVQALEPLPIVYVVGKPKVEQLSNMIVRSYKCS 130

RESULT 10
Q9ERB7 PRELIMINARY; PRT; 399 AA.
AC Q9ERB7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA 2 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.

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RA Ramesh G., Kondaiah P., Seshagiri P.B.;
RT "Differential expression and selective localization of transforming
RT growth factor-beta isoforms in the hamster uterus during estrous
RT cycle.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007214; AAG02247.1; -.
FT NON_TER 1 1
FT NON_TER 399 399
SQ SEQUENCE 399 AA; 46078 MW; AGFF8E65EAFD5148 CRC64;

Query Match 76.0%; Score 482; DB 11; Length 399;
Best Local Similarity 76.9%; Pred. No. 1.6e-46;
Matches 80; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
Db 296 ALDRAAYCFRNVDNCCRLPLYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSDTHQYK 355

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGRTPKVEQLSNM 104
Db 356 VLSLYNTLNPEASASCCVSHDLEPLTILYIGNTPKIEQLSNM 399

RESULT 11
Q9NIS3 PRELIMINARY; PRT; 81 AA.
AC Q9NIS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 3 (FRAGMENT).
GN TGF-B3.
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Wagener A., Blottner S., Fickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus
RT capreolus)";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF152592; AAF73231.1; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9250 MW; 8515C856478E4BCC CRC64;

Query Match 73.0%; Score 463; DB 6; Length 81;
Best Local Similarity 98.8%; Pred. No. 4.4e-45;
Matches 80; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 EENCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
Db 1 EENCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 60

QY 72 ASASPCCVQDLEPLTILYV 92
Db 61 ASASPCCVQDLEPLTILYV 81

RESULT 12
Q9MYZ1 PRELIMINARY; PRT; 91 AA.
AC Q9MYZ1;

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TGF BETA 2 (FRAGMENT).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARIAN FOLLICLE;
RA Wang B., Zhang Y.;
RT "Goat ovarian TGF beta 2 cDNA sequence.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF276986; AAF87742.1; -;
DR InterPro; IPR001839; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 91 91
SQ SEQUENCE 91 AA; 10412 MW; 59694FP30EAA1FAA CRC64;

Query Match 68.6%; Score 435; DB 6; Length 91;
Best Local Similarity 79.1%; Pred. No. 7.2e-42;
Matches 72; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 9 RNLENCVRLYIDFRDGLGWKWHKPGYANFCSPCYLRSADTHTSTVLGLYNTL 68
Db 1 RNVQDNCCLRLYIDFRDGLGWKWHKPGYANFCAGCPYLWSADTQHSRVLNTI 60

QY 69 NPEASAPCCVPQDLEPLTILYVGRTPKVE 99
Db 61 NPEASAPCCVSDLEPLTILYIGTPKIE 91

RESULT 13
Q9R184 PRELIMINARY; PRT; 101 AA.
AC Q9R184;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGFBI OR TGF-BETA.
OS Meriones unguiculatus (Mongolian jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPH NODE;
RA Rao U.R., Klei T.R.;
RT "cDNA cloning of gerbil transforming growth factor-beta by PCR.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF161218; AAD45726.1; -;
DR HSP; P01137; 1KLA.
DR InterPro; IPR001839; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFBI; 1.

KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >101 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 1 10 BY SIMILARITY.
FT DISULFID 9 72 BY SIMILARITY.
FT DISULFID 71 71 INTERCHAIN (BY SIMILARITY).
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 11724 MW; ABF1CFDA264AEFD CRC64;

Query Match 66.6%; Score 422; DB 11; Length 101;
Best Local Similarity 73.3%; Pred. No. 2.4e-40;
Matches 74; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 7 CERNLENCVRLYIDFRDGLGWKWHKPGYANFCSPCYLRSADTHTSTVLGLYN 66
Db 1 CFSSTKNCVRLYIDFRDGLGWKWHKPGYANFCGLGCPYINSLHTQYSKVLALYN 60

QY 67 TLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVK 107
Db 61 QHNPASAPCCVPQALEPLIVYVGRPKVEQLSNMFEVR 101

RESULT 14
Q28241 PRELIMINARY; PRT; 86 AA.
AC Q28241;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT).
GN TGFBI OR TGF-BETA-2.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ANTLER;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U62111; AAB05257.1; -;
DR HSP; P08112; 2TGI.
DR InterPro; IPR001839; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFBI; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >86 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 4 67 BY SIMILARITY.
FT DISULFID 66 66 INTERCHAIN (BY SIMILARITY).
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9848 MW; A5AE8B62D78E80E5 CRC64;

Query Match 65.0%; Score 412; DB 6; Length 86;
Best Local Similarity 79.1%; Pred. No. 2.7e-39;
Matches 68; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 12 ENCCVRLYIDFRDGLGWKWHKPGYANFCSPCYLRSADTHTSTVLGLYNTLN 71
Db 1 QDNCCLRLYIDFRDGLGWKWHKPGYANFCAGCPYLWSADTQHSRVLNTINPE 60


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QY 72 ASASPCCVQDLEPLTILYVGRTPK 97
Db 61 ASASPCCVSODLEPLTILYMGTPK 86

RESULT 15
O93449 PRELIMINARY; PRT; 382 AA.
AC O93449; Q91217;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA PRECURSOR.
GN TGF-BETA OR TGF.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEUKOCYTE;
RX MEDLINE=99242020; PubMed=10227481;
RA Daniels G.D., Secombes C.J.;
RT "Genomic organisation of rainbow trout, Oncorhynchus mykiss TGF-
RT BETA."
RL Dev. Comp. Immunol. 23:139-147(1999).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=LEUKOCYTE;
RX MEDLINE=98390168; PubMed=9722928;
RA Hardie L.J., Laing K.J., Daniels G.D., Grabowski P.S., Cunningham C.,
RA Secombes C.J.;
RT "Isolation of the first piscine transforming growth factor beta gene:
RT analysis reveals tissue specific expression and a potential regulatory
RT sequence in rainbow trout (Oncorhynchus mykiss).";
RL Cytokine 10:555-563(1998).
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY
CC MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AJ007836; CAA07707.1; -.
DR EMBL: X93303; CAA67685.1; -.
DR HSSP: P01137; IKLA.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR InterPro: IPR002400; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD000357; -. 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR SMART: SM00204; TGFB; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 270
FT CHAIN 271 382
FT DISULFID 278 286
FT DISULFID 285 348
FT DISULFID 314 379
FT DISULFID 318 381
FT DISULFID 347 347
FT CARBOHYD 73 73
FT CARBOHYD 108 108
FT CARBOHYD 113 113
FT CARBOHYD 124 124
FT CARBOHYD 259 259
FT CONFLICT 371 372
FT CONFLICT 377 377
FT CONFLICT 382 AA; 44136 MW; 93BD4D3540084B92 CRC64;
SQ SEQUENCE 382 AA; 44136 MW; 93BD4D3540084B92 CRC64;

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Query Match 63.7%; Score 404; DB 13; Length 382;
Best Local Similarity 69.0%; Pred. NO. 1e-37;
Matches 69; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 13 ENCCVRPLIIDFRODLGKWKVHEPKGYANFCSPGCPYLRSDTTHSTVGLYNTLNPEA 72
Db 283 ESCCKRLYIDFRKDLGKWKIHEPTGYFANYCIGCTCTWNTENKYSQVLALYKHHNPGA 342
QY 73 SASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
Db 343 SAQCCCVQVLEPLPIIYVGRHQKVEQLSNMIVASCRC 382

RESULT 16
O9PWA9 PRELIMINARY; PRT; 382 AA.
AC O9PWA9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA PRECURSOR.
GN TGF-BETA.
OS Morone chrysops x Morone saxatilis (white bass x striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=45352;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=KIDNEY;
RX MEDLINE=20394636; PubMed=10938723;
RA Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
RA Tompkins W.A.F.;
RT "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
RT chrysops) transforming growth factor-beta (TGF-beta), and development
RT of a reverse transcription quantitative competitive polymerase chain
RT reaction (RT-qPCR) assay to measure TGF-beta mRNA of teleost fish.";
RL Fish Shellfish Immunol. 10:61-85(2000).
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
CC PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF140363; AAD46997.1; -.
DR HSSP: P01137; IKLA.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFB_propeptide; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR SMART: SM00204; TGFB; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 270
FT CHAIN 271 382
FT DISULFID 278 286
FT DISULFID 285 348
FT DISULFID 314 379
FT DISULFID 318 381
FT DISULFID 347 347
FT CARBOHYD 73 73
FT CARBOHYD 108 108
FT CARBOHYD 113 113
FT CARBOHYD 124 124
FT CARBOHYD 259 259
FT SITE 235 237
FT SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;
SQ SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;

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Query Match 62.5%; Score 396; DB 13; Length 382;

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Best Local Similarity 69.0%; Pred. No. 8.3e-37;
Matches 69; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

Qy 13 ENCCVRPLYIDFRODLGKWKVHEPKGYVANFCGPGPYLRSDTHTSVGLYNTLNPEA 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 ETCCVRSYIDFRODLGKWKIHKPTGYNANYCMGCTIYWAENKYSQILAYKHHNPCA 342

Qy 73 SASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 343 SAOPCCVQALEPLILYVGRQHKVEQLSNMVKSKCS 382

RESULT 17
Q9PTQ2 PRELIMINARY; PRT; 376 AA.
AC Q9PTQ2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA PRECURSOR.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin Z., Kuang J.;
RT "Molecular cloning of carp transforming growth factor beta 1.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF136947; AAF22573.1; -.
DR HSSP; P01137; IKLA.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 22
FT PROPEP 23 264
FT CHAIN 265 376
FT DISULFID 272 280
FT DISULFID 308 373
FT DISULFID 312 375
FT DISULFID 341 341
FT CARBOHYD 76 76
FT CARBOHYD 125 125
FT CARBOHYD 167 167
FT SITE 230 232
FT SITE 232 232
SQ SEQUENCE 376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;

Query Match 59.1%; Score 375; DB 13; Length 376;
Best Local Similarity 59.6%; Pred. No. 1.9e-34;
Matches 65; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

Qy 3 DTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYVANFCGPGPYLRSDTHTSVL 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 ETQVCTDKSGCCVRSYIDFRODLGKWKIHKPTGYNANYCMGCTIYWAENKYSQILAYKHHNPCA 342

Qy 63 GLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKC 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 ALYKHNPASACQRCVQVNLNPLFIYVGRQHKVEQLSNMVKSKC 375

RESULT 18
Q9QW26 PRELIMINARY; PRT; 76 AA.
AC Q9QW26;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA ISOFORM 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93253033; PubMed-8486763;
RA Nishida M., Springhorn J.P., Kelly R.A., Smith T.W.;
RL J. Clin. Invest. 91:1934-1941(1993).
DR HSSP; P08112; 2TGT.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

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ID Q9QW26 PRELIMINARY; PRT; 76 AA.
AC Q9QW26;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA ISOFORM 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93253033; PubMed-8486763;
RA Nishida M., Springhorn J.P., Kelly R.A., Smith T.W.;
RL J. Clin. Invest. 91:1934-1941(1993).
DR HSSP; P08112; 2TGT.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

Query Match 53.5%; Score 339; DB 11; Length 76;
Best Local Similarity 76.3%; Pred. No. 4.3e-31;
Matches 58; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 36 PKGYANFCGPGPYLRSDTHTSVGLYNTLNPEASPCVQDLEPLTILYVGR 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 PKGYANFCAGACPYLRSSDTHTKVLSTNTINPEASPCVQDLEPLTILYVGR 60

Qy 96 PKVEQLSNMVKSKC 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PKIEQLSNMIVRACNC 76

RESULT 19
Q42306 PRELIMINARY; PRT; 87 AA.
AC Q42306;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE;
RA Daniels G.D., Belosevic M., Secombes C.J.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AJ001040; CAA04494.1; -.
DR HSSP; P01137; IKLA.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

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[illegible]

Query Match	35.2%	Score 223;	DB 13;	Length 62;
Best Local Similarity	58.1%;	Pred. No. 4.6e-18;		
Matches	36;	Conservative 10;	Mismatches 16;	Indels 0; Gaps
Qy	23	DFRDLGKKWVHEPKGYIANFCSGPCPYLRSDTTHSTVLGLYNTLNPEASASCCVPPQD	82	
		: : : : : : : : : : : : : : : :		
Db	1	DFRDLGXWTHKKTGYHANCYCMGCTYVWNAENKYSILALYKHHPGASQAQCCVPPQA	60	
Qy	83	LE 84		
Db	61	LE 62		

RA	Ostbye T.K.;			
RT	"the myostatin gene is expressed in multiple organs of Atlantic			
RT	salmon."			
RL	Submitted.			
RL	Submitted (DEC-2000) to the EMBI/GenBank/DBJ databases.			
DR	EMBL; AJ297267; CAC19541.1; -			
FW	Signal.			
KW	Signal.	1	21	POTENTIAL.
FT	CHAIN	265	373	MYOSTATIN.
FT	CHAIN			
SQ	SEQUENCE	373 AA;	41878 MW;	C355D71D83B66C4D C8G64;

Query Match 33.7%; Score 213.5; DB 13; Length 373;

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Best Local Similarity 38.0%; Pred. No. 3.6e-16;
Matches 41; Conservative 13; Mismatches 37; Indels 17; Gaps 4;

QY 12 EENCVRPLYIDFRODLGKWWHEPKGYANFCGPGCPYLSADTHSTVLGLYNTLNP 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 276 ESRCCRYPLTVDF-EDFGWDWLIAPKRYKANYCSECEYMHQKYPHT---HLVKNANPR 331
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 72 ASASPCCVQDLEPLTILY-----VGRTPKVEQLSNMVMVVKSCKS 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 332 GTAGPCCTPTKMSPINMLYFNKRKEQIYKIPSI-----VVDRCGCS 373

RESULT 23
Q9YGV1
ID Q9YGV1 PRELIMINARY; PRT; 354 AA.
AC Q9YGV1;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE DERRIERE.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Sun B.I., Bush S.M., Collins-Racie L.A., Lavallie E.R.,
RA DiBalsio-Smith E.A., Wolfman N.M., McCoy J.M., Sive H.L.;
RT "derriere: a TGF-beta family member required for posterior development
RT in Xenopus.";
RL Development 126:1467-1482(1999).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF065135; AAD19837.1; -
DR HSSP: P18075; IBMP.
DR InterPro: IPR001111; -
DR InterPro: IPR001839; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00688; TGF-beta; 1.
DR PRODOM: PD000357; -; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 354 AA; 40316 MW; 879CAE9A23F2E42F CRC64;

Query Match 32.8%; Score 208; DB 13; Length 354;
Best Local Similarity 42.3%; Pred. No. 1.4e-15;
Matches 44; Conservative 15; Mismatches 35; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRODLGKWWHEPKGYANFCGPGCPY-----LRSADTHSTVLGLYNTL 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 CKKRRLYIDFK-DVGQWQWLIAPKRYKANYCSECEYPLTLEMLRG--TNHVLQTLVHSV 309
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 NPEASPCCVQDLEPLTILYVGRTPKV-EQLSNMVMVVKSCKC 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 310 EPENTPLPCCAPTLPSPISMLYDNNVLRHVEDMVMVDECGC 353

RESULT 24
Q90723
ID Q90723 PRELIMINARY; PRT; 373 AA.
AC Q90723;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GROWTH FACTOR CVG1.
GN CVG1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
NCBI_TaxID=9031;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN;
RA Shah S.B., Hume C.R., Dodd J.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: U55871; AAB01194.1; -
DR HSSP: P18075; IBMP.
DR InterPro: IPR001111; -
DR InterPro: IPR001839; -
DR InterPro: IPR002400; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00688; TGF-beta; 1.
DR PRODOM: PD000357; -; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41405 MW; E2ACFCCCD3A4C8B5 CRC64;

Query Match 32.6%; Score 207; DB 13; Length 373;
Best Local Similarity 41.2%; Pred. No. 1.9e-15;
Matches 42; Conservative 18; Mismatches 36; Indels 6; Gaps 4;

QY 15 CCVRPLYIDFRODLGKWWHEPKGYANFCGPGCPYLSAD---TTHSTVLGLYNTLNP 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 272 CKPRLYISF-SDVGWQWLIAPKRYKANYCSECEYPLTLEMLNSTHAILQTMVHSLDP 330
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 EASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVMVVKSCKC 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 331 EGTPOPCCVPLSPISILYDNNVLRHVEDMVMVDECGC 372

RESULT 25
Q98950
ID Q98950 PRELIMINARY; PRT; 373 AA.
AC Q98950;
DT 01-FEB-1997 (TremBLrel. 02, Created)
DT 01-FEB-1997 (TremBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE VGL.
GN CVG1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
NCBI_TaxID=9031;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97147815; PubMed=8939612;
RA Seleiro E.A.P., Connolly D.J., Cooke J.;
RT "Early developmental expression and experimental axis determination by
RT the chicken Vgl gene.";
RL Curr. Biol. 6:1476-1486(1996).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: U73003; AAC60038.1; -
DR HSSP: P18075; IBMP.
DR InterPro: IPR001111; -
DR InterPro: IPR001839; -
DR InterPro: IPR002400; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00688; TGF-beta; 1.
DR PRODOM: PD000357; -; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41503 MW; 9FADC8212145602E CRC64;

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Query Match          32.6%; Score 207; DB 13; Length 373;
Best Local Similarity 41.2%; Pred. No. 1.9e-15;
Matches 42; Conservative 18; Mismatches 36; Indels 6; Gaps 4;

QY 15 CCVRPLVYIDFRODLGKWK-VWHEPKGYANFCSPGCPYLRSD---TTHSTVGLGYNLNP 70
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 272 CKPRRLYISF-SDVGWENWIIAPQGYMANYCIGCECFPLTAELNSTNHAILQTMVHSLDP 330
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 71 EASAPCCVPQDLPLETLILYVGRTPKV-EQLSNMVVKSKCK 111
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 331 EGTPOPCVPRVLSPIISILYDSDNVLRHYEDMVVDECG 372
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 26
Q9TSY2 PRELIMINARY; PRT; 162 AA.
AC Q9TSY2;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE MYOSTATIN (FRAGMENT).
GN MSTN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20078370; PubMed=10612246;
RA Stratil A., Kopecky M.;
RT "Genomic organization, sequence and polymorphism of the porcine
RT myostatin (GDF8; MSTN) gene.";
RL Anim. Genet. 30:468-470(1999).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AJ237920; CAB40844.1; -.
DR HSSP; PI8075; IBMP.
DR InterPro; IPR001839; -.
DR pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
DR KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;

Query Match          32.3%; Score 204.5; DB 6; Length 162;
Best Local Similarity 39.4%; Pred. No. 1.6e-15;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 ENCCVRPLVYIDFRODLGKWKVWHEPKGYANFCSPGCPYLRSD---TTHSTVGLGYNLNP 69
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 65 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTH-----LVHQAN 118
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 70 PEASAPCCVPQDLPLETLILYVGRTPKV-EQLSNMVVKSKCKS 112
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 119 PRGSAGPCTPTKMSPINMLYFNQKEQIYKIPAMVVDRGCGS 162
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 27
Q9GM97 PRELIMINARY; PRT; 375 AA.
AC Q9GM97;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE MYOSTATIN.
GN MSTN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

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OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Hosoyama T., Yamouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033541; BAB16046.1; -.
SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;

Query Match          32.3%; Score 204.5; DB 6; Length 375;
Best Local Similarity 39.4%; Pred. No. 3.7e-15;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 ENCCVRPLVYIDFRODLGKWKVWHEPKGYANFCSPGCPYLRSD---TTHSTVGLGYNLNP 69
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTH-----LVHQAN 331
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 70 PEASAPCCVPQDLPLETLILYVGRTPKV-EQLSNMVVKSKCKS 112
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 332 PRGSAGPCTPTKMSPINMLYFNQKEQIYKIPAMVVDRGCGS 375
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 28
Q96504 PRELIMINARY; PRT; 361 AA.
AC Q96504;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4.
GN AMPH1BP2/4.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98401944; PubMed=9733108;
RA Panopoulou G.D., Clark M.D., Holland L.Z., Lehrach H., Holland N.D.;
RT "Amph1BP2/4, an amphioxus bone morphogenetic protein closely related
RT to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
RT into evolution of dorsoventral axis specification.";
RL Dev. Dyn. 213:130-139(1998).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF068750; AAC97488.1; -.
DR HSSP; PI8075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR pfam; PF00019; TGF-beta; 1.
DR pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBIN.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
DR KW Glycoprotein.
SQ SEQUENCE 361 AA; 41517 MW; 09FF5FE6C9785DD1 CRC64;

Query Match          32.2%; Score 204; DB 5; Length 361;
Best Local Similarity 40.9%; Pred. No. 4.1e-15;
Matches 45; Conservative 15; Mismatches 40; Indels 10; Gaps 5;

QY 9 RNLENCVRPLVYIDFRODLGKWK-VWHEPKGYANFCSPGCPYLRSD---TTHSTVGLGYNLNP 62
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 254 RRLKANCRRHSLYVDF-SDVGWWDWIIAPQGYMANYCIGCECFPLTAELNSTNHAILQTMVHSLDP 310
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 63 GLYNTLNPASAPCCVPQDLPLETLILYVGRTPKV-EQLSNMVVKSKCK 111
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 311 TLVNSVNPVAPKACCVPTDLSPIISILYDSDNVLRHYEDMVVDECG 360
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RESULT 29
Q9U418          PRELIMINARY;      PRT;    411 AA.
AC
Q9U418;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4.
GN BMP2/4.
OS Branchiostoma belcheri.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasui K., Saiga H., Uemura M., Samba I.;
RT "Early body formation and expression pattern of genes encoding
RT secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF206325; AAF19841.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
DR KW Glycoprotein.
SQ SEQUENCE 411 AA; 46929 MW; F579898060F18355 CRC64;

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Query Match      32.2%; Score 204; DB 5; Length 411;
Best Local Similarity 40.9%; Pred. No. 4.7e-15;
Matches 45; Conservative 15; Mismatches 40; Indels 10; Gaps 5;

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QY 9 RNLENCVRLYIDFRODLGK-WVHEPKGYANFCGPGCPY-----LRSDTTHSTVL 62
DB 304 RRLKANCRRHSLYVDF-SDVGNDWIVAPGYQAYYCHGCPFLADHLNS--TNHAIVQ 360
QY 63 GLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
DB 361 TLVSNVPLAVPKACCVPTDLSPISMLYLNENDQVLKNYQDMVVEGCGC 410

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RESULT 30
Q9HBPO          PRELIMINARY;      PRT;    426 AA.
AC
Q9HBPO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 47.5 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qiu W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel Human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218018; AAG17260.1; -.
KW Hypothetical protein.
SQ SEQUENCE 426 AA; 47454 MW; 339276317B5B408 CRC64;

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Query Match      31.5%; Score 200; DB 4; Length 426;
Best Local Similarity 37.4%; Pred. No. 1.4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;
QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGCP-----YLRSADTTHSTVLGLYNTL 68
DB 321 CCKKQFVFK-DIGWNDWIIAPSGYHANYCEGECPSHIASTGSSLSFHSSTVINHYMR 379
QY 69 --NPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVVKSKC 112
DB 380 GHSPPFANLASCCTVTKLRPMSMLYYDQGNIIKKDIQNMIVEEGCS 426

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RESULT 31
Q9PW65          PRELIMINARY;      PRT;    404 AA.
AC
Q9PW65;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN, PITUITARY;
RA Yam K.M., Yu K.L., Ge W.;
RT "Cloning and characterization of activin beta A subunit.";
RL Mol. Cell. Endocrinol. 0:0-0(1999).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF169032; AAD50448.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRINTS; PR00670; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
DR KW Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 289 404 ACTIVIN BETA A.
SQ SEQUENCE 404 AA; 44799 MW; 3AFB41BE62A8C0DC CRC64;

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Query Match      31.2%; Score 198; DB 13; Length 404;
Best Local Similarity 38.0%; Pred. No. 2.2e-14;
Matches 41; Conservative 19; Mismatches 36; Indels 12; Gaps 6;
QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGCP-----YLRSADTTHSTVLGLYNT- 67
DB 299 CCKRQFYVFK-DIGWSDWIIAPSGYHANYCEGECPSHVASITGSSLSFHSSTVINHYMR 357
QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 112
DB 358 GYSPFNKSCCVPTLRAMSLYY-NESQIKKDIQNMIVEEGCS 404

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RESULT 32
Q91696          PRELIMINARY;      PRT;    367 AA.
AC
Q91696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN D PRECURSOR.

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OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=95275314; PubMed=7755637;
 RA Oda S., Nishimatsu S., Murakami K., Ueno N.;
 RT "Molecular cloning and functional analysis of a new activin beta
 subunit: a dorsal mesoderm-inducing activity in Xenopus";
 RL Biochem. Biophys. Res. Commun. 210:581-588(1995).
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; D49543; BAA08494.1; -;
 DR HSSP; P18075; LBMP.
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta-propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; -; 1.
 DR ProSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR Glycoprotein; Signal.
 FT SIGNAL 1 253 POTENTIAL.
 FT CHAIN 254 367 'ACTIVIN D',
 SQ SEQUENCE 367 AA; 41729 MW; C7B6334BD606FA04 CRC64;

Query Match 31.2%; Score 197.5; DB 13; Length 367;
 Best Local Similarity 36.0%; Pred. No. 2.3e-14;
 Matches 41; Conservative 25; Mismatches 35; Indels 13; Gaps 6;
 QY 10 NLEEN---CCVRPLIDFRQDLGWK-WVHEPKGYANFCGPGCPYLRS-----ADTHST 60
 DB 256 NCDQSNLCCKRDYVDFK-DIGWMDWIIPKGYQINCYCMGLCPMHIAAGPMAASFHTT 314
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKCS 112
 DB 315 VLNLKANNIQTAVNSCCVPTRRPLMLYF--DRNNVLKTDIADMIVEACGCS 367

RESULT 33
 Q9MZ18
 ID Q9MZ18 PRELIMINARY; PRT; 185 AA.
 AC Q9MZ18;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE MYOSTATIN (FRAGMENT).
 GN MSTN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lian Z., Jin H., Li N.;
 RT "Cloning of intron 2 of the myostatin gene in sheep";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; AF266758; AAF78069.1; -;
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProSITE; PS00250; TGF_BETA; 1.
 DR Glycoprotein.
 KW NON_TER 1 185
 FT NON_TER 185
 SQ SEQUENCE 185 AA; 20923 MW; BA963420A3A552850 CRC64;

Query Match 31.0%; Score 196.5; DB 6; Length 185;
 Best Local Similarity 38.4%; Pred. No. 1.4e-14;
 Matches 38; Conservative 16; Mismatches 40; Indels 5; Gaps 3;
 QY 12 EENCVRPLIDFRQDLGWKWHPEPKGYANFCGPGCPYLRSADTHSTHVLGLYNTLPE 71
 DB 90 ESRCCRYPLTVDF-EAFGWDWIIPKRYKANYCCEFLFLQKYPHT---HLVHOANPK 145
 QY 72 ASASPCCPVQDLEPLTILYVGRTPKV--EQLSNMVKSKC 109
 DB 146 GSAGPCCTPKMSPINMLYFNKKEQLIYKIPGMVVDRC 184
 RESULT 34
 Q98860
 ID Q98860 PRELIMINARY; PRT; 413 AA.
 AC Q98860;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ACTIVIN BETA-A SUBUNIT.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=96295508; PubMed=8702409;
 RA Yamamoto T., Nakayama Y., Abe S.;
 RT "Expression of activin beta subunit genes in Sertoli cells of newt
 testes";
 RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; D84516; BAA12693.1; -;
 DR HSSP; P18075; LBMP.
 DR InterPro; IPR000491; -;
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta-propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00670; INHIBINB.
 DR ProDom; PD000357; -; 1.
 DR ProSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF-beta; 1.
 KW Glycoprotein.
 SQ SEQUENCE 413 AA; 46303 MW; 46F66D112AA1B010 CRC64;

Query Match 30.4%; Score 193; DB 13; Length 413;
 Best Local Similarity 38.3%; Pred. No. 8.2e-14;
 Matches 41; Conservative 17; Mismatches 39; Indels 10; Gaps 6;
 QY 15 CCVRPLIDFRQDLGWK-WVHEPKGYANFCGPGCP-YLR-----SADTHSTHVLGLYNT- 67
 DB 308 CCKKQFYVSEK-DIGWSDWVIAPPGYATANYCEGDCPMYITGSGSPSFHAAVINOYRMR 366
 QY 68 -LNPEASAPCCVPQDLEPLTILY-VGRTPKVELSNMVKSKCS 112
 DB 367 GYSPTSVKSCCVPTKLRAMSLYDDGQNIKKDIQNMVVEECGS 413
 RESULT 35
 P91720
 ID P91720 PRELIMINARY; PRT; 614 AA.
 AC P91720;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE DECAPENTAPLEGIC PROTEIN.

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GN DPP.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97225212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL Genetics 145:297-309(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U63855; AAC47555.1; -.
DR HSSP; P18075; 1BWP.
DR FlyBase; FBgn0013109; Dvir\dpp.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Glycoprotein.
KW SEQUENCE 614 AA; 69055 MW; D0F20A4093403DCE CRC64;
SQ

Query Match 30.3%; Score 192; DB 5; Length 614;
Best Local Similarity 40.0%; Pred. No. 1.6e-13;
Matches 44; Conservative 14; Mismatches 42; Indels 10; Gaps 5;

QY 9 RNLENCVRLYIDFRDLGK-WVHEPKGYANFCGCPY-----LRSDTTHSTVL 62
Db 507 KNEEDNCRRHSLYVDF-ODVGSWDIVAPPGYDAYCHGKQFPLADHLNS--TNHAVVQ 563
QY 63 GLYNTLNPEASASPCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
Db 564 TLVNLNPGKVPKACCVPTQLEGISMLYLNQRTVVLKYNQDMTVVGGCG 613

RESULT 36
O02424 SEQUENCE FROM N.A.
ID O02424 PRELIMINARY; PRT; 365 AA.
AC O02424;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN HOMOLOG.
GN DBL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Yandell M.D., Ross R.M., Suzuki Y., Wood W.B.;
RT "Characteristics of dbl-1, a C. elegans decapentaplegic homologue,
RT support a conserved role for BMP-family signaling in bilaterian
RT development.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF004395; AAC27729.1; -.
DR HSSP; P18075; 1BWP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.

Query Match 30.3%; Score 192; DB 5; Length 614;
Best Local Similarity 40.0%; Pred. No. 1.6e-13;
Matches 44; Conservative 14; Mismatches 42; Indels 10; Gaps 5;

QY 9 RNLENCVRLYIDFRDLGK-WVHEPKGYANFCGCPY-----LRSDTTHSTVL 62
Db 507 KNEEDNCRRHSLYVDF-ODVGSWDIVAPPGYDAYCHGKQFPLADHLNS--TNHAVVQ 563
QY 63 GLYNTLNPEASASPCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
Db 564 TLVNLNPGKVPKACCVPTQLEGISMLYLNQRTVVLKYNQDMTVVGGCG 613

RESULT 36
O02424 SEQUENCE FROM N.A.
ID O02424 PRELIMINARY; PRT; 365 AA.
AC O02424;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN HOMOLOG.
GN DBL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Yandell M.D., Ross R.M., Suzuki Y., Wood W.B.;
RT "Characteristics of dbl-1, a C. elegans decapentaplegic homologue,
RT support a conserved role for BMP-family signaling in bilaterian
RT development.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF004395; AAC27729.1; -.
DR HSSP; P18075; 1BWP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.
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DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 365 AA; 41768 MW; 937BFF3459F02C7E CRC64;

Query Match 30.2%; Score 191.5; DB 5; Length 365;
Best Local Similarity 39.6%; Pred. No. 1.1e-13;
Matches 42; Conservative 16; Mismatches 41; Indels 7; Gaps 5;

QY 12 ENCCVVR-PLYIDFRDLGK-WVHEPKGYANFCGCPYLRSD---TTHSTVLGLYN 66
Db 260 ESNLCRRDTFYVDF-DDLNWQDWIMAPKGYDAYQCQSCPNPMPAQLNATNHAIQSLH 318
QY 67 TLNPEASASPCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
Db 319 SLRPDEVPPPCVPTETSPLSILYMDVKVIVIREYADMRVESC 364

RESULT 37
O76514 PRELIMINARY; PRT; 365 AA.
ID O76514;
AC O76514;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CET-1.
GN CET-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Morita K., Chow K.L., Ueno N.;
RT "Body length and Male Tail Ray Pattern Formation of C. elegans are
RT Regulated by a Member of TGFb Family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF074395; AAC26791.1; -.
DR HSSP; P18075; 1BWP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 365 AA; 41781 MW; 4DCEFE5C528BA3FF CRC64;

Query Match 30.2%; Score 191.5; DB 5; Length 365;
Best Local Similarity 39.6%; Pred. No. 1.1e-13;
Matches 42; Conservative 16; Mismatches 41; Indels 7; Gaps 5;

QY 12 ENCCVVR-PLYIDFRDLGK-WVHEPKGYANFCGCPYLRSD---TTHSTVLGLYN 66
Db 260 ESNLCRRDTFYVDF-DDLNWQDWIMAPKGYDAYQCQSCPNPMPAQLNATNHAIQSLH 318
QY 67 TLNPEASASPCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
Db 319 SLRPDEVPPPCVPTETSPLSILYMDVKVIVIREYADMRVESC 364

RESULT 38
O91403 PRELIMINARY; PRT; 313 AA.
ID O91403;
AC O91403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
```


Db 367 MNPSNPPSCCVPSKLSPIISILYIDAGNNVYKQYEDMVVSCGC 411

RESULT 41

Q9DGF2 ID Q9DGF2 PRELIMINARY; PRT; 115 AA.
AC Q9DGF2
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT "Cloning and sequencing of carp and medaka activin subunit genes."
RL Fisheries Sci. 64:680-685(2000).
DR EMBL; AB009403; BAB17596.1; -.
FT NON_TER 1 115
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 13139 MW; 8C8C7C7A784E51D2 CRC64;

Query Match 29.8%; Score 189; DB 13; Length 115;
Best Local Similarity 36.4%; Pred. No. 6.2e-14;
Matches 39; Conservative 20; Mismatches 36; Indels 12; Gaps 6;

Qy 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNT- 67

Db 11 CCKRQFYVNEK-DIGWSDWIAPSGYHANYCEGDCPIHVASIMGSALSFSHTVINHYRMR 69

Qy 68 -LNPEASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111

Db 70 GYSPFNKSCCVPTLRAMSL-YCNEEQKIIRKDIQNNMIVECGC 115

RESULT 42

Q9DGE8 ID Q9DGE8 PRELIMINARY; PRT; 115 AA.
AC Q9DGE8
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT "Cloning and sequencing of carp and medaka activin subunit genes."
RL Fisheries Sci. 64:680-685(2000).
DR EMBL; AB009407; BAB17600.1; -.
FT NON_TER 1 115
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 13127 MW; 9062BE7BC85BA432 CRC64;

Query Match 29.8%; Score 189; DB 13; Length 115;
Best Local Similarity 36.4%; Pred. No. 6.2e-14;
Matches 39; Conservative 20; Mismatches 36; Indels 12; Gaps 6;

Qy 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNT- 67

Db 11 CCKRQFYVNEK-DIGWSDWIAPSGYHANYCEGDCPIHVASIMGSALSFSHTVINHYRMR 69

Qy 68 -LNPEASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111

Db 70 GYSPFNKSCCVPTLRAMSL-YCNEEQKIIRKDIQNNMIVECGC 115

RESULT 43

Q9H512 ID Q9H512 PRELIMINARY; PRT; 177 AA.
AC Q9H512
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE BA50A15.1 (BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1))
DE (FRAGMENT).
GN BMP7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL157414; CAC08434.1; -.
FT NON_TER 1 177
FT NON_TER 177 177
SQ SEQUENCE 177 AA; 19985 MW; 3DD2ABDD09D6323D CRC64;

Query Match 29.8%; Score 189; DB 4; Length 177;
Best Local Similarity 34.8%; Pred. No. 9.7e-14;
Matches 40; Conservative 22; Mismatches 39; Indels 14; Gaps 5;

Qy 10 NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPYLRSA---DTT 57

Db 63 NVAENSSDQKQCKHLYVSFR-DLGWDWIIAPEGYAAYCEGECAPPLNSYNMNTN 121

Qy 58 HSTVLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKV-EQLSNMVVKSKC 111

Db 122 HAIVQTLVHFNPETVPKPCAPTQLNAISLVLYFDDSSNVILKKYRNMVVRACGC 176

RESULT 44

Q9GT26 ID Q9GT26 PRELIMINARY; PRT; 438 AA.
AC Q9GT26
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GBB-60A-LIKE PROTEIN AS60A.
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Anopheles.
OX NCBI_TaxID=30069;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE ANIMAL;
RA Crampton A.L., Luckhart S.;
RT "Isolation and characterization of As60A, a transforming growth factor
B gene, from the malaria vector Anopheles stephensi."
RL Cytokine 0:0-0(2000).
DR EMBL; AF284816; AAG13400.1; -.
SQ SEQUENCE 438 AA; 49824 MW; 124BA66DAA832E84 CRC64;

Query Match 29.8%; Score 189; DB 5; Length 438;
Best Local Similarity 36.5%; Pred. No. 2.5e-13;
Matches 38; Conservative 23; Mismatches 37; Indels 6; Gaps 4;

Qy 13 ENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSA---TTHSTVLGLYNTL 68

Db 335 KSCRQIQLYVSKF-DLQWHEWIIAPEGYAYCEGECFNPLNAHMTNTHAIVQTLVHLN 393

QY 69 NPEASAPCCVPQDLEPLTILYVGR-TPKVEQLSNMVKSCKC 111
 Db 394 HPTKVPCCAPTKLIPISVLYHIDEANWNLKRYKNMVKSCGC 437

RESULT 45
 Q91350 PRELIMINARY; PRT; 370 AA.
 AC Q91350;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ACTIVIN BETA B SUBUNIT.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93273083; PubMed=8500654;
 RA Dohrmann C.E., Hemmati-Brivanlou A., Thomsen G.H., Fields A.,
 RA Wolf T.M., Melton D.A.:
 RT "Expression of activin mRNA during early development in Xenopus
 RT laevis.";
 RL Dev. Biol. 157:474-483(1993).
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; S61773; AAB26863.1; -;
 DR HSP; P18075; 1BMP.
 DR InterPro: IPR001111; -;
 DR InterPro: IPR001839; -;
 DR InterPro: IPR002400; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF_beta_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; -; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein.
 SQ SEQUENCE 370 AA; 41678 MW; AD21502AC45FIDE9 CRC64;

Query Match 29.7%; Score 188.5; DB 13; Length 370;
 Best Local Similarity 38.3%; Pred. No. 2.4e-13;
 Matches 41; Conservative 19; Mismatches 36; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFRODLGW-KWHEPKGYANFCSGPCP-YLR-----SADTHTSTVLGLYNT- 67
 Db 266 CCRQFYIDFRL-IGWDDWIIAPKRYKANYCSGECEFFVLOKYPHTH-----LVHQAN 324

QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKVEQ-LSNMVKVKSCKCS 112
 Db 325 GLNP-GTVNSCCPTKLTSMYLFDEYNIVKRDVPNMIVDCGCA 370

RESULT 46
 Q9W759 PRELIMINARY; PRT; 96 AA.
 AC Q9W759;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE MYOSTATIN (FRAGMENT).
 GN MSTN.
 OS Cairina moschata (Muscovy duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cairina.
 OX NCBI_TaxID=8855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlos M., Pallova P., Karpisek M., Londynova J., Stankova I.,
 RA Svoboda I., Vernerova N., Ruzicka V.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; AF151692; AAD42221.1; -;
 DR HSP; P18075; 1BMP.
 DR InterPro: IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT 96
 SQ SEQUENCE 96 AA; 11040 MW; 383BC564EBD6EF18 CRC64;

Query Match 29.7%; Score 188; DB 13; Length 96;
 Best Local Similarity 41.2%; Pred. No. 6.6e-14;
 Matches 35; Conservative 12; Mismatches 30; Indels 8; Gaps 3;

QY 12 EENCVRPLYIDFRODLGW-KWHEPKGYANFCSGPCP--YLRSDATHTSTVLGLYNTLN 69
 Db 7 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEFFVLOKYPHTH-----LVHQAN 60

QY 70 PEASAPCCVPQDLEPLTILYVGR 94
 Db 61 PRGSAGCCCTTKMSPINMLYFNGK 85

RESULT 47
 Q9W753 PRELIMINARY; PRT; 399 AA.
 AC Q9W753;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE GROWTH AND DIFFERENTIATION FACTOR 6.
 GN GDF6.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chang C., Hemmati-Brivanlou A.;
 RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
 RL Development 0:0-0(1999).
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; AF155125; AAD38402.1; -;
 DR HSP; P18075; 1BMP.
 DR InterPro: IPR001111; -;
 DR InterPro: IPR001839; -;
 DR InterPro: IPR002405; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF_beta_propeptide; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein.
 SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

Query Match 29.7%; Score 188; DB 13; Length 399;
 Best Local Similarity 39.2%; Pred. No. 2.9e-13;
 Matches 40; Conservative 20; Mismatches 36; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGW-KWHEPKGYANFCSGPCPY-LRS--ADTHTSTVLGLYNTLPN 70
 Db 298 CSKPLHVNFK-ELGWDWIIAPLEYEAHHCYGVDFPLRSHLEPTNHAIITLMSMNP 356

QY 71 EASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSCKC 111
 Db 357 GSTPPSCCVPTKLTIPISILYIDAGNNVYKQYEDMNVVESC GC 398

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RESULT 48
Q9USE8      PRELIMINARY;      PRT;      405 AA.
AC Q9USE8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE PF-BMP2/4.
GN PF-BMP2/4.
OS Ptychodera flava.
OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;
OC Ptychodera.
OX NCBI_TaxID-63121;
RN [1]
RP SEQUENCE FROM N.A.
RA Harada Y.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Okai N., Taguchi S., Tagawa K., Satoh N.;
RT "Developmental expression of hemichordate orthologs of BMP-4, otx and
RT dlx: insights into deuterostome archetype and evolution of chordate
RT body plan.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AB028219; BAA89012.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00688; TGF_beta_propeptide; 1.
DR PRINTS; PR00669; INHIBIN.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 405 AA; 45936 MW; D2EB2D2C7560ED13 CRC64;

Query Match      29.7%; Score 188; DB 5; Length 405;
Best Local Similarity 38.7%; Pred. No. 3e-13;
Matches 43; Conservative 17; Mismatches 39; Indels 12; Gaps 6;

Qy 9 RNLENCVRLYIDFRQDLGWK-WVHEPKGYANFCSPCPY-----LRSADTTHSTVTL 62
Db 298 RKLKPCRRRSILYDF-SDVGNNDIVAPGYNAPYCGECFPPLADHLNS--TNHAIQV 354
Qy 63 GLYNTLPNASASPCVQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
Db 355 TLVHSVSKASAVPQACCVPTLSPLSML-YLDEYDKVILKNYQEMVVEGCGC 404

RESULT 49
Q9PTF9      PRELIMINARY;      PRT;      432 AA.
AC Q9PTF9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 7.
GN BMP7.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID-7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Dick A., Hild M., Bauer H., Imai Y., Malfeld H., Schlier A.F.,
RA Talbot W.S., Bouwmeester T., Hammerschmidt M.;
RT "Essential role of Bmp7 (snailhouse) and its prodomain in dorsoventral
RT patterning of the zebrafish embryo.";

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RL Development 0:0-0(2000).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF201379; AAF17558.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF_beta_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 432 AA; 48923 MW; C982AF80E1652156 CRC64;

Query Match      29.7%; Score 188; DB 13; Length 432;
Best Local Similarity 35.5%; Pred. No. 3.2e-13;
Matches 38; Conservative 22; Mismatches 37; Indels 10; Gaps 5;

Qy 12 EENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSPCPY-----PYLRSADTTHSTVTLGLY 65
Db 328 KQCKKHELYVSFR-DLQWDWIIAPEGVAAVYCEGCVPLNSYMA--TNHAIQVTLV 384
Qy 66 NTLNPEASASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
Db 385 HFINPVPKPCCAPTQLHGLISVLYFDSSNVILKKYRNMMVVRACGC 431

RESULT 50
Q9DFV1      PRELIMINARY;      PRT;      345 AA.
AC Q9DFV1;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Vg1.
OS Eleutherodactylus cystignathoides.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
OC Eleutherodactylus.
OX NCBI_TaxID-122124;
RN [1]
RP SEQUENCE FROM N.A.
RA Dai X.Z., Wells D.;
RT "Vg1 gene in the Direct Developing Frog, Syrrhophus cystignathoides
RT camp.",
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248497; AAG09784.1; -.
SQ SEQUENCE 345 AA; 40102 MW; DE29048D20DD85AA CRC64;

Query Match      29.5%; Score 187; DB 13; Length 345;
Best Local Similarity 39.4%; Pred. No. 3.3e-13;
Matches 41; Conservative 16; Mismatches 37; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSPCPY-----LRSADTTHSTVTLGLYNTL 68
Db 244 CKRRLYIDFKA-VGMQNWVIAPIPHGYFANYCHGECYPLTMMLRGNS--HAILQTLAHSF 300
Qy 69 NPEASASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
Db 301 APEDVPLCCVPIKMAPISMLFYDNDNVLRHYDNMAVDECGC 344

RESULT 51
Q9DGN4      PRELIMINARY;      PRT;      413 AA.
AC Q9DGN4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
GN GDF16.
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10906478;
RA Vokes S.A., Krieg P.A.;
RT "Gdf16, a novel member of the growth/differentiation factor subgroup
RT of the TGF-beta superfamily, is expressed in the hindbrain and
RT epibranchial placodes."
RL Mech. Dev. 95:279-282(2000).
DR EMBL: AF239676; AAF99597.1; -.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 23 POTENTIAL.
SQ SEQUENCE 413 AA; 46510 MW; 5F1B0D7D97E591F6 CRC64;

Query Match 29.5%; Score 187; DB 13; Length 413;
Best Local Similarity 39.2%; Pred. No. 3.9e-13;
Matches 40; Conservative 19; Mismatches 37; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRDLGW-KWHEPKGYANFCSGPCPY-LRS--ADTHSTVLGLYNTLNP 70
DB 312 CSKKPLLVNFK-ELGDDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIQTLMNSMDP 370
QY 71 EASAPCCVPQDLEPTILYY-VGRTPKVEQLSNMVKSCK 111
DB 371 ESTPPSCCVPSKLSILYIDSGNNVYKQYEDMWVESCSC 412

RESULT 52
Q25211 PRELIMINARY; PRT; 178 AA.
AC Q25211;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DECAPENTAPLEGIC (FRAGMENT).
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
OX NCBI_TaxID=39708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE ANIMAL;
RX MEDLINE=94287189; PubMed=7912449;
RA Carroll S.B., Gates J., Keys D.N., Paddock S.W., Panganiban G.E.,
RA Selegue J.E., Williams J.A.;
RT "Pattern formation and eyespot determination in butterfly wings."
RL Science 265:109-114(1994).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DB EMBL: L42141; AAB46367.1; -.
DR HSSP: P18075; IAMP.
DR InterPro: IPR001839; -.
DR InterPro: IPR002405; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGFb; 1.
DR Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 178 AA; 20443 MW; 30D3A7E55458EADAE CRC64;

Query Match 29.3%; Score 186; DB 5; Length 178;
Best Local Similarity 34.8%; Pred. No. 2.1e-13;
Matches 40; Conservative 21; Mismatches 34; Indels 20; Gaps 5;

QY 9 RNLENCVVRPLYIDFRDLGW-KWHEPKGYANFCSGPCPYLRS---ADTHSTVLGL 64

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DB 71 KEAREICQRPLEFVDF-ADVGSWDIIVAPHGYDAYCOGDFPLSDHLNGTNHAIQVOTL 129
QY 65 YNTLNPEASAPCCVPQDLEPTILYYVGRTPKVEQLSNMVKSCK-----CKC 111
DB 130 VNSVNPAAVPKACCVPTQLSSISMLY-----MDEVNNVVLKNYQDMVMVVGCGC 177

RESULT 53
Q9W6C0 PRELIMINARY; PRT; 261 AA.
AC Q9W6C0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148135; PubMed=10022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
RA Foerzler D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily."
RL Genome Res. 9:121-129(1999).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF113023; AAD20829.1; -.
DR HSSP: P18075; IAMP.
DR InterPro: IPR001839; -.
DR InterPro: IPR002405; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGFb; 1.
DR Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 261 AA; 29414 MW; 77346E977036A104 CRC64;

Query Match 29.3%; Score 186; DB 13; Length 261;
Best Local Similarity 39.2%; Pred. No. 3.2e-13;
Matches 40; Conservative 20; Mismatches 36; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRDLGW-KWHEPKGYANFCSGPCPY-LRS--ADTHSTVLGLYNTLNP 70
DB 160 CSRKPLLVNFK-ELGDDWIIAPLDYEAHCEGLCDPLRSHLEPTNHAIQTLMNSMDP 218
QY 71 EASAPCCVPQDLEPTILYY-VGRTPKVEQLSNMVKSCK 111
DB 219 ESTPPSCCVPSKLSILYIDSGNNVYKQYEDMWVESCSC 260

RESULT 54
Q9DGE9 PRELIMINARY; PRT; 115 AA.
AC Q9DGE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.

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OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT *Cloning and sequencing of carp and medaka activin subunit genes.*;
RL Fisheries Sci. 64:680-685(2000).
DR EMBL: AB009406; BAB17599.1; -
FT NON_TER 115
FT NON_TER 115
SQ SEQUENCE 115 AA; 12666 MW; CD38FA0DD7BD52A6 CRC64;

Query Match 29.3%; Score 185.5; DB 13; Length 115;
Best Local Similarity 37.7%; Pred. No. 1.5e-13;
Matches 40; Conservative 20; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRLPYIDFQDLGKWK-WHEPKGYIANFCGPGCP-VYLR-...SADTTHSTVLGLYNT- 67
Db 12 CCROQFIDFRL-TGNDWIITAPAGYIGNYCEGSPAYLAGVPGSASSFHTAVVQYRMR 70
QY 68 -LNPEASASCCVPPQDLPLEPTILYVGTGPKVEQ-LSNMVVKSKC 111
Db 71 GMSPP-GSVNSCCIPKLTSMLSMLYDDEYNIVKRDVPNMIVEECGC 115

RESULT 55
Q91597
ID Q91597 PRELIMINARY; PRT; 390 AA.
AC Q91597;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1 PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Moos M., Wang S., Krinks M.;
RT *Anti-dorsalizing morphogenetic protein is a novel TGF-beta homolog
expressed in the Spemann organizer.*;
RL Development 121:4293-4301(1995).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: U2155; AAC59736.1; -.
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF.BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 390 ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1.
SQ SEQUENCE 390 AA; 44367 MW; DEC8IA001349C895 CRC64;

Query Match 29.3%; Score 185.5; DB 13; Length 390;
Best Local Similarity 36.3%; Pred. No. 5.5e-13;
Matches 41; Conservative 20; Mismatches 41; Indels 11; Gaps 6;

QY 9 RNLEEN-...CCVRLPYIDFQDLGKWK-WHEPKGYIANFCGPGCPY-...LRSADTTHST 60
Db 278 RSVEDQLPCORHLYVDF-EEIGWSGWIISPRGYAHCKGSPFLPGQNMPTNAT 336
QY 61 VLGLYNTLN-PEASASCCVPPQDLPLEPTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 337 VQSIINALKLTGKGVSSCCVPPDKLFSINLLYFDDENNVLLKQYDDMVAGSCGC 389

RESULT 56
Q94580
ID Q94580 PRELIMINARY; PRT; 683 AA.
AC Q94580;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BONE MORPHOGENIC PROTEIN A.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya T., Morita K., Ueno N., Satoh N.;
RT *An ascidian homologue of vertebrate BMPs-5-8 is expressed in the
midline of the anterior neuroectoderm and in the midline of the
ventral epidermis of the embryo.*;
RL Mech. Dev. 57:181-190(1996).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: D83183; BAAL1835.1; -.
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF.BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Glycoprotein.
KW Glycoprotein.
SQ SEQUENCE 683 AA; 78693 MW; A0A157AE2518B686 CRC64;

Query Match 29.3%; Score 185.5; DB 5; Length 683;
Best Local Similarity 38.7%; Pred. No. 9.8e-13;
Matches 43; Conservative 16; Mismatches 43; Indels 9; Gaps 5;

QY 9 RNLEEN-...CCVRLPYIDFQDLGKWK-WHEPKGYIANFCGPGCPYLRSD-...TTHSTV 61
Db 573 KKLKGTQACHREELVSP-QDVNWEDWIIAPSGYMAVRCSECDPPLSANMNATNHAIV 631
QY 62 LGLYNTLPEASASCCVPPQDLPLEPTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 632 QTLVHLKSKLPFCPCCTPDLDLSISLVYDDHNNVYVYKRYNMVVLSCAC 682

RESULT 57
Q93573
ID Q93573 PRELIMINARY; PRT; 126 AA.
AC Q93573;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT *Neuronal patterning by BMPs: A requirement for GDF7 in the generation
of a discrete class of commissural interneurons in the mouse spinal
cord.*;
RL Genes Dev. 0:0-0(1998).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF089086; AAC97113.1; -.

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DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 29.2%; Score 185; DB 13; Length 136;
Best Local Similarity 36.1%; Pred. No. 1.9e-13;
Matches 39; Conservative 23; Mismatches 40; Indels 6; Gaps 5;

QY 9 RNLEENCVRPLYIDFRQDLGW-KWVHEPKGYANFCGCPY-LRS--ADTTHSTVLGL 64
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 KKAKTRCSRKPLHNFK-ELGWDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIQTLL 77
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 65 YNTLNPEASPCCVQDLEPLTILYY-VGRTPKVEQLSNMVKSKC 111
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 MNSMPESTPPSCCVSKLSPISILYIDSGNNVYKQYEDMVVETCGC 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 58
QYXZ69
ID Q9XZ69 PRELIMINARY; PRT; 204 AA.
AC Q9XZ69;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENT).
OS BMP2/4.
GN Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Tripneustes.
OX NCBI_TaxID=7673;
RN [1]
RP MEDLINE=99262121; PubMed=10329409;
RX Hwang S.-P.L., Chen C.A., Chen C.-P.;
RA "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RT closely related to vertebrate BMP2 and BMP4 with maximal expression at
RT the later stages of embryonic development.";
RL Biochem. Biophys. Res. Commun. 258:457-463(1999).
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF133305; AAD30538.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 204 AA; 23697 MW; CE829BDC2AA9F077 CRC64;

Query Match 29.2%; Score 185; DB 5; Length 204;
Best Local Similarity 36.7%; Pred. No. 3.2e-13;
Matches 40; Conservative 19; Mismatches 42; Indels 8; Gaps 5;

QY 9 RNLEENCVRPLYIDFRQDLGW-KWVHEPKGYANFCGCPYLRSA--DTTHSTVLGL 64
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 KRLKANCRRHPLYVDF-SDVHNDWIVAPAGYQYCHGECPPFLAEHLNTHAIVQTL 155
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 65 YNTLNPEASPCCVQDLEPLTILYYVGRTPKV--EQLSNMVKSKC 111
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 VNSVNPALVPRACCVPTLSAISML-YLDEYKVKVLKNYQDMVVEGCGC 203
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 59
Q9WUK5
ID Q9WUK5 PRELIMINARY; PRT; 351 AA.
AC Q9WUK5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Rossmannith W., Peter B., Schulte-Hermann R.;
RT "Rat activin beta C and beta E: sequence and expression.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF140031; AAD30132.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001318; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRINTS; PR00672; INHIBINBC.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 351 AA; 39335 MW; 6B219BF6C3E180A1 CRC64;

Query Match 29.2%; Score 185; DB 11; Length 351;
Best Local Similarity 37.7%; Pred. No. 5.6e-13;
Matches 43; Conservative 20; Mismatches 39; Indels 12; Gaps 6;

QY 9 RNLEENCVRPLYIDFRQDLGW-KWVHEPKGYANFCGCPYLRSA-----TTHSTV 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 QGLSRMCCRQEFFVDFR-EIGHWDWIIQEGYAMNFCGQCP-LHVAGMPGISASFTAV 297
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 62 LGLY--NTLNPEASPCCVQDLEPLTILYYVGRTPKVE-QLSNMVKSKCS 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 LNLKANTDAGTARRGSCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 351
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 60
Q9PWR8
ID Q9PWR8 PRELIMINARY; PRT; 392 AA.
AC Q9PWR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA B SUBUNIT PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Ge W., Miura T., Kobayashi H., Peter R.E., Nagahama Y.;
RT "Cloning of cDNA for goldfish activin beta B subunit, and the
RT expression of its messenger RNA in gonadal and non-gonadal tissues.";
RL J. Mol. Endocrinol. 0:0-0(0).
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF004669; AAB61468.1; -.

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RESULT	65	
Q9YGH7		
ID	Q9YGH7	PRELIMINARY; PRT; 424 AA.
AC	Q9YGH7	
DT	01-MAY-1999	(TReMBLrel. 10, Created)
DT	01-MAY-1999	(TReMBLrel. 10, Last sequence update)
DT	01-MAR-2001	(TReMBLrel. 16, Last annotation update)
DE	OSTEOGENIC PROTEIN-1 HOMOLOG PRECURSOR.	
GN	XOP-1H.	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodinae; Xenopus.	

GN	GDF5.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=99146893; PubMed=10021348;
RX	Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
RA	Ladher R., Allen S., Macpherson S., Luyten F.P., Archer C.W.;
RA	"Mechanisms of GDF-5 action during skeletal development.";
RL	Development 126:1305-1315(1999).
CC	-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR	EMBL: AF123389; AAD30451.1; -.
DR	HSSP: P18075; IBMP.
DR	InterPro: IPR001111; -.
DR	InterPro: IPR001839; -.
DR	InterPro: IPR002405; -.
DR	Pfam: PF00019; TGF-beta; 1.
DR	Pfam: PF00688; TGF-beta; 1.
DR	PRINTS: PR00669; INHIRIN.
DR	PROSITE: PS00250; TGF_BETA; 1.
DR	SMART: SM00204; TGFbeta; 1.
DR	Glycoprotein.
QW	SEQUENCE 500 AA; 55952 MW; 1DE8385A31119A598 CRC64;
SQ	Glycoprotein.

Query Match 28.9%; Score 183; DB 13; Length 500;
Best Local Similarity 37.0%; Pred. No. 1.4e-12;
Matches 40; Conservative 23; Mismatches 39; Indels


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AC O57573;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN.
GN ZBMP-2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE EMBRYO;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49971; BAA24406.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46845 MW; 049EC3BA083DEBDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;
Matches 42; Conservative 20; Mismatches 28; Indels 19; Gaps 8;

QY 14 NCVRPLYIDFRDLGW-KWVHEPKGYANFCGCPY-----LRSADTTHSTVLGLYNT 67
DB 310 NCRRLHYVDF-SDVGWNEWIVAPPGYHAFYCHGCPPLPDHLNS--TNHAIVQTLVNS 366
QY 68 LN---PEASASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
DB 367 VNSNIPKA----CCIPTLSPIALL-YLDEYEKVLKNYQDMVVEGCGC 410

RESULT 72
O93369 ID O93369 PRELIMINARY; PRT; 411 AA.
AC O93369
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2.
GN BMP2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RX MEDLINE=98072322; PubMed=9409664;
RA Kishimoto Y., Lee K.H., Zon L., Hammerschmidt M., Schulte-Merker S.;
RT "The molecular nature of zebrafish swirl: BMP2 function is essential during early dorsoventral patterning.";
RL Development 124:4457-4466(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RA Lee K.H., Marden J.J., Thompson M.S., MacLennan H., Kishimoto Y., Pratt S.J., Schulte-Merker S., Hammerschmidt M., Johnson S.L., Postlethwaite J.H., Beier D.C., Zon L.I.;
RT "Cloning and Genetic Mapping of Zebrafish BMP-2.";
RL Dev. Genet. 23:0-0(1998).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF072456; AAC25595.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46873 MW; 01A4C8CA012F1EDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;

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AC O57573;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN.
GN ZBMP-2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE EMBRYO;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49971; BAA24406.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46845 MW; 049EC3BA083DEBDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;
Matches 42; Conservative 20; Mismatches 28; Indels 19; Gaps 8;

QY 14 NCVRPLYIDFRDLGW-KWVHEPKGYANFCGCPY-----LRSADTTHSTVLGLYNT 67
DB 310 NCRRLHYVDF-SDVGWNEWIVAPPGYHAFYCHGCPPLPDHLNS--TNHAIVQTLVNS 366
QY 68 LN---PEASASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
DB 367 VNSNIPKA----CCIPTLSPIALL-YLDEYEKVLKNYQDMVVEGCGC 410

RESULT 71
O13108 ID O13108 PRELIMINARY; PRT; 411 AA.
AC O13108
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BMP2-4.
GN BMP2-4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98036031; PubMed=9370264;
RA Martinez-Barbera J.P., Torresson H., Darocha S., Krauss S.;
RT "Cloning and expression of three members of the zebrafish Bmp family: Bmp2a, Bmp2b and Bmp4.";
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U82232; AAC60286.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.

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RESULT 79
O9XYQ8 PRELIMINARY; PRT; 289 AA.
AC O9XYQ8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4 (FRAGMENT).
GN BMP2/4.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;
RT "A BMP pathway regulates cell fate allocation along the sea urchin
RT animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF119713; AAD28039.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 289 289
SQ SEQUENCE 289 AA; 33599 MW; 99E175C7DBC3C58B CRC64;

Query Match 27.9%; Score 177; DB 5; Length 289;
Best Local Similarity 35.8%; Pred. No. 3.7e-12;
Matches 39; Conservative 19; Mismatches 43; Indels 8; Gaps 5;

QY 9 RNLENCVRLYIDFRQDLGK-WVHEPKGYANFGSGPCPYLRSA---DTHTSTVLGL 64
Db 180 KRLKNCRRHLYVDF-SDVHNDWIVAPGYQAYCGECFPFLAEHLNTNTNHAIVQTL 238
QY 65 YNTLNPASASPCVPODLEPLTILYVGRTPKV--EQLSNMVKSKC 111
Db 239 VNSVNPALPRACCVPTLSAISM-LYLDEYKVLKQYQDMVVEGCGC 286

RESULT 80
O57574 PRELIMINARY; PRT; 400 AA.
AC O57574;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE GENETIC PROTEIN 4.
GN ZBMP-4 OR BMP4.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Osteichthys;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-WHOLE EMBRYO;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signalling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97447702; PubMed=9303442;
RA Hwang S.P., Tsou M.F., Lin Y.C., Liu C.H.;
RT "The zebrafish BMP4 gene: sequence analysis and expression pattern
RT during embryonic development.";
RL DNA Cell Biol. 16:1003-1011(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Hwang S.P., Tsou M.F., Lin Y.C., Liu C.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49972; BAA24407.1; -.
DR EMBL; AF056336; AAC13302.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB-propeptide; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR KW Glycoprotein.
SQ SEQUENCE 400 AA; 45757 MW; E175AB41D18C2171 CRC64;

Query Match 27.5%; Score 174.5; DB 13; Length 400;
Best Local Similarity 37.7%; Pred. No. 9.9e-12;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVRLYIDFRQDLGK-WVHEPKGYANFGSGPCPY----LRSADTHTSTVL 62
Db 294 KKRNCRRHLYVDF-SDVHNDWIVAPGYQAYCGECFPFLADHLNS--TNHAIVQ 350
QY 63 GLYNTLN---PEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVKSKC 111
Db 351 TLVNSVNTNIPKA----CCVPTLSAISM-LYLDETRVLKQYQDMVVEGCGC 399

RESULT 81
Q26468 PRELIMINARY; PRT; 191 AA.
AC Q26468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA (FRAGMENT).
OS Schistocerca americana (American grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Schistocerca.
OX NCBI_TaxID=7009;
RN [1]
RP SEQUENCE FROM N.A.
RA Newfield S.J., Gelbart W.M.;
RT "Identification of two Drosophila TGF-beta family members in the
RT grasshopper Schistocerca americana.";
RL J. Mol. Evol. 41:155-160(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87090408; PubMed=3467201;
RA Padgett R.W., Johnston R.D., Gelbart W.M.;
RT "A transcript from a Drosophila pattern gene predicts a protein
RT homologous to the transforming growth factor-beta family.";
RL Nature 325:81-84(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89072730; PubMed=3201241;
RA Wozney J.M., Rosen V., Celeste A.J., Mittleman L.M., Whitters M.J.,
RA Kriz R.W., Hewick R.M., Wang E.A.;
RT "Novel regulators of bone formation: molecular clones and
RT activities.";
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RL Science 242:1528-1534(1988).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U23785; AA811169.1; -.
DR HSP; P18075; I BMP..
DR InterPro; IPR000169; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PROSITE; PS00639; THIOLEPROTEASE_HIS; UNKNOWN1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 191 AA; 21879 MW; FA73DF060878F4C0 CRC64;

Query Match 27.3%; Score 173; DB 5; Length 191;
Best Local Similarity 34.3%; Pred. No. 6.7e-12;
Matches 37; Conservative 17; Mismatches 48; Indels 6; Gaps 4;

QY 9 RNLEENCVRPLYIDPRODLGW-KWHEPKGYANFCGPGPYLRSA---DTTHSTVLGL 64
   :: I IIII::: ::: I ::: I ::: I ::: I ::: I ::: I ::: I
Db 84 KQORSTCRHRPLVDPR-EVGDDWIVAPPGYEGWYCHGDCPPLSAHNMSTNHAVVQTL 142
   ::: I ::: I ::: I ::: I ::: I ::: I ::: I ::: I ::: I

QY 65 YNTLNPASASCCVPPQDLPTILYVGRTPKV-EQLSNMVKSKC 111
   I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
Db 143 MNSMNLGVPKACCIPTQTSISMLYIDBESKVLKYNHEMAYVGGCC 190

RESULT 82
O76147 PRELIMINARY; PRT; 400 AA.
AC O76147;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-WAR-2001 (TREMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN (FRAGMENT).
GN DJBMP.
OS Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Turbellaria;
OC Tricladida; Pluticicola; Dugesidae; Dugesia.
OX NCBI_TaxID=6161;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GI; TISSUE=WHOLE ANIMAL;
RA Orit H., Kato K., Agata K., Watanabe K.;
RT "Molecular cloning of bone morphogenetic protein (BMP) gene from the
   planarian Dugesia japonica."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AB010966; BAA32087.1; -.
DR HSP; P18075; I BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 400 AA; 47031 MW; 34220CB5140CB5A4 CRC64;

Query Match 27.3%; Score 173; DB 5; Length 400;
Best Local Similarity 35.1%; Pred. No. 1.5e-11;
Matches 40; Conservative 18; Mismatches 50; Indels 6; Gaps 4;

QY 3 DFNVCFRNLEENCVRPLYIDFQDLGW-KWHEPKGYANFCGPGPYLRSA---TTH 58
   I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
Db 287 DTSYMPGHEEDQRYPLIVTFK-EVGWSKIIAPQNIAYNYCKGNCYPPLSDNFNATNH 345

QY 59 STVVLGYNTLNPASASCCVPPQDLPTILYVGR-TPKVELSNMVKSKC 111
   ::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::

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Db 346 AITQLLVHGLKDLISIPKPCVYPYHLHPETLLYLNNEGDAALLREFKDMVSVCSC 399

RESULT 83
Q9VQG9 PRELIMINARY; PRT; 586 AA.
AC Q9VQG9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CG16987 PROTEIN.
CG16987.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
   Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
   Cherv J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
   Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
   Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
   Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
   Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
   Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
CC -!- SIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION
   DOMAIN.
DR EMBL; AE003582; AAF51204.1; -.
DR HSP; P18075; I BMP.
DR FlyBase; FBgn0031461; CG16987.
DR InterPro; IPR000130; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.

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DR SMART; SM00204; TGFβ; 1.
KW Glycoprotein; Hydrolase; Metalloprotease; Zinc.
SQ SEQUENCE 586 AA; 67184 MW; 582582D7F370D549 CRC64;

Query Match 27.2%; Score 172.5; DB 5; Length 585;
Best Local Similarity 36.6%; Pred. No. 2.5e-11;
Matches 41; Conservative 17; Mismatches 45; Indels 9; Gaps

QY 7 CFRNLEENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRS--ADTTHSTVL 62
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 476 CSSGNT--CCEHLYISFR-DIGHSNWILKEGYNAYFCRSCSSVASVTOASHHSIM 533
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 63 GLYNT--LNPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSKC 111
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 534 KILSTSGANKSLELVPCCTAKQYSSQLQVMDSSNTATVKTLPNMNVESGCG 585

RESULT 84
O97390 PRELIMINARY; PRT; 301 AA.
ID O97390
AC O97390;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MGDF PRECURSOR.
GN MGDF.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoidae; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA LeLong C., Mathieu M., Favrel P.;
RT "Structure and expression of mgdf, a new member of the TGF-beta
   superfamily in Crassostrea gigas (Mollusca Bivalvia).";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
   EMBL; AJ130967; CAA10268.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFβ_propeptide; 1.
DR PRINTS; PR00569; INHIBINA.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFβ; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 36
FT CHAIN 37 301
FT CHAIN 37 301
SQ SEQUENCE 301 AA; 34723 MW; 5217AD88239C9009 CRC64;

Query Match 27.1%; Score 172; DB 5; Length 301;
Best Local Similarity 36.4%; Pred. No. 1.4e-11;
Matches 40; Conservative 19; Mismatches 41; Indels 10; Gaps

QY 9 RNLEENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPC--PYLRSAD-TTHSTVLGL 64
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 KKNYQCRKRELNVDFKA-VGMNDWIFAPPGYNAYICDGSCHWPYDDHMVYNHAIQDL 252
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 YNTLNPEASAPCCVPQDLEPLTILY----YGRTPKVEQLSNMVKSKC 111
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 VNSIDPRAAPKPCVPTLSLSLLYTDHGAVLVKLYQ--DMVVEGCGC 300

RESULT 85
O16123 PRELIMINARY; PRT; 428 AA.
ID O16123
AC O16123;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

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Query Match      27.1%; Score 172; DB 5; Length 428;
Best Local Similarity 36.0%; Pred. No. 2e-11;
Matches 41; Conservative 16; Mismatches 43; Indels 14; Gaps 5;

QY 3 DTWYCRNLEENCVRPLYIDFRODLGW-KWHEPKGYANFCGPGPYLRSA---DTTH 58
      ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
Db 323 DKNYCRRT-----QLLVDF-NELNMWDILAPSSYSAIQCGECPNLTFHNTN 373
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
QY 59 STVLGYNTLNPEASAPCCVPQDLPLTILY-VGRTPKVEQLSNMVKSKC 111
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
Db 374 AIVOGLNSVDPLNVPAPCCVPTMESLAIYIDVEGKIVIKNYPDMVEVLSGCC 427

RESULT 87
Q9VQC6 PRELIMINARY; PRT; 588 AA.
AC Q9VQC6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DPP PROTEIN.
GN DPP OR CG9885.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AE003583; AAF51250.1; -.
DR HSP: P18075; IBMP.
```

```
DR FlyBase; FBgn0000490; dpp.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00869; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
SQ SEQUENCE 588 AA; 65867 MW; 2C8166C1BD2F666B CRC64;

Query Match      27.1%; Score 172; DB 5; Length 588;
Best Local Similarity 35.8%; Pred. No. 2.8e-11;
Matches 39; Conservative 16; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLEENCVRPLYIDFRODLGW-KWHEPKGYANFCGPGPYLRSA-----TTTSTVLG 63
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
Db 481 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYVCHGKCF-PLADHFNSTHNAVQT 538
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
QY 64 LYNTLNPEASAPCCVPQDLPLTILYVGR-TPKVEQLSNMVKSKC 111
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
Db 539 LVNNPNPKVKACCCVPTQLDSVAMLYLNDQSTVVVKNYQEMTVVCGGC 587
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||

RESULT 88
Q90390 PRELIMINARY; PRT; 102 AA.
AC Q90390;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=BLOOD;
RC MEDLINE=93290666; PubMed=8512569;
RA Ge W., Gallin W.J., Strobeck C., Peter R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
RT structural conservation during vertebrate evolution.";
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: L15339; AAA49162.1; -.
DR HSP: P18075; IBMP.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 102 102
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11849 MW; 0F5E17FA198F94D9 CRC64;

Query Match      27.1%; Score 171.5; DB 13; Length 102;
Best Local Similarity 40.08; Pred. No. 5.2e-12;
Matches 34; Conservative 14; Mismatches 28; Indels 9; Gaps 4;

QY 15 CCVCRPLYIDFRODLGW-KWHEPKGYANFCGPGCP-----YLRSDTTHSTVLGLNT- 67
      ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
Db 5 CCKRQFYVNFK-DIGWSDIATAPSGYHANYCEGDCPSHVASITGSALSFHSHYHMR 63
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
QY 68 -LNPEASAPCCVPQDLPLTILY 91
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
Db 64 GYSPFNNIKCCVPTRLRAMSLY 88
      : ||| : : : : : ||||| : : ||| : : : : : ||| : : : : : |||
```

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RESULT 89
Q9MZV5
ID Q9MZV5 PRELIMINARY; PRT; 337 AA.
AC Q9MZV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 (FRAGMENT).
GN BMP4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Johanson J.A., Breen M., Lepine A., Murphy K.E.;
RT "Identification and chromosomal localization of the gene encoding
RT canine bone morphogenetic protein 4 (bmp4).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF136233; AAF82188.1; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 337 AA; 38792 MW; BC91231431FDC27 CRC64;

Query Match 26.9%; Score 170.5; DB 6; Length 337;
Best Local Similarity 37.7%; Pred. No. 2.3e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTHSTVL 62
Db 231 RKKKNKRRRLYVDF-SDVGNDWIVAPPGYQAFYCHGDCFPFLADHLNS--TNHAIVQ 287
QY 63 GLYNTLN---PEASASPCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSCK 111
Db 288 TLVNSVNSIPKA----CCVTELSAISML-YLDEYDKVLKNVOEMVVEGCGC 336

RESULT 90
Q9W6T8
ID Q9W6T8 PRELIMINARY; PRT; 120 AA.
AC Q9W6T8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA A PROTEIN (FRAGMENT).
GN ACTIVIN BETA A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodaway A., Takeda H., Koshida S., Price B.M., Smith J.C., Patient R.,
RA Holder N.;
RT "Activin is an inducer of mesoderm in the zebrafish germ ring.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AJ238980; CAB43091.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBIN.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
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DR SMART; SM00204; TGF; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13583 MW; D6B395EB4B4D705 CRC64;

Query Match 26.7%; Score 169; DB 13; Length 120;
Best Local Similarity 34.3%; Pred. No. 1.2e-11;
Matches 36; Conservative 21; Mismatches 36; Indels 12; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPYLSADTH-----STVLGLYNT- 67
Db 11 CCKRQFYVNFK-DIGWNDWIIAPSGYHANYCEGDCASNVASITGNSLSRSTVISHYRIR 69
QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSCK 109
Db 70 GYSPFTNIKSCVPTLRAMSLY-NEEQKIVKDIQNMIVEEC 113

RESULT 91
O42303
ID O42303 PRELIMINARY; PRT; 257 AA.
AC O42303;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONTACT (FRAGMENT).
GN CONTACT.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398455; PubMed=9256353;
RA Bruneau S., Mourrain P., Rosa F.M.;
RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT cell lineages in the developing pectoral fins and head and is
RT regulated by retinoic acid.";
RL Mech. Dev. 65:163-173(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; Y12005; CAA72733.1; -.
DR HSP; P18075; 1BMP.
DR ZFIN; ZDB-GENE-990415-39; contact.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein.
FT NON_TER 1
FT CHAIN 140 257 POTENTIAL.
SQ SEQUENCE 257 AA; 29787 MW; 6D64F0542F948849 CRC64;

Query Match 26.7%; Score 169; DB 13; Length 257;
Best Local Similarity 34.3%; Pred. No. 2.6e-11;
Matches 37; Conservative 25; Mismatches 40; Indels 6; Gaps 5;

QY 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSPGCPY-LRS--ADTHSTVLGL 64
Db 150 KNPGRKCNKRLHVNFK-EMGWDDWIIAPLEVEAFICDGVCDPPIRSHLEPTNHAIIQTL 208
QY 65 YNTLNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSCK 111
Db 209 MNSMDPRSTPTCCVPTLRAMSLY-NEEQKIVKDIQNMIVEEC 256

RESULT 92
Q98861
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DR PROSITE; PS00250; TGF_BETA; 1.  

DR SMART; SM00204; TGFβ; 1.  

KW Glycoprotein.  

SQ SEQUENCE 400 AA; 45757 MW; 427D1DB8FE12D025 CRC64;  

  

Query Match 26.6%; Score 168.5; DB 13; Length 400;  

Best Local Similarity 36.9%; Pred. No. 4.7e-11;  

Matches 41; Conservative 16; Mismatches 41; Indels 13; Gaps 7;  

  

QY 9 RNLEENCVRPLYIDFRQDLGWK-WVHEPKGYVANFCSGPCPY-----LRSADTTHSTVL 62  

| | | | | : | | | | | : | | | | | : | | | | | :  

Db 294 KRRNRKRRLHAYVDFF--SDVGWNDWIIVAPPGYQAYYGCGECPFLADHLNS--TNHAIVQ 350  

| | | | | : | | | | | : | | | | | : | | | | | :  

QY 63 GLYNLTPEASASCCVPQDLEPTILYYVGRTPKV--EQLSNMVKSKKC 111  

| | | | | : | | | | | : | | | | | : | | | | | :  

Db 351 TLNVSVTNT-PKWCCVPTLSAISML-YLDETRRVLLKNYQEMVVEGCGC 399  

| | | | | : | | | | | : | | | | | : | | | | | :  

  

RESULT 94  

Q9ZIV8 ID Q9ZIV8 PRELIMINARY; PRT; 421 AA.  

AC Q9ZIV8;  

DT 01-MAY-1999 (TrEMBLrel. 10, Created)  

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  

DE BONE MORPHOGENETIC PROTEIN 10.  

GN BMP10.  

OS Mus musculus (Mouse).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  

OX NCBI_TaxId=10090;  

RN [1]  

RP SEQUENCE FROM N.A.  

RA Celeste A.;  

RT "Mouse Bone Morphogenetic Protein 10 (BMP-10) Genomic Sequence, Full Coding Region of exon 2.";  

RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.  

SC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.  

DR EMBL; AF101440; AAC77461.1;  

DR EMBL; AF101439; AAC77461.1; JOINED.  

DR HSSP; PI8075; IBMP.  

DR InterPro; IPR001111;  

DR InterPro; IPR001839;  

DR InterPro; IPR002405;  

DR Pfam; PF00019; TGF-beta; 1.  

DR PRINTS; PR00688; TGFβ-propeptide; 1.  

DR ProDom; PD00669; INHIBINA.  

DR ProDom; PD000357; 1.  

DR PROSITE; PS00250; TGF_BETA; 1.  

DR SMART; SM00204; TGFβ; 1.  

KW Glycoprotein.  

SQ SEQUENCE 421 AA; 47917 MW; 703422876A64A18F CRC64;  

  

Query Match 26.6%; Score 168.5; DB 11; Length 421;  

Best Local Similarity 35.8%; Pred. No. 5e-11;  

Matches 39; Conservative 17; Mismatches 46; Indels 7; Gaps 5;  

  

QY 9 RNLEENCVR-PLYIDPRODLGW-KWVHEPKGYANFCSGPCPYLRS--ADTTHSTVLG 63  

| | | | | : | | | | | : | | | | | : | | | | | :  

Db 313 RNAKGNYCKKTPLYIDFK-EIGWDSWIIAPGVEAECEGVCNVPLAEHLTPTKHAIQA 371  

| | | | | : | | | | | : | | | | | : | | | | | :  

QY 64 LYNTLNPEASASCCVPQDLEPTILYY-VGRTPKVEQLSNMVKSKKC 111  

| | | | | : | | | | | : | | | | | : | | | | | :  

Db 372 LVHLKNSQKAKACCVPDKLPDISILYLDRGVVTVTKFYEGMAVSEGC 420  

| | | | | : | | | | | : | | | | | : | | | | | :  

  

RESULT 95  

Q9DET1 ID Q9DET1 PRELIMINARY; PRT; 102 AA.  

AC Q9DET1;  

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
```


DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)
DE	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	GROWTH DIFFERENTIATION FACTOR 5	PRECURSOR (FRAGMENT).
OS	Gallus gallus	(Chicken).
OS	Eukaryota:	Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
OC	Archosauria:	Aves; Neognathae; Galliformes; Phasianinae;
OC	Gallus.	
OX	NCBI_TaxID=9031;	
OX	[1]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=LEG BUD;	
RC	MEDLINE=99119368; PubMed=9918693;	
RA	Merino R., Macias D., Ganan Y., Economides A.N., Wang X., Wu Q.,	
RA	Stahl N., Sampath K.T., Varona P., Harle J.M.;	
RT	"Expression and function of Gdf-5 during digit skeletogenesis in the	
RT	embryonic chick leg bud.;"	
RT	Dev. Biol. 206:33-45(1999).	
CC	-I- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.	
DR	EMBL; AF075441; AAD14568.1; -.	
DR	HSSP; P18075; LBMP.	
DR	InterPro: IPR001111; -.	
DR	InterPro: IPR001839; -.	
DR	InterPro: IPR002405; -.	
DR	Pfam: PF00019; TGF-beta; 1.	
DR	Pfam: PF00868; TGF-propeptide; 1.	
DR	PRINTS; PR00669; INHIBINA.	
DR	PROSITE; PS00250; TGF BETA; 1.	
DR	SMART; SM00204; TGFb; 1.	
KW	Glycoprotein. 1	
FT	NON_TER 1	
FT	NON_TER 324	
FT	SEQUENCE 324 AA; 37206 MW; 0B8A7CB111375007 CRC64;	

		Query Match	26.0%	Score 165;	DB 13;	Length 324;
		Best Local Similarity	34.0%;	Pred. No.	9.4e-11;	
		Matches	35;	Conservative	24;	Mismatches 32; Indels 12; Gaps 5;
QY	9	RNLEENCCVRPLVIDFRDQLGW-KWVHEPKGYVANFCGCPDY-LRS--ADTHTSTVIUGL 64	:	:	:	:
Dd	226	KNLKARCRRALKHVNFK-DMGWDWIILAPLEYEAYHCGLCEPFLRSHLEPTNHAIQTLL 284	:	:	:	:
QY	65	YNTLNPEASPPCVPDGLEPIILYYVGRTPKVEQLSNMVKV 107	:	:	:	:
Dd	285	MNSGDPESTPTTCVPRLSPISILE-----IDSANNNVVYK 320	:	:	:	:

RESULT	99
Q90388	
ID	PRELIMINARY; PRT; 102 AA.
AC	Q90388;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DD	01-NOV-1996 (TrEMBRel. 01, Last sequence update)
DE	01-MAR-2001 (TrEMBRel. 16, Last annotation update)
DE	ACTIVIN BETA-B-1 SUBUNIT (FRAGMENT).
OS	Carassius auratus (Goldfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OX	Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX	NCBI_taxID=7957;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BLOOD;
RA	MEDLINE=93290666; PubMed=8512569;
RX	Ge W., Gallin W.J., Stroheck C., Peter R.E.:
RT	"Cloning and sequencing of goldfish activin subunit genes: strong
RT	structural conservation during vertebrate evolution."
RL	Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC	- !- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR	EMBL; L15340; AAA49160.1; -.
DR	HSP; F18075; IJMP.
DR	InterPro; IPRO01839; -.
DR	Pfam; PF00019; TGF-beta; 1.

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DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 102
FT NON_TER 102
SQ SEQUENCE 102 AA; 11358 MW; 222222E5A828A7C CRC64;

Query Match      25.9%; Score 164; DB 13; Length 102;
Best Local Similarity 38.8%; Pred. No. 3.7e-11;
Matches 33; Conservative 16; Mismatches -26; Indels 1

Qy 15 CCVRPLYIDFRODLGKK-WVHEPKGYANFCSGPCP-YLR- - -SADTTHSTVLG
   || : ||||| ||| : ||||| ||| : ||| : ||| : ||| :
Db 6 CCRQFQYIDFRL-IGNWDIIAPGYGNYGNCGSCPAYMGVPGSASFPTAVVN

Qy 68 -LNPEASAPCCVPQDLEPLTILYY 91
   :| : || : ||| : ||| : ||| : ||| : ||| :
Db 65 GISP-GSVNSCCIPTKLSTMSLYF 88

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RESULT 100	
P79707	
ID	P79707 PRELIMINARY; PRT; 83 AA.
AC	P79707;
DT	01-MAY-1997 (TREMBLrel. 03, Created)
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	VG-1 (FRAGMENT).
OS	Cynops pyrrhogaster (Japanese common newt).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX	NCBI_TaxID=8330;
RN	[1]

[L]
RN
KP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takeshima K.,
RT Kaneda T.;
RR "serial expression of the genes in a mesodermalizing ectoderms of
RL early Cynops gastrula.";
RT Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR ENBL; D89444; BAAL13959.1; ..
DR HSSP; P18075; BMP.
DR InterPro; IPRO01839; .-
DR Pfam; PF000019; TGF-beta; 1.
DR ProSite; PS00250; TGF-BETA; 1.
DR SMART; SMOU204; TGFB; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT TER 83 83
SQ SEQUENCE 83 AA; 9530 MW; 1538F5G763FC4A67 CRC64;

Query Match	25.6%; Score 162; DB 13; Length 83;
Best Local Similarity	43.3%; Pred. No. 5e-11;
Matches	Conservative 13; Mismatches 21; Indels 4; Gaps 2;
Qy	29 GWK-WWHEPKGYANFCGCPYLRSA---DTHSTVGLYNTLNPEASPCCVPDGLE 84 :- : :- :- :-
Db	1 GWNWVIAPQGYMANYCHGCPPPLTEILNGTNHAIQTLLVHSMEPEDTPQCCVPVRLS 60
Qy	85 PLTIYY 91 :-
Db	61 PISMLY 67 :-

Search completed: October 30, 2001, 08:54:14
Job time: 123 sec

